

# Chapter 13

## Cereals

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### 13.1 Rice

#### *13.1.1 Why Conserve Rice Germplasm*

Rice is the staple food for more than half of the world's human population. Average global consumption is 52.9 kg/capita/year. However, in countries such as Bangladesh, Cambodia, Lao PDR, Myanmar, and Viet Nam, average consumption is more than 150 kg/capita/year (FAO 2011). Rice is grown in more than 100 countries, with a global total of more than 150 million hectares planted with rice, much of which is in the tropics or sub-tropics. The top five producers in 2007 were China, India, Indonesia, Bangladesh, and Viet Nam (FAO 2011). A significant proportion of the rice crop is grown by millions of small farmers and agricultural workers who are dependent on rice for their livelihood.

It is predicted that the human population will reach more than nine billion by 2050 (UN 2011) and estimated that rice production needs to increase by 1.5% per year in order to meet people's needs and keep rice affordable. In order to meet increasing demand, it is essential that rice scientists and breeders have access to the entire rice gene pool, so that they can incorporate desirable genes into varieties that are evermore productive and tolerant of abiotic and biotic stresses.

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### 13.1.2 *The Rice Genepool*

The genus *Oryza* consists of 25 species (USDA-ARS-NGRP 2011). The two cultivated species, *O. sativa* L. and *O. glaberrima* Steud., together with six other species are grouped within the *O. sativa* complex and have the AA-genome. Asian rice, *O. sativa* appears to have been domesticated approximately 9,000 years BC in the Yangtze River basin in China, whilst domestication of African rice occurred later, ~3500 BC (Vaughan et al. 2008a, b; Molina et al. 2011). Key factors in the domestication of Asian rice (African rice is less well studied) were the loss of shattering and loss of strong secondary dormancy. The commonality of the mutant for non-shattering grains suggests that domestication arose as a single event, from the wild rice *O. rufipogon* Griff. Early domestication and extensive geographical spread of *O. sativa* has resulted in a huge amount of genetic diversity. There are two main variety groups: indica rice which is mainly grown in tropical and subtropical regions, and japonica rice which is grown in more temperate climates. The use of isozyme markers has identified four additional variety groups, aus, ashwina, rayada, and aromatic; SSR markers and SNPs have further suggested distinction between tropical and temperate japonica varieties, the tropical japonica group corresponding approximately to a group still sometimes referred to as javanica. In the late 1960s, high-yielding varieties bred by the International Rice Research Institute (IRRI) marked the Green Revolution for rice. Cultivars of *O. sativa* are now grown in many countries, whilst *O. glaberrima* is still largely confined to West Africa. Since the late 1990s, breeders have started to produce varieties known as NERICA (New Rice for Africa) by crossing *O. sativa* and *O. glaberrima*. These inter-specific varieties are higher yielding than *O. glaberrima*, yet tolerate the drier, less fertile African soils.

Within the *Oryza* genus there are three other species complexes (Vaughan and Morishima 2003): the *officinalis* complex consists of 12 species, one with each of BB, EE, or FF genomes, three with BBCC, and three with each of CC and CCDD genomes; *ridleyi* comprises *O. ridleyi* Hook.f. and *O. longiglumis* Jansen with the HHJJ genome; *O. meyeriana* Baill. and *O. neocaledonica* Morat have the GG genome and *O. schlechteri* Pilg. has an HHKK genome. The three species with the CCDD genome, *O. latifolia* Desv., *O. grandiglumis* (Döll.) Prodoehl, and *O. alta* Swallen and *O. glumaepatula* Steud. (AA) occur in Latin America. Five wild species occur in Africa (two with AA genome, one with CC, and one with BBCC); one of these, *O. eichingeri* Peter (CC) is also found in Sri Lanka. *O. australiensis* Domin (EE) is restricted to tropical Australia; *O. schlechteri* and *O. longiglumis* Jansen (HHJJ) are only found in New Guinea; *O. rhizomatis* D.A. Vaughan (CC) is restricted to Sri Lanka. Other species are generally more widely distributed across southeast and south Asia. Many of these crop wild relatives (CWR) can be found growing in damp or wet habitats close to fields of cultivated rice and may be classed as agricultural weeds. Some wild *Oryza* species with the AA genome readily hybridize with cultivated rice; the resultant offspring are described as weedy rice, although this description may also include cultivar hybrids or derivatives. Weedy rice also represents

a potentially significant problem in rice cultivation. Conversely, there are instances where genes from rice CWR have been used in breeding programs to improve cultivated rice. For example *O. australiensis*, *O. officinalis* Wall, and *O. latifolia* have been used as a source of genes conferring resistance to brown plant hopper and *O. australiensis*, *O. brachyantha* A. Chev. and Roehrich, and *O. minuta* J. Presl. and C. Presl. have been used to confer resistance to blast bacterial blight. Accurate identification of wild species is difficult, and complicated by the natural occurrence of inter-specific hybrid swarms. This hampers the effective conservation and use of wild rice accessions.

### 13.1.3 Existing Collections

There are more than 1,750 genebanks around the world, of which more than 10% hold some rice germplasm. Based on country reports submitted between 2006 and 2008 (FAO 2010) and a 2007 survey carried out for the development of the Global Strategy for the Ex Situ Conservation of Rice Genetic Resources (Global Crop Diversity Trust 2010), there are in excess of 750,000 genebank accessions of *Oryza* species. Overall there are very many more accessions of the Asian cultivated rice, *O. sativa* than of the African cultivated rice, *O. glaberrima*, a reflection of its wider cultivation and greater genetic diversity. The proportion of all collections that are wild species is less than 3%. However, gaining an understanding of the amount of genetic diversity all these collections represent, in particular those of *O. sativa*, is difficult, not least since within countries there may be multiple collections held by different institutes with a mandate for rice research. Some collections may be extensively duplicated in another genebank, and both genebanks may be maintaining and distributing that germplasm using different genebank management systems and accession numbers. Other collections may be more unique, and may not even be safety duplicated to another genebank in case of e.g., natural disasters which result in the loss of accessions. This is less likely given recent efforts, in particular by the Global Crop Diversity Trust (GCDT), to ensure that accessions are available as part of a rational system of rice conservation and use, and that there are black box samples as safety back-up in a genebank, preferably on another continent, and/or in the Svalbard Global Seed Vault (SGSV) in Norway (Global Crop Diversity Trust 2010).

