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Role of Plant Genetic Resources in Food Security

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9.1 Introduction

Within the last 13 000 years many crop species were domesticated and spread to a range of agri-ecological environments, varying by species (Hancock 2012a). There was manual selection for both food and agronomic characteristics, and natural selection for adaptation to new agro-ecological environments. Such selection was affected by available gene pools, continuing sources of genetic diversity from wild relatives and mutations, natural selection pathways from stabilising to directional, and both allo- and auto-polyploidy, to result in unique gene pool patterns for each crop (Hancock, 2012b; Cortes et al., 2013). The distribution of wheat was expanded greatly with the addition of the *Aegilops tauschii* D genome to tetraploid durum wheat, thereby enabling hexaploid wheat to adapt to a much wider agroecological range from the subtropics to high latitudes, and to provide a wider diversity of food uses (Hancock, 2012c).

The global agricultural patterns that have evolved over many centuries are now threatened by unprecedented climatic changes. Levels of CO₂ and various pollutants will continue to rise with unprecedented population growth, associated rises in both minimum and maximum temperatures, and in-crop temperature spikes which are expected to be beyond those experienced in crop evolution (Lobell et al., 2008). Levels of soil moisture available to crops may be less reliable in regions dependent on rain-fed agriculture, as precipitation patterns change to become more irregular. Worldwide agriculture will be challenged both to feed an ever increasing population and to adapt to more unpredictable local environments, as crop stresses become more severe this century (Hatfield and Prueger, 2015).

This chapter will review the role of plant genetic resources under potential scenarios for world agriculture to address the challenges of climate change and population increase, and outline research initiatives for major crops put forward by the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), the International

Institute for Tropical Agriculture (IITA) and the International Center for Agricultural Research in the Dry Areas (ICARDA).

9.2 Climate Change and Agriculture

Climate change adaptation strategies include:

- Crop-specific relocation to more reliable, stable zones;
- changing to stress tolerant crops within existing zones;
- targeting of intra-specific genetic diversity for abiotic stress tolerances;
- breeding across gene pools within species;
- crop wild relatives as a source of novel genetic diversity for abiotic stresses;
- application of genetic engineering tools to enhance stress tolerances, and
- exploration of under-utilised species (Padulosi et al., 2011).

9.3 Adjusting Crop Distribution

Crops for high value processing, such as viticulture for wine, may shift to other production areas. Wine grape production may shift from semi-arid regions in southern Australia to cooler and moister regions further south in Tasmania (Webb et al., 2011). Rainfed barley cultivation is expanding to dry areas in the temperate cropping zone due to their earliness, allowing them to escape the increasing frequency of late droughts (Siddique et al., 1990).

Pearl millet followed by sorghum is more adapted to low rainfall than maize, and both provide more suitable alternatives to maize as cropping zones contract with climate change in sub-Saharan Africa (Lobell et al., 2008). However, there is a comparative premium for maize as a food, and hence a cultural imperative to investigate options for breeding drought and heat stress tolerant maize (Cairns et al., 2013). Since their introduction to various agri-ecological zones in sub-Saharan Africa in the 15th century, maize, common beans (*Phaseolus*), peanuts, pigeon peas, and wheat have become important locally produced foods, but a question remains as to whether new cultural transitions to alternative food sources can be achieved over a much shorter time frame, within this century, driven by climate change.

9.4 Within Crop Genetic Diversity for Abiotic Stress Tolerances

Widely distributed crops may include landraces or farmers' varieties at village level that are adapted to extreme environments. In West Asia and North Africa, wheat and barley landraces are still widely used under harsh conditions in the drylands and mountainous areas showing their inherent adaptation to drought and extreme temperatures and to low input agriculture (Mazid et al., 2013). Traditional 'Fadama' wheats in northern Nigeria were sown in wide rows up to one (1) m apart in flood plains as rivers receded after the summer rains, with no further water supply. Chipping of the clay soil between

rows kept weeds down and created a mulch, thus conserving water (Redden et al., 1979). These wheats have yet to be tested for drought tolerance under different agro-ecological conditions.

A few cowpea landraces in a large collection from sub-Saharan West Africa exhibited seed set when exposed to temperatures above 40°C in Nevada, and were confirmed to have heat tolerance for pollen development in controlled environments (Hall, 2011).

Using climatic histories of pea landrace collection sites in China, Li Ling et al. (2013) prioritised pea accessions for frost tolerance during flowering. Some of these accessions have now been shown to likely possess frost tolerance with field screening in a frost prone location near Handorf, in the Adelaide hills, Australia (Davies et al., 2016 in preparation). Collection of landraces from extreme agro-ecological environments can provide germplasm that is useful in breeding for abiotic stress tolerances, provided that there are good screening procedures in place, since landraces occurring in regions of abiotic stress could have escape mechanisms such as very early flowering (Hall, 2011).

9.5 Broadening the Available Genetic Diversity Within Crops

Inter-crossing of previously isolated gene pools within crops has proved beneficial for improved grain yield, with backcrossing of winter X spring wheat hybrids into respective winter and spring wheat breeding programs of the International Centre for Wheat and Maize Improvement (CIMMYT) (Kronstad and Rajaram, 1990), and for wider adaptation and yield improvement of rice for African environments from crosses between *Oryza indica* x *Oryza glaberrima* (Fujii et al., 2004). Inter-crossing of the separately evolved Meso-American and Andean (plus north-Andean) gene pools of common bean (*Phaseolus vulgaris* L.) generated new sources of disease resistances and nutrition for each gene pool and increased the available genetic diversity for exploitation in targeted breeding programs (Islam et al., 2002).

9.6 Crop Wild Relatives as a Novel Source Of Genetic Diversity

Crop wild relatives (CWR) provide an important source of novel genetic diversity for crop improvement. They include progenitors and cross-compatible species in the primary and secondary gene pools (embryo rescue may be required for difficult to cross relatives), and the tertiary gene pool of more distantly related relatives, from which novel genes can only be introgressed with genetic engineering or special techniques. While the collection of CWR in the field can be targeted for stress tolerance by researching the climate histories and agro-ecological characteristics of potential collection sites, this does not guarantee success. Antecedent gene pool diversity, genetic bottlenecks, recent selection environments and evolution of escape mechanisms are potential complications (Baute et al., 2015). Careful screening and verification are also needed to check whether gene expression in CWR can be successfully introgressed into the improved genetic backgrounds of crops (Tanksley and McCouch, 1997, Baute et al., 2015).

Major gene traits for disease resistance have been successfully introgressed into wheat from tertiary CWR (Zhang et al., 2004, Falim et al., 2012); however, abiotic

stress tolerance expressions are often complex and controlled by QTLs which are more difficult to introgress, with expression also affected by the genetic background (Reynolds et al., 2009).

