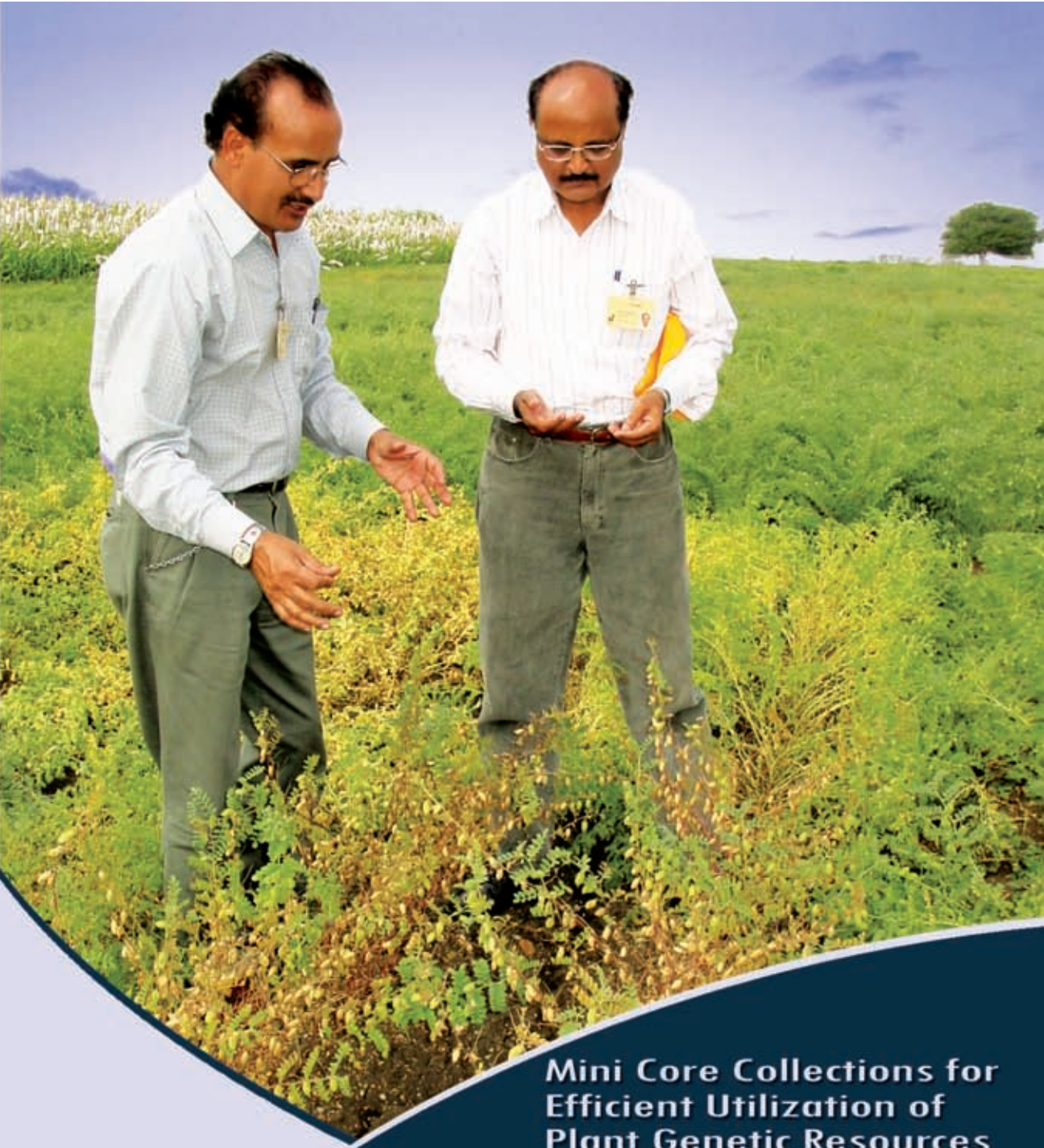

Mini Core Collections for Efficient Utilization of Plant Genetic Resources in Crop Improvement Programs

Information Bulletin No. 78

ICRISAT
Science with a human face

International Crops Research Institute for the Semi-Arid Tropics

Citation: Upadhyaya HD, Pundir RPS, Dwivedi SL and Gowda CLL. 2009. Mini Core Collections for Efficient Utilization of Plant Genetic Resources in Crop Improvement Programs. Information Bulletin No. 78. Patancheru 502 324, Andhra Pradesh, India: International Crops Research Institute for the Semi-Arid Tropics. 52 pp. ISBN 978-92-9066-519-9. Order code IBE 078.