The largest single collection is that held in-trust and made freely available under the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) at IRRI. In May 2011, the T.T. Chang Genetic Resources Center at IRRI had 112,884 accessions of *O. sativa*, 2,828 accessions of *O. glaberrima*, and 4,389 accessions of wild *Oryza* species (Table 13.1). The second largest collection is held by India's National Bureau of Plant Genetic Resources (NBPGR), with 86,119 accessions of which approximately 1% is wild species (FAO 2010). There are also large collections in China: the Chinese Academy of Agricultural Sciences (CAAS) holds more than 80,000 accessions (Global Crop Diversity Trust 2010)

**Table 13.1** Major ex situ collections of rice and maize

Institution	Country	Number of accessions			
		<i>Oryza sativa</i>	<i>O. glaberrima</i>	Other <i>Oryza</i> species (23)	
<b>Rice</b>					
International Rice Research Institute (May 2011)	International (Philippines)	112,884	2,828	4,389	
National Bureau of Plant Genetic Resources (FAO 2010)	India	ca. 85,250	Unknown	ca. 860	
Chinese Academy of Agricultural Sciences (Global Crop Diversity Trust 2010)	China	67,783	0	12,000	
China National Rice Research Institute (December 2010)	China	75,106	17	2,053	
National Institute of Agrobiological Sciences (FAO 2010)	Japan	ca. 44,000	Unknown	ca. 450	
<b>Maize</b>					
International Center for Maize and Wheat Improvement (May 2011)	International (Mexico)	<i>Zea mays</i> subsp. <i>mays</i> 27,052	Teosintes ( <i>Zea</i> sp.) 227	<i>Tripsacum</i> sp. 161	
National Center for Genetic Resources Preservation	USA	27,649	459	190	
Banco Portugues de Germoplasma Vegetal (FAO 2010)	Portugal	24,529	0	0	
North Central Regional Plant Introduction Station (May 2011)	USA	19,582	ca. 325	ca. 50	
Chinese Academy of Agricultural Sciences (FAO 2010)	China	19,088	0	0	
Instituto Nacional de Investigaciones Forestales y Agropecuarias (FAO 2010)	Mexico	14,067	ca. 136	ca. 50	

whilst the Chinese National Rice Research Institute (CNRI) reported having, at the end of 2010, 75,106 accessions of *O. sativa*, 17 accessions of *O. glaberrima*, and 2,053 of 11 other *Oryza* species [pers. comm]. Collections of between 20,000 and 45,000 accessions are held by the National Institute of Agrobiological Sciences (NIAS) in Japan; the Rural Development Agency in Korea; the National Center for Genetic Resources Preservation in the USA; AfricaRice (another international agricultural research organization located in Benin); and the Biotechnology Research Development Office (BRDO) in Thailand.

Most of the accessions (>85%) held by NBPGR in India, by CAAS and CNRI in China, and by other national genebanks, were collected in-country; the Napok Agricultural Center in Laos reported that all their accessions were collected in country (Global Crop Diversity Trust 2010). Both India and China have conducted extensive in-country collecting missions, often without collaboration, and as such, these collections are likely to contain a high proportion of unique germplasm. Collections with a national focus are also more likely to be dominated by landraces (rather than for example, breeding lines or advanced cultivars). In contrast, not surprisingly, the international collections held by IRRI and by AfricaRice have high proportions of regionally-collected germplasm (Asia and West Africa, respectively). Indeed many national collections have been duplicated to IRRI or AfricaRice, usually for maintenance and distribution as a regular accession. Genebanks in countries that are not traditional rice producing countries tend to have a larger proportion of their collection that is introduced material for breeding and other fundamental research. The Dale Bumpers National Rice Research Center in the USA for example, reported that 93% of their 23,090 accessions were breeding lines (FAO 2010). This USA collection, like the collection held by NIAS in Japan, perhaps has a more temperate focus than the Asia-based collections.

The largest ex situ collection of wild rice species is held by CAAS, China; in 2007 CAAS reported having 12,000 accessions of wild species, approximately 15% of the entire collection (Global Crop Diversity Trust 2010). The Cambodian Agricultural Research and Development Institute (CARDI), the National Agricultural Research Centre of Pakistan, and the SADC Plant Genetic Resources Centre in Zambia also have relatively high proportion of wild species germplasm (10–30% of their total accessions), although in terms of numbers, the second largest collection of wild rice species is held by IRRI. However, most genebanks have relatively few (<100 accessions) or no wild rice germplasm.

#### **13.1.4 Networks and Resources**

The major national genebanks in Asia have been supported by the strong national programmes in each of the countries, commensurate with the high importance attached to rice in the region. However, there is a need for greater cooperation and rationalization to understand the extent of duplication and, conversely, the gaps in the rice gene pool which are not in conserved ex situ, and to ensure efficiency. In

regions outside of Asia, rice is a lower priority for research and conservation and hence rice collections in those regions tend to be small, scattered, and not well resourced. A partial “rice registry” has been constructed to help identify accessions with common ancestry, cross-referencing rice accessions held in the USA Department of Agriculture, CAAS China, and the IRRI and AfricaRice genebanks. The *Oryza* accessions held by IRRI and AfricaRice can also be requested via a single on-line portal, the System-wide Information Network for Genetic Resources (SINGER: <http://singer.cgiar.org>). SINGER has been incorporated into Genesys (<http://www.genesys-pgr.org/>), a more general global portal for searching germplasm from national as well as international collections based on a broader range of passport and characterization data.