Yield improvements have been achieved in tomato (Iltis 1988, Tyack and Deppenwolf, 2015) and wheat (Ortiz et al., 2007) with CWR introgressions, and CWR contributed drought stress tolerance in synthetic wheats (Lage and Trethowan, 2008, Jones, Gosman Horsnell et al., 2013), though it may be necessary to break linkages with undesirable traits. In the CIMMYT wheat breeding program, synthetics, or reconstructed hexaploid wheats from *Triticum durum* X *Aegilops tauschii* crosses, have been widely used to select for resistances to diseases and insects, tolerance of drought, heat and salinity stresses, and for grain yield improvement (Ogbonnaya et al., 2008, Ortiz et al., 2007, Ortiz 2015).

The tetraploid *Brassica napus* (canola) with A and C genomes has been enhanced for both major genes and quantitative traits with introgressions from CWR and from diploid progenitor crops [*B. rapa* (A genome), and *B. oleracea* (C genome)] and other tetraploid *Brassica* crops, and in *B. napus* resynthesised from the diploid progenitors (Salisbury and Barbetti, 2011). Major genes have been introgressed from CWR for disease and pest resistance traits, and for male sterility into rice, as well as quantitative traits for drought tolerance, grain yield and biomass, and there have been similar CWR contributions for improvement of durum wheat, maize, potato, chickpea and lentil (Porceddu and Damania, 2015).

9.7 Genomics, Genetic Variation and Breeding for Tolerance of Abiotic Stresses

Candidate genes for drought/heat adapted traits have been identified in the domestic gene pools of crops, for expression of osmotic adjustment, transpiration efficiency, photosynthetic resilience and levels of water soluble carbohydrates (Xue and McIntyre, 2011). However, the molecular bases of such trait expressions are often unknown, even with identification of many stress induced processes and factors, such as anti-oxidant enzymes, reactive oxygen species molecules (ROS), osmoprotectant protein stabilisers and heat shock chaperones. A stress associated trait may be linked to an expression change in another trait or yet to be identified biochemical process (Xue and McIntyre, 2011). In addition, acclimation of plants to stress may increase expressions of stress tolerance genes. Plants have evolved many regulatory loci for stress mediating genotypic interactions with the external environment, including photoperiod adaptation, changes in the mRNA levels of genes for removal of ROS, signaling proteins and proteins for post transcriptional regulation of RNA, and enzymes for key pathways of DREB, and abscisic acid syntheses (Xue and McIntyre., 2011, Weller et al., 2012).

The molecular bases of these processes are increasingly amenable to investigation with next generation sequencing (NGS), as well as more traditional approaches such as EST sequences in genome wide searches for phenotypic expressions. However, positional cloning of a gene/regulatory sequence associated with a phenotypic expression is not proof of causation (Langridge and Fleury, 2011).

NGS has an application in the discovery of single nucleotide polymorphisms, association mapping and markers for introgressions from wild relatives and from alien species (Varshney et al., 2009). Further advances to a third generation technology can

be expected in the future, as well as analyses of allopolyploid genomes with homologous syntenies for enhancing both yield and nutritional traits (Xue and McIntyre, 2011, Walley and Moore, 2015).

For many crops novel genes for drought and for heat tolerance from CWR can be identified with molecular tools such as genome wide searches of comparative functional genomics, and analyses of known candidate genes (Upadhyaya et al., 2011). Although gene transcripts from CWR may differ widely from those for crops, CWR sequences are increasingly available with a high density of markers for crop progenitors, such as *Cicer reticulatum* for chickpea and *Aegilops tauschii* for bread wheat (Jhanwar et al., 2012, You et al., 2011). Such markers, in combination with physiological and biochemical knowledge of traits, can assist with NGS mapping of differentially expressed functional genes (Xue et al., 2008, Varshney et al., 2009). NGS enables germplasm collections to be screened for novel alleles from CWR (Langridge and Fleury, 2011).

Transgenic techniques expand options for sourcing novel traits; via inter-specific DNA transfer with agrobacterium infection, genome editing of targeted lesions, mutagenic 'Tilling' to introduce a single DNA base change mirroring CWR variation; screening of CWRs for sequenced polymorphisms and 'Ecotilling' comparison with a reference crop relative (Walley and Moore, 2015). Transfer of synthesised DNA into target organisms is also envisaged. These developments considerably widen the range of available genetic variation for improving the tolerances of crops to drought and heat stresses.

9.8 Under-utilised Species

Crops with restricted regional distribution, and neglected species, could play an important role in the adjustment of agriculture to future climate change uncertainties in temperature and rainfall. Such species include a wide range of end-uses, food, beverages, oil, nutrition, aromatics, fibre and medicine, but have been little researched (Padulosi et al., 2011). Strategically, they provide a diversified agricultural portfolio with improved opportunities for agriculture to withstand climate change, through resilience of agroecosystems.

The west African Bambara groundnut (*Vigna subterranea*) is drought tolerant and adapted to harsh climates and marginal soils, but has unpredictable yield and a long cooking time (Padulosi et al., 2011). Similarly, various minor millets in southern India are drought resistant and have excellent nutrition. *Chenopodium pallidicaule*, known locally as kañiwa and having notable frost tolerance, is cultivated around Lake Titicaca, in Bolivia and Peru. Stress tolerant perennial species for food and nutrition with exceptional abiotic stress tolerances include tamarind, custard apple, neem, Indian gooseberry and the drought hardy trees of *Promopsis* spp. (Padulosi et al., 2011). These under-utilised species provide options for coping with the risks of climate change, and to anticipate possible shocks by adjusting planting dates and using crop mixtures. However, there is a conservation gap, with a general absence of under-utilised species conserved *in-situ* in national ecological reserves, or *ex-situ* in gene bank collections.

In temperate crop zones, dryland fruit trees (olive, almond, etc.) and several species found in forests such as *Argana spinosa*, *Crateagus* sp., *Zizyphus* sp. have the potential to be grown in dry areas using water saving irrigation and rain water harvesting techniques.

Under-utilised species can provide new agricultural opportunities with climate change. Holubec et al. (2015) describe the recent domestication of honeysuckle berry (*Lonicera caerulea* L.) and other wild fruits in sub-arctic zones for their nutritional and medicinal value, with the transition to domestication proceeding stepwise from collection of genetic resources to cultivation and plant breeding. This is a case where global warming may assist the development of new crop options.

Agriculture may adjust to climate change in various ways; with agro-ecological farming systems, increased local crop diversity for food risk management, genetic engineering techniques with exploitation of CWR for genetic adaptation of major crops, and increased attention to under-utilised crops.

9.9 Genetic Resources in the Low Rainfall Temperate Crop Zone

The International Center for Agricultural Research in the Dry Areas (ICARDA) with a CGIAR mandate for agricultural development in the non-tropical drylands is playing a crucial role in conserving and using genetic resources of cereals, food legumes, temperate forages and range species. Its active collection contains around 150 000 accessions most of which are landraces, wild relatives and native species, collected mainly from the Vavilovian Centers of diversity in the Mediterranean, Fertile Crescent, Abyssinian and Central Asia regions (Table 9.1).