Abstract

Plant genetic resources are the basic raw materials for crop improvement to enhance productivity and an insurance against unforeseen threats to agricultural production. Continuous progress in crop improvement depends on discovery of new sources of genetic variation, accurate identification of lines with beneficial traits, and their judicious use. Core collections (~10% of the entire collection) and mini core collections (~10% of the core or ~1% of the entire collection) have been suggested as a gateway to enhanced utilization of germplasm by crop improvement scientists. Using passport, characterization and evaluation data, core and/or mini core collections have been developed in chickpea, groundnut, pigeonpea, pearl millet, sorghum, finger millet and foxtail millet at ICRISAT, Patancheru, India. Evaluation of these subsets has resulted in identification of new sources of genotypic variation: drought and salinity tolerance in chickpea, groundnut and pigeonpea; low temperature tolerance (at germination) in groundnut; sorghum stalks with high sugar content; resistance to pest and diseases in chickpea, groundnut, pigeonpea and sorghum; early maturity, large seed size and/or high grain (or pod) yield in chickpea and groundnut; early maturity and high grain yield in pigeonpea; and high grain and fodder (green) yield in pearl millet, finger millet and foxtail millet. The concept and process of developing mini core has been recognized worldwide as an "International Public Good" (IPG). Many national programs have shown immense interest in evaluating mini core for identification of new sources of variation for use in crop improvement programs. To date, 84 sets of mini core of chickpea, groundnut, pigeonpea, sorghum, pearl millet, foxtail millet and finger millet have been supplied to researchers in 13 countries. Feedback revealed that researchers in national programs were able to identify new sources of variation for beneficial traits such as early maturity, resistance to pest and diseases, large seed size, and high grain yield. Seeds of mini core collections are available to researchers globally for research and training.

Mini Core Collections for Efficient Utilization of Plant Genetic Resources in Crop Improvement Programs

Information Bulletin No. 78

Hari D Upadhyaya, RPS Pundir, SL Dwivedi and CLL Gowda

ICRISAT
Science with a human face

International Crops Research Institute for the Semi-Arid Tropics
Patancheru 502 324, Andhra Pradesh, India

2009

Contents

Foreword

Like any other CGIAR genebank, ICRISAT has a large germplasm collection (119,074 accessions) of chickpea, groundnut, pigeonpea, sorghum, pearl millet and small millets in its Patancheru-based genebank in India. In spite of such large collections, there has been very limited use of germplasm in crop improvement programs. One of the reasons for low use of germplasm is lack of information about the usefulness of the collections preserved in genebanks. To enhance the use of germplasm, it is necessary for the germplasm to be properly characterized and for information to be extracted in a holistic manner to identify a set of genetically diverse germplasm. A core collection (10% of entire collection) has been suggested as a scientific basis to enhance utilization of germplasm in crop improvement. Towards this end, we have developed core collections in chickpea, groundnut, pigeonpea, sorghum, pearl millet and small millets. However, in some cases, we found that even the core collection consists of too large a number of germplasm accessions. For example, there are 2,247 accessions in the sorghum core collection, which itself will be unmanageable to effectively and accurately conduct multilocation agronomic evaluation. To overcome this limitation, Upadhyaya and Ortiz in 2001 postulated the concept and process of developing a “mini core collection” that represents the core collection for over 80% of its genetic variability. For developing a mini core, we evaluated core collections for agronomic and seed quality traits and used that dataset to construct mini core collections, which are now available in chickpea, groundnut, pigeonpea, sorghum and pearl millet, fully representing variability present in the core (or entire collection), but with a sufficiently reduced number of accessions.

This bulletin provides descriptive information about constructing core and mini core collections from the entire collection, and the statistical parameters used to measure the representativeness of the

mini core to the core or entire collection. We have also demonstrated that by evaluating such reduced subsets, it is still possible to identify new sources of variation that are genetically diverse and possess beneficial traits. We earnestly believe that this publication will be globally useful to researchers engaged in genetic enhancement of crops.