In contrast to the absence of networks for the conservation of rice germplasm, the International Network for Genetic Evaluation of Rice (INGER) is a good example of an effective network for its utilization. INGER is a partnership of national agricultural research and extension systems (NARES) and international centers including IRRI, AfricaRice, and the Centro Internacional de Agricultura Tropical (CIAT), that started in 1975. The INGER partner institutions collaborate mainly through the distribution of pre-defined “nurseries”, or sets of germplasm selected on the basis of their perceived potential value for particular situations or qualities. All the passport and evaluation data is also shared. The germplasm is now exchanged following the standard material transfer agreement of the ITPGRFA. Over the last 30 years or so, it has been credited with the release of 667 varieties in 62 countries. The Latin-American fund for irrigated rice (Fondo Latinoamericano para el Arroz de Riego; FLAR) has a similar purpose to INGER but is more restricted in genetic scope and in membership, geographic coverage, and germplasm sharing.

### 13.1.5 Future

Given the total number of rice accessions that are held in genebanks globally, it is clear that there is considerable national and international commitment to the maintenance of this resource. This commitment is doubtless promoted by the continued use of ‘new’ germplasm in rice breeding programs. However, there is a bottleneck in the use of a large proportion of rice collections, due to limitations in the amount of phenotypic data that has been collected. More advanced and faster phenotyping techniques and facilities, for example as planned as part of the Global Rice Science Partnership (GRiSP), together with the increasing availability of DNA sequences should facilitate better selection of accessions for use in breeding programs (conventional breeding methods and for example, through marker assisted selection or genetic modification). Generation of large data sets for numerous accessions will require sophisticated data storage and analysis. The International Rice Information System (<http://iris.irri.org>) is a database system for germplasm pedigree, evaluation, genomic, and environmental data (Bruskiewich et al. 2003).

The conditions under which collections are stored vary between genebanks and not all genebanks store their seed germplasm according to the international standards for genebanks (FAO/IPGRI 1994). Of particular concern is unique germplasm that is only held in genebanks that are able to store rice seeds under short-term storage conditions or whose storage conditions or pre-storage drying conditions depend on ambient temperature and humidity. Genetic erosion of such collections is inevitable without investment to upgrade drying facilities and/or temperature-controlled storage. Further, there are strong indications of gaps in coverage particularly of wild rice species outside south and east Asia. This under-representation of crop wild relatives in *ex situ* collections is going to be addressed by a new initiative led by the GCDT to collect and conserve the wild relatives of rice and other major food crops. Characterisation and pre-breeding activities will help identify useful traits for introduction into advanced cultivars.

## 13.2 Maize

### 13.2.1 Why Conserve Maize Germplasm

Maize (*Zea mays* L. subsp. *mays*) is currently produced on nearly 100 million hectares in 125 developing countries and is among the three most widely grown crops in 75 of those countries (FAO 2011). Although much of the world's maize production (approximately 78%) is utilized for animal feed, human consumption in many developing and developed countries is steadily increasing. For example, maize is the most important cereal crop for food in sub-Saharan Africa and Latin America. Further, with human population growth, the demand for maize in the developing world will double between now and 2050, and by 2025, maize is likely to become the crop with the greatest production globally (Rosegrant et al. 2008).

A great deal of genetic variability is present within and between the many diverse lines, varieties, and races of maize (Goodman and Brown 1988). Maize genetic resources constitute an immensurable treasure for humankind. Their conservation and the investigation of existing variation and possible current and future uses provide:

- Resources for agricultural improvement to reduce hunger and poverty.
- A solid knowledge base for future generations of researchers.

The value of germplasm within genebanks is mostly measured by the extent of utilization of their genetic variation (mostly for breeding programmes). Landraces have the value of adaptation to specific cultivated regions or ecological conditions. Wild species may contain special genes such as those conferring disease resistance, climate adaptation, or nutritional quality.

In some areas, where populations of Native Americans predominate, their landraces of maize are still being cultivated and can still be collected today. However,

economic forces are seriously eroding the wellbeing of the small farmers in Mexico with a resulting serious reduction in the number of landraces being grown and a reduction of land area devoted to most races. As a result, some races of maize have been displaced by modern cultivars while others, including virtually all the teosintes, are threatened as a result of modern farming and ranching practices.

### 13.2.2 *The Maize Genepool*

Maize was domesticated in southern or southwestern Mexico, most likely from teosinte or some extinct wild maize closely related to teosinte (Wilkes 2004; Sluyter and Dominguez 2006). While maize covered much of the New World at the time of colonisation, the teosintes have a much more restricted geographic distribution; mainly central and southwestern Mexico, with limited populations in northern Mexico, Guatemala, and Nicaragua. The genetic diversity of maize, being an out-crossing crop, is extremely broad. Maize landraces exhibit significant morphological variation and genetic polymorphism (Ortiz et al. 2010). Thus, maize has gained adaptation and productivity in all continents through introductions and breeding and is widely grown between 55°N and 55°S (Guidry 1964) and from sea level to 3,800 m (Taba 1997).

Maize has been divided into about 300 races (Goodman and Brown 1988). A maize race has been defined as ‘a group of related individuals with enough characteristics (genes) in common to permit their recognition as a group’ (Anderson 1944). It is reported that the total number of unique New World maize germplasm accessions exceeds 27,000 [survey carried out in 2006 for the development of the *Global Strategy for the Ex Situ Conservation and Utilization of Maize Germplasm* (Global Crop Diversity Trust 2007)]. The major types of cultivated maize (*Zea mays* L.) under conservation are characterised by their kernel types: dent, flint, floury, sugary, pop, and morocho (a soft floury texture inside the grain, surrounded by a hard flint texture). Grain may be white, yellow, purple, orange yellow, red, sun red, mottled, or brown.