New collecting missions are organized annually based on the gap analysis using DIVA-GIS tool (www.diva-gis.org; Hijmans et al., 2005) to fill the geographic distribution gaps in the existing collections but also to target landraces and wild relative species for climate change adaptive traits such as drought, heat and salinity tolerance. Landraces, wild relatives and forage and range species with such traits are selected

Table 9.1 Total number of accessions held in-trust by ICARDA genebank (as of February 2015).

Crop	Number of accessions
<i>Aegilops</i>	4282
Bread wheat	14 731
Durum wheat	19 797
Primitive wheat	913
Wild <i>Triticum</i>	1607
Barley	29 703
Wild <i>Hordeum</i>	2058
Total cereals	73 091
Total food legumes	31 747
Total forages and range species	43 209
Total genebank holdings	148 047

using aridity index, soil salinity maps and information acquired during the missions either from national experts or through local knowledge of communities. In wheat, species such as *Aegilops kotchyii*, *Ae. searsii*, *Ae. vavilovii* could provide potential genes for drought and heat tolerance and *Ae. biconis* is known to have high salt tolerance.

The continuum between collecting, conserving and using is very important in developing new varieties with higher and stable yields and with better end-use quality. Therefore, mining genebanks holdings for useful traits is an important step towards efficient use of genetic resources. Focused Identification of Germplasm Strategy (FIGS), developed by ICARDA and its partners in Australia and the Vavilov Institute in Russia, presents an alternative to the random sub-setting and core collection efforts, enabling the identification of sought traits in manageable sized subsets constructed specifically for each trait (Street et al., 2008). FIGS approach uses the environmental information of the germplasm collection to develop algorithms correlating the environmental parameters with the traits of interest. This approach has shown its relevance in identifying useful traits in cereals and food legumes (El-Bouhssini et al., 2009, Endresen et al., 2011, Bari et al., 2012, Khazaei et al., 2013), and is now routinely used at ICARDA for rationalizing the distribution of accessions held in its genebank. The efficiency of FIGS approach in mining genetic resources is proven by identifying novel diversity for several stresses (Table 9.2), and is used to rationalize the distribution of accessions to allow partners to get subsets with higher frequencies to find sought traits.

The subsets are jointly evaluated with other researchers, and selected landraces and genetic stocks identified to have valuable genes are used as parental germplasm by breeders. However, when genes are identified in wild relatives, an important pre-breeding step is required which will introgress genes of interest into advanced breeding lines of crops without dragging along linked undesirable genes. The value of pre-breeding is shown in case of wheat through the widening of the genetic base of both bread and durum wheats using *Aegilops* and wild *Triticum* species. Bread wheat has benefited from the synthetic hexaploid wheat crosses and more than 35% of the elite breeding germplasm generated by CIMMYT and ICARDA include genes derived from *Aegilops tauschii* (Ogbonnaya et al., 2013). Durum wheat improvement at ICARDA has benefited from crosses with *Triticum turgidum* subsp. *dicoccoides* and other wild and primitive *Triticum* species for resistance to biotic and abiotic stresses and for quality

Table 9.2 New sources of resistance/tolerance to major biotic and abiotic stresses identified using the Focused Identification of Germplasm Strategy (FIGS).

Crop	Biotic and abiotic stress	References
Wheat	Russian wheat aphid	El-Bouhssini et al., 2011
	Hessian fly	El-Bouhssini et al. 2014
	Sunn pest	El-Bouhssini et al. 2009
	Rusts	Bari et al., 2012; Andressen et al., 2012 ; Bari et al., 2014
Faba bean	Drought	Khazaei et al., 2013

attributes (Porceddu and Damania, 2015). Similarly, the wild progenitor of barley, *Hordeum vulgare* subsp. *spontaneum* could provide valuable traits to cultivated barley.

Ex situ conservation of genetic resources should be complemented with efforts to promote the *in situ*/on-farm conservation of landraces and wild relatives mainly in hot spot diversity areas or in areas where genes of climate adaptive traits could be found. This approach allows the dynamic conservation of a larger genetic base along with associated local knowledge (Maxted et al., 1997).

Efforts are undertaken jointly with CIMMYT to genotype all wheat genebank accessions to be able to use genotyping information to target novel allelic variation for various traits and to conduct association mapping.

9.10 Forage and Range Species

Livestock play a major role in sustaining the livelihoods of local communities living under harsh conditions in Central and West Asia and North Africa region (CWANA) and in mitigating and adapting to climate change adversity. In dry areas, local breeds are predominant and their feeding is tightly linked to the availability of forages and access to rangelands. However, range species are subject to intensive overgrazing which has reduced their share in the livestock feeding calendars, calling for collective efforts to improve and better manage the rangelands through rehabilitation and restoration using drought and heat tolerant native species (Peacock et al., 2003). For most of these species and local livestock breeds, *in situ*/on-farm conservation and sustainable use of rangelands need to be promoted through community-based approaches using low-cost technological, institutional, value adding and alternative income options along with enabling policies.

9.11 Genetic Resources in the Humid Tropics

The International Institute for Tropical Agriculture (IITA) is a CGIAR Institute based in sub-Saharan Africa (SSA) and focusing on research for food security and poverty alleviation in that region (<http://www.iita.org>) as described in its refreshed strategy (IITA, 2012). It has breeding programs for maize, cowpea, soybean, cassava, yam and banana/plantain which have had significant impact on livelihoods in many countries across Africa. The Genetic Resources Center (GRC) of IITA is based at its headquarters in Ibadan, Nigeria and holds important international collections with a total of around 33 000 accessions (Table 9.3). These are predominantly of the staple crops that IITA breeds but in addition it has germplasm of a number of less widely grown crops, often described as 'orphan' or neglected and underutilised species, with considerable potential for a greater role in agriculture. Amongst these are African yam bean (*Sphenostylis stenocarpa*), Bambara groundnut (*Vigna subterranea*) and taro or cocoyam (*Colocasia esculenta*).

The cowpea collection, with 15 000 accessions, is the largest of this species in the world with strong representation from SSA, particularly West Africa. Core and mini core collections have been developed in this crop and widely utilised (Mahalakshmi et al., 2007). This crop has several near relatives, which are potentially important sources of resistance to diseases and pests. The parasitic weed *Striga* is an important cause of yield losses of

Table 9.3 Germplasm Accessions held at the Genetic.

Resources Centre, IITA.	Number of accessions
Cowpea (<i>Vigna unguiculata</i> L.)	15 379
Soybean (<i>Glycine max</i> L. Merr)	4841
Cassava (<i>Manihot esculenta</i> Crantz)	3499
Yam (<i>Dioscorea</i> spp.)	3156
Bambara groundnut (<i>Vigna subterranea</i> L. Verdc)	1752
Maize (<i>Zea mays</i> L.)	1565
Miscellaneous legumes	558
Wild Vigna (<i>Vigna</i> species L.)	1543
Banana/plantain (<i>Musa</i> spp.)	546
African yam bean [<i>Sphenostylis stenocarpa</i> (Hochst.) Harms]	456

cowpea in the Guinea savannah and Sudan savannah zones of West Africa (Tignegre et al., 2013). Resistance to this parasite has been observed in wild relatives but crossing barriers remain a challenge. Recent work at IITA has shown that landraces from the same geographical areas as resistant CWRs also show resistance but this requires further confirmation and utilisation in variety development.