Authors
Hari D Upadhyaya,
RPS Pundir, SL Dwivedi and CLL Gowda

Preface

ICRISAT has the responsibility to collect, conserve, characterize, document and provide the genetic resources of the cultivated and wild relatives of its five mandate crops and six small millets for use in crop improvement programs globally. Continued progress in varietal development depends on discovery of new sources of genetic variation, accurate identification of lines with beneficial traits, and their judicious use in crop improvement. ICRISAT genebank at Patancheru, India has assembled more than 119,000 accessions of chickpea, groundnut, pigeonpea, pearl millet, sorghum and of six small millets. Past experience revealed that there has been scanty use of germplasm in crop improvement programs. Crop breeders in general are reluctant to use exotic germplasm, and rather prefer their own working collection of germplasm for cultivar development, thus, leading to narrowing the genetic base of newly developed cultivars. This could lead to catastrophes in the event of new and emerging challenges (such as climate change) to agricultural production. Additionally, the spread of high yielding crop cultivars could replace the prevalent landraces and local cultivars, leading to plant diversity erosion.

Clearly, there is a need to capture the genetic variation from the existing collections to a manageable level to enable germplasm curators preserve such variation (before being lost), and at the same time find ways to increase the use of diverse germplasm with beneficial traits for developing elite genetic materials to meet new and emerging challenges to agricultural production. Core collection (10% of entire collection) has been suggested as a gateway to enhance utilization of germplasm in crop breeding. However, in some situations, even the core (where core itself is too large) has not been economically useful to accurately identify germplasm with beneficial traits. To overcome this problem, the genetic

resources scientists at ICRISAT postulated the mini core collection (10% of core collection or 1% of entire collection) concept, representing over 80% variability from the core collection. This bulletin summarizes the progress made in developing core and mini core collections of our mandate crops that when evaluated resulted in new sources of genetically diverse germplasm with beneficial traits.

I am pleased to record my appreciation of the genetic resources scientists for such a novel approach ("mini core" concept) that has been recognized worldwide as an International Public Good (IPG). More importantly, the researchers in national programs are showing great interest in using mini core collections to identify new sources of variation for use in crop breeding and genomics.

William D Dar
Director General
ICRISAT

Acknowledgment

The authors acknowledge the contribution of Patancheru-based ICRISAT scientists, Vincent Vadez, L Krishnamurthy, RP Thakur, R Sharma, S Pande and HC Sharma, and former scientist J Kashiwagi, for screening core and/or mini core collections for resistance to biotic and abiotic stresses. Likewise, we gratefully acknowledge the contribution of Asian NARS for evaluating the core and/or mini core collections. The contribution of S Singh and MT Reddy of Genetic Resources Unit in preparation of this bulletin is also acknowledged.

About the authors

HD Upadhyaya Principal Scientist and Head, Genebank, ICRISAT, Patancheru PO 502 324, AP, India.

RPS Pundir Former Visiting Scientist (Genetic Resources), ICRISAT, Patancheru PO 502 324, AP, India.

SL Dwivedi Visiting Scientist (Genetic Resources), ICRISAT, Patancheru PO 502 324, AP, India.

CLL Gowda Global Theme Leader – Crop Improvement, ICRISAT, Patancheru PO 502 324, AP, India.

Introduction

Crop domestication was initiated about 12,000 years ago when human beings started growing crops of their choice rather than gathering them from the wild. When this transition from gathering to cultivating plants took place, there was a genuine interest in selection, collection and utilization of crop plants. Cultivated plants became part of human heritage since then. Several wild and weedy species that were not domesticated continue to evolve and hybridize with cultivated ones in nature, thus, enhancing the plant genetic diversity.

Nikolai Ivanovich Vavilov (1951) recognized the importance of plant genetic diversity in agriculture. He traveled extensively to sample plant diversity for utilization in agriculture, and emphasized the importance of plant introduction and exploration for new genes, an important feature of agricultural research.

Development and spread of high yielding crop cultivars have replaced the prevalent landraces and local cultivars, leading to plant diversity erosion. This loss of native crop landraces and cultivars prompted the Food and Agriculture Organization (FAO) and the World Bank to create new institutions for the collection and preservation of plant genetic resources - the *ex-situ* genebanks. Over six million germplasm accessions have been collected and/or assembled and conserved worldwide in 1,308 genebanks (FAO 1998).