The primary maize genepool consists of cultivated maize and diploid teosintes (Tallury and Goodman 2001). Teosintes comprise seven taxa divided into two sections and five species. All but one species is diploid,  $2n=20$ , and inter-fertile with cultivated maize. There is also one species of perennial, tetraploid teosinte (*Zea diploperennis*). Teosinte was originally divided into six races (Wilkes 1967), but since the discovery of *Z. diploperennis*, species and subspecies names have come into favour for teosinte (Wilkes 2004).

The genus *Tripsacum* is the genus most closely related to *Zea*, and all species within this genus constitute the secondary gene pool of maize (Tallury and Goodman 2001). *Tripsacum* species have multiples of  $x=8$  chromosomes (Anderson 1944; Stebbins 1950) and are perennials. Maize and *Tripsacum* have been hybridized (e.g., de Wet and Harlan 1978), but the offspring have varying degrees of sterility and no spontaneous hybrids have been confirmed. There are at least 16 species of



*Tripsacum*, ranging from the USA to Bolivia (de Wet et al. 1983). A tertiary gene pool consists of the distantly related Asiatic genera *Coix*, *Selerchne*, *Pollytoca*, and *Chinache* as well as genera in the tribe Andropogoneae (Tallury and Goodman 2001). No members of the tertiary gene pool have been used for maize improvement or backcrossed to cultivated maize.

### 13.2.3 Existing Collections

Maize ex situ germplasm collections include landraces (maize races), improved populations (synthetics, varieties, and cycles of selection), inbred lines (early generation homozygous), reference hybrids, genetic stocks (natural genes and transgenes) and wild species housed as caryopsis and clones (Taba 1997). Not all accessions have been classified by race, and not all can be classified due to hybridization.

The two most recent surveys of global maize collections include that for the *Global Strategy for the Ex Situ Conservation and Utilization of Maize Germplasm* (Global Crop Diversity Trust 2007) and the Second Report on the State of the World's Plant Genetic Resources for Food and Agriculture (SOWPGR2; FAO 2010). The SOWPGR2 surveyed 281 collections and reported almost 328,000 accessions worldwide, including approximately 33% land races and 1% wild relatives. The Global Strategy reported on unique landrace collections and reported over 42,000 accessions in 34 collections worldwide (Global Crop Diversity Trust 2007).

The largest single collection in the world, with over 27,000 accessions, is housed at The International Center for Maize and Wheat Improvement (CIMMYT) in Mexico (Table 13.1). CIMMYT's maize collection is held in Trust and made freely available under the ITPGRFA. The other key international collection of the Americas is the North Central Regional Plant Introduction Station (NCRPIS) in Ames, IA, USA. The National Center for Genetic Resources Preservation (NCGRP) in Ft. Collins, CO, USA holds duplicates for a number of collections and has over 39,000 accessions overall. However, it has very few accessions that are unique to the Center. In addition the Maize Genetic Co-operation Stock Center in Urbana, IL, USA is a bank specifically for genes. The maize stock center houses virtually all of the mutants of maize, various chromosomal stocks, multiple mutant stocks, and various other stocks of interest to the maize genetics community. All centers have back-up collections either between them, at the SGSV in Norway, or both.

The national centers of major importance are in Brazil, Colombia, Mexico, and Peru. These four centers were the original stock centers of the National Research Council Rockefeller Foundation collections of the 1940s–1960s. These collections comprised the original strains available in current collections and were the basis of maize race definition and description. Other national collections of major importance include BPGV-DRAEDM, Portugal, ICGR-CAAS, China, and INIFAP, Mexico (FAO 2010).

### ***13.2.4 Networks and Resources***

While there are numerous regional germplasm networks in the Americas, Africa, Asia, and Europe, most of the networks are more concerned with general information exchange rather than regeneration and active germplasm exchange. The networks that have been the most effective for maize are LAMP (Latin American Maize Project) and the Latin America Maize Regeneration Project. Over 12,000 Latin American accessions were evaluated through LAMP, sequentially identifying the more promising ones for further breeding work, and eventually identifying an elite set of about 300 accessions. The regeneration project eventually regenerated most of the maize accessions of Latin America, including those of LAMP.

The LAMP project eventually led to the GEM (Germplasm Enhancement of Maize) project in the USA, a cooperative public/private endeavor to quickly expand the germplasm base of commercial maize. Elite germplasm accessions are crossed to private lines from US or foreign companies (or to public lines from foreign countries), families are derived by selfing, and top crosses are tested cooperatively to identify superior families. These superior families are first distributed to cooperators (US and international) and then, with a year's delay, to the general public anywhere in the world via the NCRPIS at Ames, IA, USA. Together, these three projects represent much of the current leadership for protection, promotion, and utilization of maize germplasm resources.

### ***13.2.5 Future***

The proper utilization of germplasm collections requires access to information on its morphological, agronomic, and genomic characters as well as access to the germplasm material itself. The GCDT is working with national partners worldwide to regenerate unique and imperiled collections. One important outcome of this endeavor is that duplicates of these materials will be donated to CIMMYT to become part of its collection and thus available for all.

The government of Mexico has recently announced the program "MasAgro; the Sustainable Modernization of Traditional Agriculture." As part of this 10-year initiative, smallholder farmers are working with agricultural research and development organizations to raise and stabilize their crop yields, increase their incomes, and reduce the effects of climate change on Mexico's agricultural output (<http://www.cimmyt.org>). A subproject, Seeds of Discovery (SeeD), will undertake the genetic characterization of each accession in the CIMMYT genebank. In addition, subsets of CIMMYT's holdings will be evaluated for traits of agronomic importance and end-use quality. These activities will be carried out in collaboration with international and national institutions.

Finally, the inception of the GRIN-Global database (<http://www.grin-global.org>) should make information across collections available to users worldwide. Together,

these undertakings promise to augment utilization on a global level as well as add to the conservation of materials that could otherwise become lost.