Climate change predictions for SSA show that in many areas the challenges of drought and heat are likely to grow in the coming decades (Lobell et al., 2011). This is of particular concern in the savannah areas south of the Sahel, but the predicted changes in rainfall patterns mean that drought tolerance will also be an important trait in crops such as yam which are commonly grown in the humid forest zone further south. The drought tolerant maize for Africa (DTMA) project has developed new varieties of this crop for the low and mid altitudes of West Africa (Tambo and Abdoulaye, 2012).

Cassava (*Manihot esculenta*) is a staple food across many parts of Africa. Breeding programs at IITA are developing varieties with increased yield, disease resistance and quality attributes including increased levels of beta-carotene (Boakye et al., 2013). Some studies have indicated that cassava may become even more important in parts of Africa in the future as climate change increases its relative advantage over other crops (Jarvis et al., 2012).

Yams (*Dioscorea* spp.) are a multi-species crop with two predominant cultivated types *D. rotundata* and *D. alata* and some close relatives. *D. rotundata* in particular is a very important crop in West Africa and yam breeding at IITA has utilised the more than 3300 accessions held by GRC. As with other crops, molecular methods are increasingly being applied to yams to characterise diversity, identify potential duplicates and associate genotypic differences in key traits.

It seems likely that one effective approach to enhanced food security is to increase the role of crops that are currently underutilised or grown on relatively small areas and where research and breeding efforts have been very limited. This may be particularly the case when we consider the importance of nutritional security (diet quality, for instance mineral and vitamin intake) as well as calorific intake alone.

A number of underutilised crops have significant potential, particularly within systems where their nitrogen fixation abilities can play a major role in enhancing soil fertility for other crops. For example, African yam bean is a leguminous crop which is considered to have considerable unrealised potential to contribute to food security in many parts of sub-Saharan Africa (Adewale et al., 2015). However, as with many 'orphan' crops there is a lack of good data about current production and usage. More studies have been carried out on Bambara groundnut and again this crop has considerable potential. Studies are underway to analyse the variation in drought tolerance between accessions of this crop, with collaboration between IITA and the Crops For the Future Research Centre (CFFRC) who have previously carried out a number of studies on the genetics and breeding of this crop (OluKolu et al., 2012).

9.12 Genetic Resources in the Semi-arid Tropics and Representative Subsets

ICRISAT genebank at Patancheru, India has the largest collections of chickpea, groundnut, pigeonpea, pearl millet, and sorghum and of six small millets, totalling 123 921 accessions from 144 countries (<http://www.icrisat.org/gene-bank-home.htm>; accessed on December 31, 2015). About 90% of these germplasm collections are preserved under long term storage (-20°C) and 100% under medium term storage (4°C and 20-30% RH) conditions. ICRISAT made a safety deposit of 108 352 germplasm accessions at the Svalbard global seed vault (SGSV), Norway for preservation under permafrost conditions. About 96% of the total collection has been characterized for morpho-agronomic traits using prescribed descriptors, and 45% for seed nutritional traits (mostly oil and protein contents).

Reduced subsets such as core (Frankel, 1984) and mini core (Upadhyaya and Ortiz, 2001) collections, selected on the basis of passport, characterization and evaluation data to represent the diversity of the entire collection, have been recognized as a gateway to enhance utilization of germplasm in plant breeding. Both core and/or mini core collections (Tables 9.4–9.5) and genotype-based reference sets (www.generationcp.org) have been formed for ICRISAT mandate crops. These representative sets are available to researchers globally after signing the Standard Material Transfer Agreement (<http://10.3.1.36:8080/what-we-do/crops/SMTA.pdf>) with ICRISAT. The concept and process of forming mini core collections (Upadhyaya et al., 2009a) has been recognized as 'International Public Goods'.

9.13 Plant Phenomics

Precise phenotyping is the key to finding gene(s) and its allelic variants, analyze their expression, and thereafter introduce agronomically beneficial alleles into new cultivars. Plant phenomics is a rapidly emerging area and comprises tools that offer a suit of new technologies to accelerate progress in understanding gene function and environmental responses. It will bridge the gap between genomics, plant function and agricultural traits and will enable breeders to develop improved germplasm or cultivars with specific

Table 9.4 Core collections in ICRISAT mandate crops and small millets.

Crop	Accessions used (#)	Traits used (#)	Core collection accessions (#)	Reference
Barnyard millet	736	21	89	Upadhyaya et al., 2014b
Chickpea	16 991	13	1956	Upadhyaya et al., 2001
Finger millet	5940	14	622	Upadhyaya et al., 2006a
Foxtail millet	1474	23	155	Upadhyaya et al., 2008
Groundnut	14 310	14	1704	Upadhyaya et al., 2003
Kodo millet	656	20	75	Upadhyaya et al., 2014b Upadhyaya et al., 2014b
Little millet	460	20	56	
Pearl millet	20 844	22	2094	Upadhyaya et al., 2009b
Pigeonpea	12 153	14	1290	Reddy et al., 2005
Proso millet	833	20	106	Upadhyaya et al., 2011c
Sorghum	22 474	21	2247	Grenier et al., 2001

Table 9.5 Mini core collections of ICRISAT mandate crops and small millets.

Crop	Entire collection (#)	Mini core collection accession (#)	% of entire collection	Traits used (#)	Reference
Chickpea	16 991	211	1.24	16	Upadhyaya and Ortiz, 2001
Finger millet	5940	80	1.34	18	Upadhyaya et al., 2010
Foxtail millet	1474	35	2.37	21	Upadhyaya et al., 2011b
Groundnut	14 310	184	1.28	34	Upadhyaya et al., 2002
Pearl millet	20 844	238	1.14	12	Upadhyaya et al., 2011d
Pigeonpea	12 153	146	1.2	16	Upadhyaya et al., 2006b
Sorghum	22 473	242	1.08	21	Upadhyaya et al., 2009c

attributes (Furbank and Tester, 2011; Cabrera-Bosquet et al., 2012). Phenomics include both forward and reverse approaches. The former uses phenotyping tools to screen germplasm for valuable traits, while the latter dissects traits to discover their mechanistic understanding and allow exploitation of this mechanism to enhance the trait value into new germplasm. To date, a number of automatic-high throughput plant growth and phenotyping platforms have been established to study, for example, root system architecture, assess biomass production and partitioning, diagnose and quantify plant responses to stresses, predict quality attributes of the produce, and provide images of plant phenotypes with low-cost 3D systems (Cobb et al., 2013; Fiorani and Schurr, 2013; Araus and Cairns, 2014; Paulus et al., 2014). ICRISAT has established an imaging platform, called LeasyScan, combined with lysimetric capacity to assess canopy traits affecting water use (Vadez et al., 2015). This platform has the potential to phenotype for traits

controlling plant water use at a high rate and precision and creates an opportunity to harness their genetics for breeding of improved cultivars. Combined with crop simulation modelling, the deciphering of trait variation can potentially allow testing the effect of altering genetic traits on plant performance across time and geographical scale.