International Agricultural Research Centers (IARCs) under the aegis of the Consultative Group on International Agricultural Research (CGIAR), including ICRISAT, have the responsibility to collect, conserve, characterize, evaluate, document and provide the genetic resources of the cultivated and wild relatives of its mandate crops for use in cultivar development programs. Assembling germplasm from various sources was initiated since the inception of ICRISAT in 1972. Initial efforts were to assemble germplasm accessions from genebanks globally and we assembled 85,590 accessions from 75 genebanks/institutions. Germplasm of mandate crops were also

collected from centers of diversity and other areas considered being of high priority. In between 1975 and 2008, ICRISAT organized 216 joint missions in 61 countries, which resulted in collection of over 33,000 accessions of five mandate crops and six small millets. ICRISAT's genebank at Patancheru, India holds (as of 30 April 2009) 119,074 accessions of chickpea, groundnut, pigeonpea, pearl millet, sorghum and of six small millets (Table 1).

Table 1. Status of germplasm accessions held at RS Paroda genebank, ICRISAT, Patancheru, India (as of 30-04-2009).

	Accessions			
Crop	Cultivated	Wild	Total	Origin (countries)
Sorghum	37,485	458	37,943	92
Pearl millet	20,844	750	21,594	50
Chickpea	19,941	326	20,267	60
Pigeonpea	13,077	555	13,632	74
Groundnut	14,968	477	15,445	92
Finger millet	5,844	105	5,949	24
Foxtail millet	1,481	54	1,535	26
Proso millet	842		842	30
Little millet	466		466	5
Kodo millet	658		658	2
Barnyard millet	743		743	9
Total	116,349	2,725	119,074	144

Use of germplasm in crop improvement

Plant genetic resources are the raw materials for the development of improved cultivars. Between 1974 and 2008, an average of 19,912 germplasm samples were supplied annually to users outside ICRISAT, and 18,695 samples to researchers within ICRISAT. However, studies have shown scanty use of germplasm in crop improvement programs globally. For example, groundnut scientists at ICRISAT used 986 unique parents (1986-2002) to develop 8,279 advanced varieties in groundnut (ICGV#), but included only 132 unique germplasm and 10 wild *Arachis* species (Upadhyaya et al. 2006b) from more than 15,400 germplasm accessions available in its genebank. The two most often used cultivars were Robut 33-1 (ICG 799) and Chico (ICG 476). Likewise, chickpea scientists at ICRISAT (1978-2004) used 12,887 parents (586 unique lines) to develop 3,548 advanced varieties (ICCV#), which included only 91 unique germplasm accessions and five wild *Cicer* species accessions. The two most frequently used cultivars were L 550 (ICC 4973) and K 850 (ICC 5003) (Upadhyaya et al. 2006a). India has one of the largest breeding programs in legumes, which released 229 cultivars of chickpea, lentil, pigeonpea, black gram and green gram through hybridization and selection (data up to 2003). Pedigree analysis of these cultivars revealed that Pb-7 in chickpea, L-9-12 in lentil, T-1 and T-190 in pigeonpea, T-9 in black gram, and T-1 in green gram were the most frequently used parents (Kumar et al. 2004). The situation is not better in other countries/crops. For example, Dixie Giant and Small White Spanish-1 contributed nearly 50% of the germplasm of Virginia Runner cultivars released in USA (Knauft and Gorbet 1989). Low use of germplasm have also been reported in wheat (Dalrymple 1986), spring barley (Vellve 1992), and maize (Cantrell et al. 1996). Clearly, there is a need to increase the use of genetically diverse germplasm with beneficial traits in crop improvement programs to develop elite genetic materials to meet the emerging challenges to agricultural production.

Pattern and impact of germplasm uses

In between 1974 and 2008, ICRISAT germplasm unit supplied 1,354,036 seed samples in 144 countries, including 654,348 samples to researchers within ICRISAT (Table 2). The following pattern emerged.