## 13.3 Sorghum

### 13.3.1 Why Conserve Sorghum Germplasm

Sorghum (*Sorghum bicolor* (L.) Moench) is the fifth most important cereal in the world after rice, wheat, maize, and barley. It is mostly grown in the semi arid tropics; the countries with the large areas of sorghum cultivation are India (7.7 million ha), Sudan (5.61 million ha), Nigeria (4.7 million ha), Niger (3.3 million ha), Burkina Faso (1.98 million ha), USA (1.95 million ha), Mexico (1.77 million ha), Ethiopia (1.62 million ha), and Mali (1.22 million ha) (FAO 2010). Sorghum constitutes the staple food for over 750 million people who live in the semi-arid tropics of Africa, Asia, and Latin America. In addition, stalk and foliage are used as fodder, fuel, and for thatching and fencing. It has a wide range of industrial uses including ethanol production, sugar and concentrated sugar syrup, popping, confectionary, etc., in developed and developing countries.

### 13.3.2 The Sorghum Genepool

*S. bicolor* (2n=20) is synonymous with *Holcus bicolor* L., *Andropogon sorghum* (L.) Brot., and *Sorghum vulgare* Pers. Sorghum was probably domesticated in the north east quadrant of Africa, an area that extends from the Ethiopia-Sudan border westward to Chad (Doggett 1970; de Wet et al. 1976). From there it was probably spread to India, China, the Middle East, and Europe. Sorghum is known by a variety of names: Guinea corn in West Africa, kaffir corn in South Africa, durra in Sudan, and mtama in eastern Africa. In India, the crop is known as jowar in the North and cholam in the South.

*S. bicolor* is considered an extremely variable crop-weed complex. It comprises wild, weedy, and cultivated annual forms which are fully inter-fertile. The cultivated forms fall in *S. bicolor* subsp. *bicolor* and are classified, in the most widely accepted system, into five basic races (bicolor, guinea, caudatum, kafir, and durra) and ten intermediate or hybrid or half races on the basis of spikelet morphology and panicle shape [guinea-bicolor, caudatum-bicolor, kafir-bicolor, durra bicolor, guinea-caudatum, guinea-kafir, guinea-durra, kafir-caudatum, durra-caudatum, and kafir-durra (Harlan and de Wet 1972; de Wet 1978)]. Sub-race names are being added to this system (Doggett and Prasad Rao 1995; Prasad Rao et al 1989). The wild forms are classified into *S. bicolor* (L.) Moench subsp. *verticilliflorum* (Steud.) Piper (synonyms: *S. arundinaceum* (Desv.) Stapf and *S. bicolor* (L.) Moench subsp.

*arundinaceum* (Desv.) de Wet and Harlan). The subspecies is further divided into four overlapping races, the most widely distributed and variable of which is *verticilliflorum*, found across the African savanna and introduced into tropical Australia, parts of India, and the Americas. The weedy forms are classified into *S. bicolor* (L.) Moench subsp. *drummondii* (Steud.) de Wet (synonyms: *S. sudanense* (Piper) Stapf and *S. drummondii* (Steud.) Millsp. and Chase), which arose and probably continues to arise from crossing between cultivated grain sorghum and close wild relatives wherever in Africa, they are sympatric. The hybrids have stabilized and occur as persistent weeds in abandoned fields and field margins. A well known forage grass, Sudan grass, belong to this complex.

The primary gene pool include the *S. bicolor* cultivated species and *S. propinquum* (Kunth) Hitchc., a wild diploid complex found in southeast Asia (Acheampong et al. 1984). The secondary gene pool includes *S. halepense* (L.) Pers., a rhizomatous tetraploid fodder, thought to be an autotetraploid of *S. propinquum* (Acheampong et al. 1984). Commonly known as Johnson grass, this is native to southern Eurasia east to India, but has now been introduced as a weed to warm temperate regions of the world. The tertiary gene pool consists of all other sections/subgenera of sorghum.

### 13.3.3 Existing Collections

World collections of sorghum comprise 235,688 accessions (FAO 2010). Substantial collections (about 62%) are in 21 genebanks including 16.1% in the genebank of the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT). At ICRISAT, sorghum germplasm was assembled by (1) introducing material gathered at various places across the world; (2) launching germplasm collection missions in priority areas; and (3) assembled from centre's own research. At present ICRISAT is the major repository for sorghum germplasm with a total of 37,949 accessions from 92 countries (Table 13.2). ICRISAT has collected 9,011 sorghum samples from 94 collection missions in 33 countries. 121 organizations located in 52 countries donated 28,932 accessions. The collection comprises 85.3% landraces, 13.2% breeding material, 1.2% wild species and 0.3% named cultivars. The germplasm maintained at ICRISAT is predominantly represented by three races: durra (23.5%), caudatum (20.6%), and guinea (14.8%). Of the ten hybrid races, only durra-caudatum (11.5%), guinea caudatum (9.2%), and durra bicolor (7.1%) are common. To enhance use of germplasm in crop improvement, a mini core collection (242 accessions, 1% of entire collection) representing the diversity of the entire collection has been developed (Upadhyaya et al. 2009a).

In addition to the world repository of sorghum germplasm at the ICRISAT genebank, considerable collections (>10,000 accessions) have been assembled at the Plant Genetic Resources Conservation Unit, Southern Regional Plant Introduction Station, University of Georgia, USDA-ARS, USA; the Institute of Crop Germplasm Resources, CAAS, China and National Bureau of Plant genetic Resources (NBPGR), India Table 13.2.