9.14 Discovering Climate Resilient Germplasm Using Representative Subsets

9.14.1 Multiple Stress Tolerances

A systematic evaluation of mini core collections has generated a number of germplasm lines resistant to abiotic and/or biotic stresses (Tables 9.6–9.7). A few of these lines also showed resistance to more than one stress, for example, accessions with multiple resistance traits in chickpea were ICC 6874 and ICC 14 402 (drought, salinity, heat, fusarium wilt, legume pod borer), ICC 12 155 (drought, salinity, heat, fusarium wilt, botrytis gray mould), ICC 335 (drought, salinity, fusarium wilt, herbicide), ICC 6279 (salinity, fusarium wilt, botrytis gray mould), and ICC 2580 (drought, salinity, herbicide) (Upadhyaya et al., 2013), while in groundnut, multi-trait accessions were ICG 12 625 (drought, low temperature, late leaf spot (LLS), aflatoxin, bacterial wilt), ICG 1668 (heat, LLS, peanut bud necrosis disease, bacterial wilt), ICG 2925 (heat, LLS, rust), ICG 8285 (drought, heat, salinity), and ICG 11 426 (early leaf spot, LLS and rust) (Upadhyaya et al., 2014a). The multi-trait germplasm identified both in chickpea and groundnut on average produced 1.5 to 2.0 t ha⁻¹ pod/seed yield.

9.14.2 Drought Tolerance

Conservative water use (less use during the vegetative growth stage could keep more soil water available during reproductive growth) (Zaman-Allah et al., 2011; Vadez et al., 2013) plus drought avoidance root traits (Kashiwagi et al., 2015; Purushothaman et al., 2013) are associated with improved grain yield of chickpea under drought stressed environments. Canopy temperature depression in chickpea measured at 62 days after sowing is positively associated with grain yield and biomass. A cooler canopy temperature at mid reproductive stage can thus be used as selection criterion for drought tolerance as it ensures greater grain yield in drought-stressed environments (Purushothaman et al., 2015). Increased water use efficiency (WUE) in groundnut confers adaptive advantage under abiotic stress conditions. Specific leaf area (SLA) and SPAD chlorophyll meter reading (SCMR) have been suggested as surrogate traits for selecting for high WUE in groundnut (Nageswara et al., 2001), although their relevance has been questioned (Vadez et al., ICRISAT, pers. commun.).

Access to water from the soil at key physiological stages is important for adaptation to drought. When assessing differences in water uptake under terminal drought stress, Vadez et al. (2013) found that drought sensitive pearl millet yielded 30-100% lower than that of tolerant lines under water stress. More importantly, they found that total volume of water extracted by tolerant and sensitive genotypes were similar under water stress; however, tolerant genotypes extracted less water prior to anthesis, and more water after

Table 9.6 Sources of resistance to abiotic stress reported using mini core collections in chickpea, pigeonpea, groundnut, finger millet and foxtail millet.

Stress	Abiotic stress resistant germplasm	Reference
Chickpea		
Drought	ICC# 283, 456, 637, 708, 867, 1205, 1422, 1431, 1882, 2263, 2580, 3325, 4495, 4593, 4872, 5337, 5613, 5878, 6874, 7272, 7323, 7441, 8261, 8950, 10399, 10945, 11121, 11944, 12155, 12947, 13124, 14402, 14778, 14799, 14815, 15868, 16524, 16796 ICC 751	Reviewed in Upadhyaya et al., 2013 Kashiwagi et al., 2013
Salinity	ICC# 283, 456, 708, 867, 1431, 2263, 2580, 3325, 4495, 4593, 4872, 5613, 5878, 6279, 6874, 7272, 7441, 8261, 9942, 10399, 10945, 11121, 11944, 12155, 13124, 14402, 14778, 14799, 15868, 16524, 16796	Reviewed in Upadhyaya et al., 2013
Heat	ICC# 283, 456, 637, 708, 1205, 1882, 2263, 4495, 5613, 5878, 6874, 7441, 10945, 11121, 11944, 12155, 13124, 14402, 14778, 14799, 14815, 15868	
Chilling stress	Reproductive stage: ICC 16348 and ICC 16349	Kumar et al., 2011
Groundnut		
Drought	ICG# 434, 442, 862, 1274, 2106, 2511, 3053, 3584, 3673, 5475, 5663, 6646, 8285, 8567, 10554, 11088, 11855, 12625, 14475	Reviewed in Upadhyaya et al., 2014a
Salinity	ICG# 4729, 5236, 862, 1668, 2925, 8285, 11219, 12879, 15042	
Salinity	ICG# 442, 862, 2106, 8285, 9842, 11855	
Low temperature	ICG# 1274, 5475, 5609, 10554, 11088, 12625	
P deficiency	ICG# 442, 3584, 3673, 5609, 5663, 9842, 14475	
Pigeonpea		
Water logging	ICP# 1279, 4575, 5142, 6370, 6971, 6992, 7057, 7148, 7375, 7426, 8012, 8255, 10228, 10397, 11320, 11477, 12515, 13571, 13577, 14294, 14444, 14900, 14903, 16309	Krishnamurthy et al., 2012
Finger millet		
Salinity	IE# 518, 2034, 2217, 2790, 2872, 3045, 3077, 3391, 3470, 3973, 4073, 4329, 4671, 4673, 4757, 4789, 4795, 4797, 5066, 6154, 6165, 6326	Krishnamurthy et al., 2014a
Foxtail millet		
Salinity	Ise# 96, 254, 388, 480, 869, 969, 995, 1629, 1851, 1888	Krishnamurthy et al., 2014b

Table 9.7 Sources of resistance to biotic stress reported using mini core collections in chickpea, groundnut, pigeonpea, pearl millet, sorghum, finger millet and foxtail millet mini core collection.