Chickpea: A total of 127,427 samples of 16,942 accessions were supplied against 1,551 requests worldwide, involving 84% of entire collection. The most frequently requested accessions were ICC 4918 (Annigeri), ICC 4973 (L 550), and ICC 5003 (K-850), all originating in India. Annigeri is early-maturing desi type, K 850 is medium maturing large-seeded desi type, and L 500 is late maturing, small-seeded kabuli type.

Groundnut: A total of 97,097 samples of 14,424 accessions were supplied against 1,384 requests worldwide, involving 93% of the entire collection. The most frequently requested accessions were ICG 799 (Robut 33-1), ICG 221 (TMV 2), and ICG 156 (M 13), all originating in India. TMV 2 is an early maturing Spanish type. Robut 33-1 is a Virginia bunch type, while M 13 is a large-seeded Virginia runner type.

Pigeonpea: A total of 68,594 seed samples of 10,743 accessions were supplied against 1,664 requests, representing 79% of the entire collection. The predominantly requested accessions were ICP 7035 (DSLR-55), ICP 26 (T 21) and ICP 7182 (BDN 1), all originating in India. ICP 7035 is vegetable type and resistant to sterility mosaic. ICP 26 is widely adapted early maturing type, while ICP 7182 is medium-maturing type.

Sorghum: A total of 253,908 seed samples of 32,501 accessions, mostly landraces, were supplied against 2,099 requests, involving 86% of the entire collection. The most frequently requested accessions were IS 18758 (E 35-1) from Ethiopia and IS 1059 and IS 5604, both *Durra-bicolor* intermediate race type from India. IS 18758 belongs to *Zerazera* landrace, released in Burkina Faso and Cameroon, and have been extensively used in hybridization programs. IS 1059 and IS 5604 are high yielding widely adapted germplasm.

Pearl millet: A total of 93,246 seed samples of 17,262 accessions were supplied against 1,147 requests, involving 80% of the entire collection.

Table 2. Status of germplasm supplied from RS Paroda Genebank, Patancheru, to researchers at ICRISAT and outside (1974-2008).

Crop		1974-78	1979-83	1984-88	1989-93	1994-98	1999-03	2004-08	Total
Sorghum	ICRISAT	19,440	97,153	62,843	12,841	1,857	16,937	19,982	231,053
Sorghum	Outside	16,471	42,156	96,054	62,708	21,205	9,085	6,229	253,908
Pearl millet	ICRISAT	2,587	15,531	9,947	5,293	4,337	7,654	7,552	52,901
Pearl millet	Outside	3,007	12,295	35,669	27,100	6,370	4,515	4,290	93,246
Chickpea	ICRISAT	25,613	47,019	21,779	40,012	21,053	13,704	15,859	185,039
Chickpea	Outside	15,760	36,255	26,013	19,400	11,276	9,973	8,750	127,427
Pigeonpea	ICRISAT	9,101	26,804	12,632	12,051	5,410	7,845	9,617	83,460
Pigeonpea	Outside	9,009	10,537	13,064	17,529	8,158	7,452	2,845	68,594
Groundnut	ICRISAT	867	24,155	27,926	7,936	2,488	13,157	19,020	95,549
Groundnut	Outside	3,682	17,226	27,552	16,482	18,134	9,267	4,720	97,097
Small millets	ICRISAT	-	-	-	-	-	912	5,434	6,346
Small millets	Outside	3,665	16,402	9,127	8,225	5,042	8,340	8,615	59,416
Total		109,202	345,533	342,606	229,577	105,330	108,841	112,913	1,354,036

IP 4021 (an early flowering accession from Gujarat, India), IP 6271 (Sogue landrace from Mali), and IP 3122 (Jakhrana landrace from India) were the most frequently requested accessions.

Small millets: A total of 59,416 seed samples of 8,968 accessions were supplied against 339 requests, involving 88% of the entire collection. Finger millet accession IE 2333 (race *Compacta*) from Kenya; foxtail millet accessions ISe 376 (race *Maxima*) from India; proso millet accession IPm 1545 (race *Contractum*) of unknown origin; non-lodging little millet accession IPmr 699 (race *Robusta*) from India; kodo millet accession IPs 197 (race *Variabilis*) from India; and barnyard millet accession IEc 51 (race *Robusta*) from India were the most frequently requested accessions.