**Table 13.2** Major ex situ collections of sorghum and millets

Institution	Country	Number of accessions
<b>Sorghum</b>		
Plant Genetic Resources Conservation Unit, University of Georgia, USDA-ARS	USA	44,993
International Crop Research Institute for the Semi-Arid Tropics (ICRISAT)	International (India)	37,949
Institute of Crop Germplasm Resources, Chinese Academy of Agricultural Sciences (CAAS)	China	18,263
National Bureau of Plant Genetic Resources (NBPGR)	India	17,466
<b>Pearl millet</b>		
International Crop Research Institute for the Semi-Arid Tropics (ICRISAT)	International (India)	22,211
National Bureau of Plant Genetic Resources (NBPGR)	India	7,444
ICRISAT-Niamey	International (Niger)	5,365
Costal Plains Experiment Station USDA-ARS Tifton	USA	5,228
<b>Eleusine spp.</b>		
National Bureau of Plant Genetic Resources (NBPGR)	India	9,522
All India Coordinated Research Project (AICRP) on Small Millets	India	6,257
International Crop Research Institute for the Semi-Arid Tropics (ICRISAT)	International (India)	5,957
<b>Setaria spp.</b>		
Chinese Academy of Agricultural Sciences (CAAS)	China	26,233
National Bureau of Plant Genetic Resources (NBPGR)	India	4,392
Institut de Recherche pour le Développement	France	3,500
<b>Paspalum spp.</b>		
National Bureau of Plant Genetic Resources (NBPGR)	India	2,180
Plant Genetic Resources Conservation Unit, University of Georgia, USDA-ARS	USA	1,385
All India Coordinated Research Project (AICRP) on Small Millets	India	1,111
<b>Echinochloa spp.</b>		
Department of Genetic Resources I, National Institute of Agrobiological Sciences (NIAS)	Japan	3,671
National Bureau of Plant Genetic Resources (NBPGR)	India	1,677
<b>Panicum spp.</b>		
N.I. Vavilov All-Russian Scientific Research Institute of Plant Industry	Russia	8,778
Chinese Academy of Agricultural Sciences (CAAS)	China	8,451
Department of Genetic Resources I, National Institute of Agrobiological Sciences (NIAS)	Japan	6,277

### 13.3.4 Networks and Resources

In collaboration with national agricultural research systems (NARS), universities, and Non-Governmental Organizations (NGOs), ICRISAT has launched expeditions to collect germplasm of its mandate crops. More than 95% of the sorghum

collection was placed under the purview of the ITPGRFA and are available to the world community using Standard Material Transfer Agreement (SMTA). ICRISAT's agreement with FAO requires safety back-up for long-term conservation. The Memorandum of Understanding (MOU) between the Nordic genebank and ICRISAT has facilitated the safety duplication of ICRISAT collections in the SGSV; ICRISAT has already deposited about 21,000 duplicate accession samples in the SGSV.

### **13.3.5 Future**

Sorghum is a multipurpose crop. The demand for sorghum grain as food is likely to remain high in the traditional producing and consuming countries which have little opportunity to produce alternative crops. Under these circumstances there will be continuous demand for sorghum cultivars that are high yielding, have a broad genetic base, and are stable under abiotic and biotic stresses. In future, ICRISAT needs to ensure that the assembled germplasm is conserved, maintained safely, and distributed to all bona fide users for utilization in crop improvement programs. The strategic research on core and mini core collections and identification of new diverse sources will enhance the use of germplasm in breeding programs. Molecular characterization of mini core and trait-specific subsets will further reveal genetic usefulness of the germplasm accessions in allele mining.

## **13.4 Pearl Millet**

### **13.4.1 Why Conserve Pearl Millet Germplasm**

Pearl millet (*Pennisetum glaucum* (L.) R. Br.) is an important food and forage crop in Africa and Asia. It is also valued for fodder (both stover and green fodder) and poultry feed in the Americas. Traditionally, pearl millet grains are used in the preparation of conventional foods such as unleavened flat breads (chapati), fermented breads (Kisra, injera, dosa, etc.), porridge, mudde or dumpling, biscuits, snacks, and malt and opaque beer. Pearl millet is mainly grown by small farmers who are dependent on pearl millet for their livelihood. Pearl millet is mainly cultivated in Niger, Nigeria, Burkina Faso, Togo, Ghana, Mali, Senegal, Central African Republic, Cameroon, Sudan, Botswana, Namibia, Zambia, Zimbabwe, and South Africa in Africa and India, Pakistan, and Yemen in Asia.

Pearl millet is probably the world's hardest crop and has great potential because of its suitability to the extreme limits of agriculture. Its importance is expected to increase under various climate change scenarios (Lane et al. 2007). Pearl millet is endowed with enormous genetic variability for various morphological traits, yield

components, adaptation and quality traits. The genetic variability accumulated over centuries is fast eroding, mainly due to the replacement of landraces by improved cultivars, natural catastrophes (droughts, floods, fire hazards, etc.), industrialization, human settlement, over-grazing, and destruction of plant habitats for irrigation projects and dams (Upadhyaya and Gowda 2009). Therefore, the conservation of pearl millet diversity is essential to combat new pests and diseases and to produce adapted varieties for the changing climatic conditions.

### 13.4.2 The Pearl Millet Genepool

The genus *Pennisetum* (L.) Rich., to which pearl millet belongs, is the largest in the tribe Paniceae and consists of over 140 species (Clayton 1972). *Pennisetum* is divided into five sections: *Gymnothrix*, *Eu-Pennisetum*, *Penicillaria*, *Heterostachya*, and *Brevivalvula*. Pearl millet belongs to the section *Penicillaria*. The genus *Pennisetum* is a heterogeneous assemblage of species with large variation in chromosome number, ranging from  $2n=10$  to  $2n=72$ , in the multiples of 5, 7, 8, and 9. There are many more species in this genus, but their chromosome number and gene-pool relationships are yet to be established (Hanna 1987). Among those studied, the lowest chromosome number ( $2n=2x=10$ ) occurs in *P. ramosum* (Hochst.) Schmeinf. Those with  $x=7$  chromosomes include the cultivated pearl millet and its wild and weedy subspecies, and *P. schweinfurthii* Pilger ( $2n=2x=14$ ) and *P. purpureum* Schumach. ( $2n=4x=28$ ). *P. massaicum* Stapf ( $2n=16$  and  $32$ ) is the only known species with  $x=8$ . All other species have the basic chromosome number of  $x=9$ . The genus includes annual as well as perennial and sexual as well as asexual, including apomictic species.