Stress	Biotic stress resistant germplasm	Reference
Chickpea		
Fusarium wilt	ICC# 1710, 1915, 2242, 2277, 2990, 3325, 4533, 5135, 6279, 6874, 7184, 7554, 7819, 9848, 12 028, 12 037, 12 155, 13 219, 13 441, 13 599, 13 816, 14 199, 14 402, 14 831, 15 606, 15 610	Reviewed in Upadhyaya et al., 2013
Dry root rot	ICC# 1710, 2242, 2277, 11 764, 12 328, 13 441	
Ascochyta blight	ICC# 1915, 7184, 11 284	
Botrytis gray mold	ICC# 2990, 4533, 6279, 7554, 7819, 9848, 11 284, 11 764, 12 028, 12 037, 12 155, 12 328, 13 219, 13 599, 13 816, 14 199, 15 406, 15 606, 15 610	
Legume pod borer	ICC# 3325, 5135, 6874, 14 402, 14 831, 15 406, 15 606	
Herbicide	ICC# 2242, 2580, 3325	
Groundnut		
Early leaf spot	ICG# 2857, 6022, 6402, 11 426	Reviewed in Upadhyaya et al., 2014a
Late leaf spot	ICG# 76, 532, 1668, 2857, 2925, 4156, 4412, 6402, 6993, 7243, 8760, 9037, 9777, 9842, 9961, 4684, 6022, 11 109, 12 000, 11 426, 12 276, 12 625, 12 672, 12 697, 13 787, 15 190	
Rust	ICG# 76, 532, 2381, 2857, 2925, 4412, 6993, 7243, 8760, 9037, 9842, 9961, 9777, 11 109, 11 426, 12 000, 12 697, 13 099, 13 787, 14 008	
<i>Aspergillus flavus</i>	ICG# 76, 2381, 4156, 6402, 8760, 12 625, 12 697, 13 787	
Peanut bud necrosis disease	ICG# 76, 1668, 4412, 4684, 11 109, 12 000, 12 672, 13 099, 14 008, 14 482, 15 190,	
Bacterial wilt	ICG# 76, 1668, 12 625	
Pigeonpea		
Fusarium wilt	ICP# 6739, 8860, 11 015, 13 304, 14 638, 14 819	Sharma et al., 2012a
Sterility mosaic	ICP# 3576, 6739, 6845, 7869, 8152, 8860, 9045, 11 015, 11 059, 11 230, 11 281, 11 320, 11 321, 11 823, 11 910, 12 410, 13 167, 13 304, 13 579, 13 633, 14 819, 14 976, 15 049, 15 185	
Pearl millet		
Blast	IP# 7846, 11 036, 21 187 resistant to four pathotypes, with 32 accessions having resistance to at least one pathotypes	Sharma et al., 2013
Downy mildew	A number of accessions resistant to individual pathotypes (Sg 384, Sg 409, Sg 445, Sg 457, Sg 510, Sg 519, Sg 526, and Sg 542), while IP# 9645, 11 943, 14 537, 14 542, 14 599, and 21 438 to multiple-pathotypes (6-7)	Sharma et al., 2015

Table 9.7 (Continued)

Stress	Biotic stress resistant germplasm	Reference
Sorghum		
Anthraco-nose, leaf blight and rust	13 accessions resistant to anthracnose, 27 to leaf blight and six to rust; with IS 473, 23 521, 23 684 being resistance to all three diseases	Sharma et al., 2012b
Grain mold	Fifty accessions resistant to downy mildew with disease incidence <10%, including IS 12 706, 26 701, 29 241, 29 269, 29 314, and 29 335 combining resistance and good agronomic traits	Sharma et al., 2010
Downy mildew	IS# 23 992, 27 697, 28 449, 28 747, 30 400, and 31 714 (disease incidence <10%); IS# 23 992 having resistant to downy mildew and grain mold	
Finger millet		
Blast	Fifty-eight accessions resistant to both neck and panicle blast, correlation between neck and panicle blast 0.92; IE# 1022, 2821, 2872, 4121, 4491, 4570, 5066, 5091, and 5537 being agronomically and nutritionally superior lines	Kiran Babu et al., 2013
Foxtail millet		
Blast	Sixteen accessions resistant to blast, with ISe 1181 and 1547 being resistant to leaf, sheath, neck, and panicle blast against four isolates	Sharma et al., 2014

anthesis and this increased water uptake after anthesis resulted in higher grain yield under terminal drought in pearl millet.

Kapanigowda et al., (2013) evaluated 140 exotic sorghum germplasm and adapted lines under irrigated and drought stressed environments, found differences in chlorophyll content, chlorophyll *a* fluorescence, leaf temperature, grain yield, and harvest index, and identified drought tolerant germplasm (PI# 510898, 53 3946, 55 0590, and 56 2166, and IS# 1212 and 2872) as evidenced by higher grain yield under drought stressed conditions.

9.14.3 Heat Tolerance

Devasirvatham et al. (2015) reported a number of chickpea accessions with varying intensity of heat tolerance. Phenology was negatively correlated with grain yield, while plant biomass, pod number, filled pod number and seed number per plant were positively correlated. Cold tolerant chickpea accessions were less affected by stress-related leaf injury and showed greater ascorbic acid and proline than cold-sensitive germplasm (Kumar et al., 2011).

High temperature (HT) stress affects grain yield in sorghum. HT stress decreases pollen viability, pollen germination, and seed set, and response of pollen to temperature varied among sorghum accessions. Genotypes with higher ceiling temperature for pollen germination (T_{max}) had a higher percentage of seed-set under HT stress

(Djanaguiraman et al., 2014). Further, response of seed set to high temperature in the field study is correlated to that in the controlled environment facility (CEF) ($R^2 = 0.69$) and poor seed set is not compensated by increased seed mass in either CEF or field experiments (Singh et al., 2015).

In pearl millet, large genetic variability in seed set at daily maximum temperature of $\geq 42^\circ\text{C}$ during flowering was noted among hybrid parental lines, germplasm and improved populations. The seed set started declining when maximum air temperature reached 42°C , reaching only 20% at 46°C . Boot-leaf-stage is more heat sensitive than panicle-emergence stage and the female reproductive system is more heat sensitive than pollen (Gupta *et al.*, 2015).

9.14.4 Tolerance of Soil Nutrient Imbalance

Soil phosphorous (P) deficiency and aluminum (Al) toxicity are the major constraints to sorghum productivity in sub-Saharan Africa. Higher P-acquisition efficiency from soils and improved internal physiological P-use efficiency are the main adaptation strategies adopted by the plants (Richardson et al., 2011). Tolerance to P-deficiency is measured by comparing the differences in grain yield between $-P$ and $+P$ soil conditions, and lines with least difference in grain yield are considered as tolerant to soil-P deficiency. West African sorghum germplasm showed abundant genetic variation both for P-acquisition and P-use efficiency (Leiser et al., 2014a, 2015). Landrace genotypes generally had higher P uptake and grain P concentration than formally bred-genotypes, which exhibited a higher P use efficiency (Leiser et al., 2014a). Grain yield under $-P$ and $+P$ conditions is significantly correlated ($r = 0.85$) (Leiser et al., 2014b).

9.15 Global Warming and Declining Nutritional Quality

Widespread micronutrient malnutrition results in an enormous negative cost to society. Global warming is associated with declining nutritional quality of food crops (Dwivedi et al., 2013). Limited research at ICRISAT has led to identification of seed nutrient dense [calcium (Ca), iron (Fe), and zinc (Zn)] germplasm, for example, 48 accessions high in Fe, 43 high in Zn, and 23 high in both Fe and Zn in groundnut (Upadhyaya et al., 2012) or 27 pearl millet accessions, mostly of Togo types, with high Fe and Zn (Rai et al., 2015). Small millet grains are highly nutritious. Two- to three-fold differences were noted in Ca among finger millet ($1.84 - 4.89 \text{ g kg}^{-1}$) and foxtail millet ($90.3 - 288.7 \text{ mg kg}^{-1}$) mini core collections, with several accessions having significantly greater Fe, Zn and Ca than controls (Upadhyaya et al., 2011a, b).