Several germplasm accessions have been used to develop cultivars and hybrids. In addition, many germplasm lines when evaluated by NARS produced higher grain yield and have been directly released as cultivars. Globally, 108 germplasm accessions (35 sorghum cultivars in 17 countries, 28 pigeonpea cultivars in 10 countries, 22 chickpea cultivars in 15 countries, 19 groundnut cultivars in 15 countries, two finger millet cultivars in one country, and a pearl millet and barnyard millet cultivar in one country), distributed to users from ICRISAT genebank, have been directly released as cultivars (Figure 1). A total of 657 cultivars have been released in 78 countries by our NARS partners from the breeding materials supplied by ICRISAT that included the germplasm lines. These cultivars have greatly benefited those countries by increasing both production and productivity.

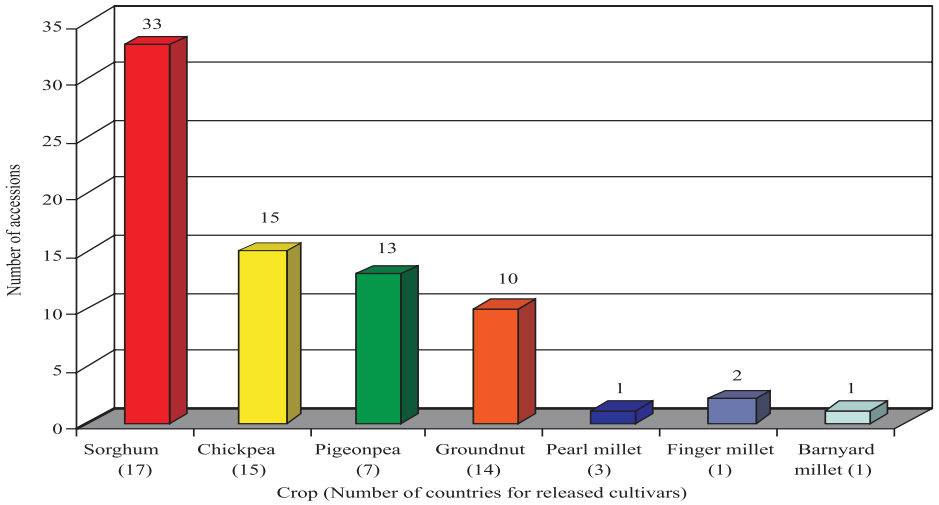

Figure 1. Number of accessions released as varieties worldwide from the basic germplasm supplied from ICRISAT genebank during 1976-2008.

Assessing diversity in germplasm

Patterns of diversity have been assessed using descriptors developed for each crop: chickpea (IBPGR, ICRISAT and ICARDA 1993), groundnut (IBPGR and ICRISAT 1992), pigeonpea (IBPGR and ICRISAT 1993a), pearl millet (IBPGR and ICRISAT 1993b), sorghum (IBPGR and ICRISAT 1993c), finger millet (IBPGR 1985a) and foxtail millet (IBPGR 1985b). Accessions in the collection were grown under field conditions for characterization/ evaluation and seed multiplication over several years. Characterization and evaluation data were recorded using the crop-specific descriptors, and analyzed subsequently to discern patterns of diversity in the global collection.

Chickpea: Using data on 21 traits from 16,820 accessions from 43 countries, Upadhyaya (2003a) assessed the pattern of diversity. The morphological traits showed differences among geographical regions in their distribution and range of variation. Accessions with no anthocyanin - a characteristic feature of Kabuli type - were less frequent in South Asia, South East Asia and Africa, however, predominant in East Asia, Mediterranean region and Europe. The patterns of variation for flower color, seed color, seed shape and surface across different regions were similar to plant color. Semi-erect and semi-spreading growth habits were evenly distributed in South Asia, whereas in the rest of the regions, except Southeast Asia, semi-erect accessions were predominant. Erect, prostrate and spreading growth habits had very low frequency across all regions except East Asia. Chickpea accessions resistant to fusarium wilt were available from all regions, though with higher proportion from South Asia, Southeast Asia and West Asia.