On the basis of crossability and following the biological concept of species, *Pennisetum* germplasm has been classified into three genepools: primary, secondary, and tertiary. The primary genepool includes all those taxa that can easily cross with the cultivated pearl millet. This includes all variability in the cultivated *P. glaucum*, and those in its wild progenitor [*P. glaucum* ssp. *violaceum* (= *monodii* Maire)] and weedy form (*P. glaucum* subsp. *stenostachyum* Kloyzsch ex. A. Br. and Bouche). The latter results from hybridization between cultivated pearl millet and its wild progenitor. The secondary genepool includes those species that also cross easily with the cultivated types, but do not produce fertile hybrids. Elephant or Napiergrass (*P. purpureum*), a rhizomatous perennial, belongs to this genepool. It is an allotetraploid ( $2n=2x=28$ ) with A'A'BB genomic constitution in which the A' genome is homologous or at least homoeologous to the A genome of the primary genepool. Its hybrids with cultivated pearl millet have  $n=21$  and are sterile, but become fertile after chromosome doubling ( $2n=6x=42$ ). The tertiary genepool includes the remainder of the species which either do not cross with cultivated pearl millet or when they do, albeit in rarest instances, the fertility in hybrids or their derivatives can only be achieved through resorting to special techniques (Hanna 1987).



### ***13.4.3 Existing Collections***

There are 65,400 accessions of pearl millet in 70 genebanks of 46 countries (FAO 2010). The long-term objective of ICRISAT is to serve as the world repository for the germplasm of its mandate crops, including pearl millet, and their wild relatives. By the end of 2010, the genebank at ICRISAT had registered 22,211 accessions of pearl millet germplasm from 51 countries, including 750 accessions of wild relatives belonging to 24 species of genus *Pennisetum* (Table 13.2). This is the largest collection of pearl millet germplasm assembled at any one place in the world. Pearl millet germplasm was assembled by (1) introducing the material that was already gathered at various places across the world; (2) launching germplasm collection missions in priority areas; and (3) assembly from center's own research. A total of 65 organizations contributed 11,381 accessions including those contributed by different disciplines at ICRISAT, in different years. The major donors of pearl millet germplasm include the Institut de Recherche pour le Développement, France (2,178); Rockefeller Foundation, India (2,022); and IBPGR (now Bioversity International), Italy (974). ICRISAT in collaboration with its partners launched a total of 216 collection missions for all its mandate crops including 76 for pearl millet germplasm in 28 countries and collected 10,830 pearl millet samples. Biological status of accessions indicated 19,063 landraces, 2,269 breeding materials, 129 advanced cultivars, and 750 wild accessions in the collection. To enhance the use of germplasm in crop improvement programs, core (2,094 accessions; Upadhyaya et al. 2009a) and mini core collections (238 accessions; Upadhyaya et al. 2011b) have been developed.

In addition to the single largest collection of pearl millet at the ICRISAT genebank, there are considerable collections at NBPGR, India; ICRISAT, Niamey; Coastal Plains Experimental Station, USDA, Tifton, USA; Institut de Recherche pour le Développement, France (4,405); Plant Genetic Resources of Canada (3,840), and Serere Agricultural and Animal Production Research Institute, Uganda (2,142). Most of these pearl millet collections were collected in-country and may, to a greater or lesser extent, be duplicates of accessions at ICRISAT (Table 13.2).

### ***13.4.4 Networks and Resources***

In collaboration with NARS, universities, and NGOs, ICRISAT has conducted expeditions to collect germplasm of its mandate crops. More than 96% of the pearl millet collection was placed under the purview of the ITPGRFA and are distributed according to the SMTA. Efforts have been made to conserve 5,205 pearl millet accessions at ICRISAT regional genebank at Niamey, Niger. In addition, ICRISAT has already deposited 8,050 duplicate accession samples at SGSV. ICRISAT's



pearl millet passport and characterization databases can be accessed through SINGER and Genesys.

### **13.4.5 Future**

In future, ICRISAT needs to ensure that the assembled germplasm is maintained in safe, secure and cost-effective manner and distributed to all bona fide users for utilization in crop improvement programs. Identifying gaps (Upadhyaya et al. 2009c, 2010a) in the collection and exploration for wild relatives and trait-specific germplasm are essential to further increase the diversity in collection. Trait-specific genetically diverse parents for trait enhancement are the primary need of the plant breeder. Strategic research on core and mini core collections and identification of new diverse sources will enhance the use of germplasm in breeding programs. Molecular characterization of mini core and trait-specific subsets will further reveal genetic usefulness of the germplasm accessions in allele mining. The aim is to identify the trait-specific genetically diverse and agronomically better germplasm lines through characterization, evaluation, and screening for the development of high yielding cultivars with a broad genetic base.

## **13.5 Small Millets**

### **13.5.1 Why Conserve Small Millet Germplasm**

Small millets are small-seeded annual coarse cereals grown throughout the world, particularly in arid, semi-arid, or mountain zones, as rain-fed crops under marginal and sub-marginal conditions of soil fertility and moisture. They include finger millet (*Eleusine coracana* (L.) Gaerth.), foxtail millet (*Setaria italica* (L.) Beauv.), proso millet (*Panicum miliaceum* L.), little millet (*P. sumatrense* Roth. ex Roem. & Schult.), barnyard millet (*Echinochloa crusgalli* (L.) Beauv.), and kodo millet (*Paspalum scrobiculatum* L.). Precise estimates of area and production are not available and data is generally combined for all the millets. South and East Asia produces about 60% of the total millet harvest; Eurasia and Central Asia, 14%; Africa, 16%; and the rest of the world, 10%. India is the leading producer contributing about 38% of the production. Finger millet is the principal small millet species grown in South Asia, followed by kodo millet, foxtail millet, little millet, proso millet and barnyard millet, in that order. Foxtail millet and proso millet are important in China and the latter is grown extensively in southern USSR. Presently, small millets are cultivated in areas where they produce a more dependable harvest than other crops. This has been largely responsible for their continued presence and cultivation in many parts of the world.