9.16 Crop Wild Relatives (CWR) - The Source of Allelic Diversity

CWR harbor gene(s) for resistance to stresses, agronomic and nutritional traits. Global use of CWR has been mainly concentrated on pest- and diseases-resistance (Dwivedi et al., 2008; Dempewolf et al., 2014; Heisey and Rubenstein, 2015). Establishing in situ

conservation of CWR, close to their natural habitats, allows new variation to arise and species to adapt to gradual changes in environmental conditions and biotic interactions. This will facilitate the capture of new variation for use and development of climate smart crops. Further, a targeted approach to develop a climate distribution map by plotting the natural occurrence of wild relatives (chickpea: Western Asia, specifically in South eastern Turkey and Syria; pigeon pea: South Asia, Southern and Eastern Africa, and Oceania; peanut: South America; pearl millet: West and Central Africa and South Asia; sorghum: Southern and Eastern Africa, West and Central Africa, South Asia, North America, and Australia) against corresponding temperature and precipitation will accelerate evaluation and capture of allelic diversity associated with abiotic stress tolerance.

Molecular and phenotypic variation assessment of ex situ genebank collections along with those recently collected from natural habitats provide opportunity to monitor changes in functional diversity arising as a consequence of climate change. For example, when wild emmer wheat (*Triticum dicoccoides*) and wild barley (*Hordeum spontaneum*) populations from Israel sampled in 1980 and again in 2008 were evaluated for flowering time and SSR allelic richness, Nevo et al., (2012) observed that populations collected in 2008 flowered earlier than those collected in 1980. They noted greater shortening of flowering after the 28-year period in wild barley (average, 10.94 d; range, 8.21-17.26 d) than in wild emmer wheat (average, 8.53 d; range, 7.19-10.45 d) populations. Wild emmer wheat lost more alleles (28) in response to 28 years of climate change than wild barley (10). Further, allele reduction in emmer is negatively correlated with altitude (-0.854*), humidity (-0.673*), and nearly significant with plant development formation (-0.568). In barley (without the Mt. Herman population), the difference is positively correlated with rainfall (0.790*) but negatively with evaporation (-0.692*) and plant development (-0.867*).

9.17 Introgression of Traits from CWR

The development of pre-breeding lines has long been advocated as a means to facilitate the transfer of genes from wild species. Pod borer (*Helicoverpa armigera*) is a major pest of chickpea and pigeonpea, with very low level of resistance in cultivated varieties. Resistance to pod borer in pigeonpea has been achieved by transferring resistance genes from *Cajanus acutifolius* and *C. platycarpus* into improved genetic background of cultivated pigeonpea (Mallikarjuna et al., 2011; Jadhav et al., 2012). Progenies involving cultivated and wild *Cicer* (*C. echinosperma*, *C. reticulatum*, *C. pinnatifidum*) are reported resistant to ascochyta blight (*Ascochyta rabiei*) and/or botrytis gray mould (*Botrytis cinerea*) in chickpea (Ramgopal et al., 2013; Kaur et al., 2013). Robust chilling tolerance at reproductive stage is reported in a *C. echinospermum* accession (Berger et al., 2012).

Leal-Bertioli et al. (2012) investigated drought related traits in cultivated (tetraploid) groundnut, its putative diploid progenitors (*A. duranensis* and *A. ipaënsis*), and synthetic varieties involving the putative donors. This study revealed that leaf area, stomata size, trichome density and transpiration profile of groundnut are substantially modified in diploid species (wild *Arachis*). Further, drought related traits in synthetics are substantially modified (i.e., tetraploidization offsets the characteristics of the wild diploids), which reveals that evaluation of synthetics is likely to be more informative than direct evaluation of wild diploids. Chromosome segment substitution lines

available in groundnut (Fonceka et al., 2012) should be investigated to find novel genetic variations for drought tolerance. Introgression lines originating from advanced backcross populations by crossing synthetics (Mallikarjuna et al., 2012) with cultivated groundnuts showed rust and late leaf spot resistance equal to that of synthetics. In addition, these lines also showed remarkable diversity offering greater opportunity to selection for agronomic traits (Kumari et al., 2014).

Sorghum races such as *vigratum*, *arundinaceum*, and *verticilliflorum* showed ecologically wide adaptation, for example, in African rainforests wherein cultivated sorghum is poorly adapted. These species thrive due to their greater drought and heat tolerance (Venkateswaran et al., 2014). *S. halepense* is adapted to very cold climates, while *S. propinquum* is adapted to the moist habitats of Southeast Asia (Upadhyaya et al., 2015). Thus, wild and weedy sorghum offer an immense opportunity to mine and transfer agronomically beneficial alleles to enhance adaptation of cultivated sorghum. Pearl millet is capable of reproducing successfully up to 42°C and it would be interesting to identify wild relatives especially from Sahel that can withstand higher temperature at their reproductive stage. *P. glaucum ssp. monodii* is the closest relative of pearl millet with abundant phenotypic diversity as observed in Sahelian region, where temperature increased by 0.2-0.8°C since the 1970s and is expected to rise further by 3-4°C (Sarr, 2012). Critical evaluation of *monodii* accessions is therefore suggested to identify drought and heat stress tolerant accessions for enhancing pearl millet adaptation to more severe drought and heat (at flowering) stress conditions.

9.18 Association Genetics to Abiotic Stress Adaptation

The diversity panels of germplasm collections, such as conventional core (Frankel, 1984)/ mini core (Upadhyaya and Ortiz, 2001) collections or reference sets (www.generationcp.org), are an ideal germplasm resource for studying linkage disequilibrium and association mapping in crop plants. Identification of candidate genes associated with abiotic stress response will accelerate breeding efforts aiming to enhance productivity under drought-stressed environments. Eighteen (18) SNPs in chickpea reference accessions were significantly associated with drought avoidance root traits, carbon isotope discrimination ($\delta^{13}\text{C}$), heat tolerance, harvest index (HI), and 100-seed weight under drought-stressed conditions (Thudi et al., 2014). Pandey et al., 2014 reported 152 significant marker trait associations (MTA) for six traits including SCMR, HI, and seed weight in the groundnut reference set under both well-watered and drought-stressed conditions.

Sehgal et al. (2015) detected significant MTA in pearl millet inbred germplasm association panel accessions. One SNP in the putative acetyl CoA carboxylase gene showed constitutive association with grain yield, grain harvest index and panicle yield under both irrigated and drought-stressed environments. Likewise, an indel in the putative chlorophyll a/b binding protein gene was significantly associated with stay-green and grain yield traits under drought stressed environments. This can be used as a functional marker for selecting high yielding genotypes with stay-green phenotype under drought stressed environments. Similar studies in sorghum on quantifying allelic associations with bioclimatic and soil gradients using 404 627 SNPs on 1943 georeferenced landraces revealed that environment explained a substantial portion of SNP variation,

independent of geographical distance, and genic SNPs were enriched for environmental associations. This suggests that genomic signatures of environmental adaptation may be useful for crop improvement (Lasky et al., 2015).

The rice protein kinase, *OsPSTOL1*, enhances P acquisition and grain yield in rice under low P (Gamuyao et al., 2012). Root length and root surface area in sorghum are positively correlated with grain yield under low P in the soil. This emphasizes the importance of P acquisition efficiency in sorghum adaptation to low-P conditions. *SbPSTOL1* genes have multiple functions in the root system, enhancing not only root morphology but also changing root system architecture, which leads to increased grain yield under low-P soils (Hufnagel et al., 2014).

Genome wide association mapping using 220 934 SNPs on 187 genetically highly diverse West African sorghum accessions revealed that a genomic region on chromosome 3 is associated with grain yield. More importantly, a major Al-tolerance gene *SbMATE* is co-located in this region, and *SbMATE*-specific SNPs show very high associations to grain yield, especially under $-P$ conditions, explaining up to 16% of the genotypic variance (Leiser et al., 2014b).

9.19 Strategic Overview

ICRISAT is actively involved in finger millet improvement, and this work is targeted at Nairobi, Kenya with emphasis to develop high-yielding finger millet varieties possessing appropriate tolerance to stresses and adapted to Eastern and Southern African agroecologies. Our previous work led researchers identify a number of promising finger millet and foxtail millet accessions, some with tolerance to abiotic and biotic stresses, of which three finger millet lines have already been released in Kenya (IE 4115) and Uganda (IE 2440 and IE 4625). In addition, five more finger millet lines (IE 3575, 4415, 4424, 6045, 6337) in India and IE 2872 in Kenya have been identified for release. Likewise, ISe 156 and ISe 1575, foxtail millet lines, have been identified for release in India.

At ICRISAT, molecular breeding for drought tolerance has been initiated, and a 'QTL hotspot' from germplasm line ICC 4958 was introgressed through marker-assisted backcross breeding in JG 11, a leading chickpea variety in India. A number of introgressed lines produced higher seed-yields in multi-location trials, as compared to JG 11, in both rainfed and irrigated conditions. Further work is in progress to introgress this QTL-hotspot region into other leading chickpea varieties in India and Ethiopia (Varshney et al., 2015).

9.20 Perspectives

The evidence to date suggests that South Asia and sub-Saharan Africa will be severely affected by global warming, while agriculture is already marginal in central Asia and northern Africa. The inhabitants in these regions have very limited capacity to adopt mitigation strategies. Development of climate smart crops together with integrated management of natural resources is a win-win situation to minimize the adverse impact of climate change and variability on the agrarian society. An important part of this strategy is discovering and harnessing natural genetic variation in germplasm

collections for improved tolerances to more extreme in-crop drought and heat stresses. Sources may include genetic variation within species, genetic variation in the crop wild relatives, and genetic modification ranging from mutation 'tilling' to biotechnology tools.

Large germplasm collections need to prioritise subsets which are manageable for screening of trait expressions, and subsequent identification of genes and associated markers for application in pre-breeding and breeding programs. Such examples include the FIGS approach developed by ICARDA for trait targeted mining of germplasm, agro-ecological mapping of pea landrace collection sites for frost tolerance during reproductive growth in China, genetic and trait diversity sets of core and mini-core collections for trait exploration at ICRISAT and IITA, with many successes for identifying abiotic tolerances and biotic stress resistances in several crops. Chickpea root traits may confer drought tolerance, landraces within Africa contain genetic variation for tolerance of low P levels in soils, and many physiological and gene regulatory traits may be implicated in heat and drought stress responses. Cowpea landraces from the Sahel with pollen tolerant to temperatures above 40°C were first screened for seed set in summer in the Nevada desert. In pearl millet such tolerance can extend over 42°C.

FIGS and agro-ecological perspectives also assist further germplasm collecting to fill diversity gaps, especially for CWR which are greatly under-represented in ex-situ collections, but which contain the greatest genetic diversity especially for tolerances of heat, drought and salinity stresses. Some CWR are adapted to a wider range of environments than the respective crops; examples are wild sorghum in rainforests, and wild millet in the Sahel.

Certain genebanks emphasise the importance of maintaining in-situ collections of CWR as sources of novel germplasm from evolutionary responses to climate change over time (Nevo et al., 2012)

Exploitation of CWR for crop improvement requires not only gene/QTL identification but also use of NGS and genetic markers to assist introgression into improved genetic backgrounds/ploidy level, where the expression of tolerance genes can be best evaluated. For polyploid crops, synthetics from CWR and backcrossing are proven strategies, in conjunction with targeted screening environments, for selection of improved yield under increased levels of abiotic stresses, notably in the wheats, millets, sorghum and groundnut. New genomic techniques also assist multiple trait mapping and selection. Significant high throughput genotyping and phenotyping platforms are available for dissecting the physiological, genetic and molecular basis of stress tolerance, and should be put to use to accelerate cultivar development.

Under-utilised minor crops are a largely overlooked resource which could provide new options for regions that are increasingly suffering from drought and heat stresses. There is a rich resource for these in the IITA genebank, including yam bean, which as a legume could have a very important role as a sustainable source of nitrogen from symbiotic fixation.

Thus there are many strategies being explored with a focus on adapting to climate change.

9.21 Summary

Agricultural research for the management of climate change must address both unprecedented world population levels which are expected to keep rising. Increased cropping risks are expected for both drought and heat stresses, especially in the reproductive growth stages, and from more virulent and aggressive disease and pest populations.

Exploration of genetic diversity for such stress tolerances is a priority for genetic resource collections at ICARDA, IITA, ICRISAT and other genebanks. Strategies include evaluation of manageable core and mini-core collections for genetic diversity and targeting of landrace collections using trait-based FIGS approaches for selection of tolerances to abiotic stresses in their source environments.

Utilisation of crop wild relatives greatly widens the genetic base of their respective cultivated crops. Evaluation is conducted on reconstituted synthetics in durum and in bread wheats, leading to joint advances for yield and abiotic stress tolerances in both the ICARDA and CIMMYT wheat breeding programs, as well as for resistances to pests and diseases in these and many other crops.

Exploitation of wild relative germplasm can now be assisted by identification of markers for abiotic stress tolerance expressions, which facilitate introgression and backcross breeding.

Important progress has been achieved for tolerance of drought stress in wheat, chickpea (via root traits), and sorghum. Reproductive heat tolerance has been improved in wheat, millet, chickpea, groundnuts and maize. Drought tolerance associated traits include: canopy temperature, root morphology, seed filling, water use efficiency as well as stay green expressions. Heat tolerance includes survival of both pollen and ovules, and seed set, under high temperatures. In addition, genetic variability has been identified for phosphorous uptake and efficiency. These factors all contribute to improvement in grain yield.

Complementary conservation agricultural practices would also be needed for climate-smart- practices. Under-utilised crops which have received little attention from research, could also provide new alternatives to help manage climate change.

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