### 13.5.2 *The Genepools of Small Millets*

All small millets belong to the family Poaceae (Gramineae). Of them, the genera *Setaria*, *Panicum*, *Paspalum*, *Echinochloa* and *Digitaria* are classified under the tribe Paniceae of sub-family Panicoideae, and the other two genera *Eleusine* and *Eragrostis* under the tribe Eragrostideae of sub-family Chloridoideae (Prasad Rao and Mengesha 1988).

#### 13.5.2.1 Finger Millet

Finger millet was domesticated in Africa, probably in the Ethiopian region. It is also known as African millet, koracan, ragi (India), wimbi (Swahili), bulo (Uganda), and teleburn (Sudan). It was introduced to India as a crop more than 3,000 years ago (Doggett 1989). Cultivated finger millet is *Eleusine coracana* (L.) Gaertn. subsp. *coracana*. The closest wild relative is *Eleusine coracana* subsp. *africana* (Kenn-O'Byrne) Hilu and de Wet. Wild finger millet (subsp. *africana*) is native to Africa but was introduced as a weed to the warmer parts of Asia and America. Cultivated finger millets are divided into races and sub-races on the basis of inflorescence morphology. Members of the race *compacta* are commonly referred to as cockscomb finger millet in both Africa and India. The race *plana* is characterized by large spikelets (8–15 mm long) that are arranged in two, more or less even rows along the rachis, giving the inflorescence branch a flat ribbon like appearance. The race *vulgaris* is the common finger millet to Africa and Asia; four sub-races are recognized on the basis of inflorescence morphology.

#### 13.5.2.2 Foxtail Millet

Foxtail millet was first domesticated in the highlands of central China: remains of the cultivated form are known from the Yang-Shao period dating back some 5,000 years. Comparative morphology suggested that foxtail millet spread to Europe and India as a cereal soon after its domestication (Prasad Rao et al. 1987). The possible ancestor is *Setaria viridis*. Foxtail millet is fairly tolerant of drought; it can escape, some droughts because of early maturity. On the basis of inflorescence morphology, foxtails millets are classified into species, sub-species, races, and sub-races.

#### 13.5.2.3 Proso Millet

Domestication of proso millet probably occurred in Manchuria (de Wet 1986). It was probably introduced into Europe about 3,000 years ago. After this date, it was introduced to the Near East and India (Zohary and Hopf 1988). On the basis of cultivated morphology study, proso millet is divided into five cultivated races.

#### 13.5.2.4 Little Millet

The possible wild progenitor of little millet is *Panicum psilopodium* which is distributed from Sri Lanka to Pakistan and eastward to Indonesia. On the basis of morphology, little millet is divided into subspecies, race, and sub-race.

#### 13.5.2.5 Barnyard Millet

*Echinochloa crusgalli* was domesticated about 4,000 years ago in Japan. *E. colona*, which occurs widely in tropical and sub-tropical areas, was domesticated in India. On the basis of morphology they are similar, but hybrids between them are sterile. *E. colona* differ from the *E. crusgalli* in having smaller spikelets with membranaceous rather than chartaceous glumes. On the basis of inflorescence morphology the genus *Echinochloa* is classified into two species, three subspecies and eight races.

#### 13.5.2.6 Kodo Millet

Kodo millet was domesticated in India about 3,000 years ago and is now produced in West Africa and India. Crossing readily occurs between cultivated and weedy races, and seed from the hybrid harvested along with those of the sown crop; racial differentiation is not distinct despite years of cultivation in India (Prasad Rao et al. 1987). On the basis of inflorescence morphology, kodo millet is classified into three races.

### 13.5.3 Existing Collections

The genebank at ICRISAT conserves a total of 10,235 accessions of small millets germplasm from 50 countries. In addition, several organizations in different countries are also conserving considerable collections. There may be some duplicates across the collections (Table 13.2).

### 13.5.4 Networks and Resources

While collecting germplasm of its mandate crops, ICRISAT has also collected small millet germplasm. Core and mini core collections of finger millet and foxtail millet have been developed. Selected germplasm sets and mini core collections have been evaluated for agronomic performance across locations in collaboration with NARS

scientists in Asia and Africa. ICRISAT has already deposited 7,399 duplicate accession samples at SGSV.

Small millets are not mandate crops of ICRISAT. To enhance use of genetic resources in crop improvement, core collections in finger millet (622 accessions; Upadhyaya et al. 2006), foxtail millet (155 accessions; Upadhyaya et al. 2008), barnyard millet (89 accessions; Upadhyaya et al. 2011b), and proso millet (106 accessions; Upadhyaya et al. 2011c), and mini core collections of finger millet (80 accessions Upadhyaya et al. 2010b) and foxtail millet (35 accessions Upadhyaya et al. 2011d) have been developed.

### 13.5.5 Future

The most important feature of minor millets is their short biological cycle; this trait is very important for risk avoidance under rainfed cultivation. In intercropping systems, they are used as short duration millets with slower maturing crops. The grain is small and can be stored for long periods without damage, ensuring continuous food supply during adverse situations such as failure of other crops. Small millets also perform better in adverse climatic conditions like severe drought (Kodo millet has the highest drought resistance). Most of the millets mature early so they can escape drought stress and they can be grown in sub-marginal conditions of soil fertility and moisture where the major cereal crops fail to realize production satisfactorily. Small millets are ideal for organic agriculture production and are often grown by subsistence level farmers with years of experience and traditional wisdom embedded in the variety choice and system of agriculture. Minor millets are nutritionally comparable or even superior to staple cereals such as rice and wheat (Gopalan et al. 2004). Millets are known as nutri-cereals; they are rich in vitamins, sulphur-containing amino acids, minerals, and phytochemicals, and have a high proportion of non-starch polysaccharides and dietary fiber. In view of all these benefits, small millets will play an important role in agriculture in the years to come.

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