Regions showed significant differences for quantitative traits. Accessions from Africa were earliest to flower, while accessions from East Asia were of late flowering type. European accessions recorded not only the highest number of pods per plant but also produced highest grain yield and largest seed size. Accessions from Africa had the smallest seed size. Seed color showed maximum diversity (Figure 2). The principal component analysis (PCA) using quantitative traits and clustering on the first three PC scores

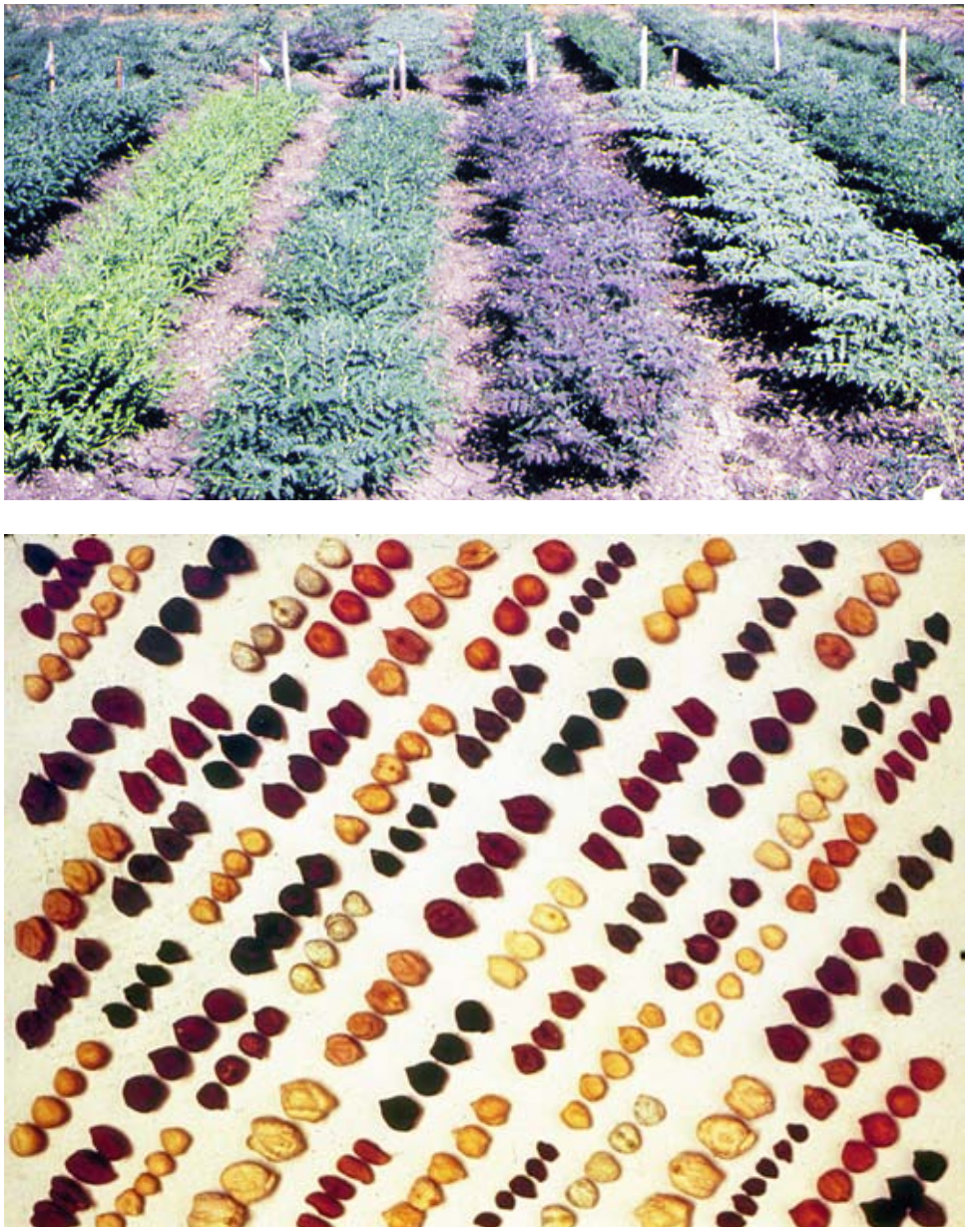

Figure 2. Diversity in plant foliage and seed size, shape and color among chickpea germplasm.

delineated two regional clusters consisting of Africa and South and Southeast Asia in the first cluster; and the Americas, Europe, West Asia, Mediterranean and East Asia in the second cluster (Figure 3) (Upadhyaya 2003a).

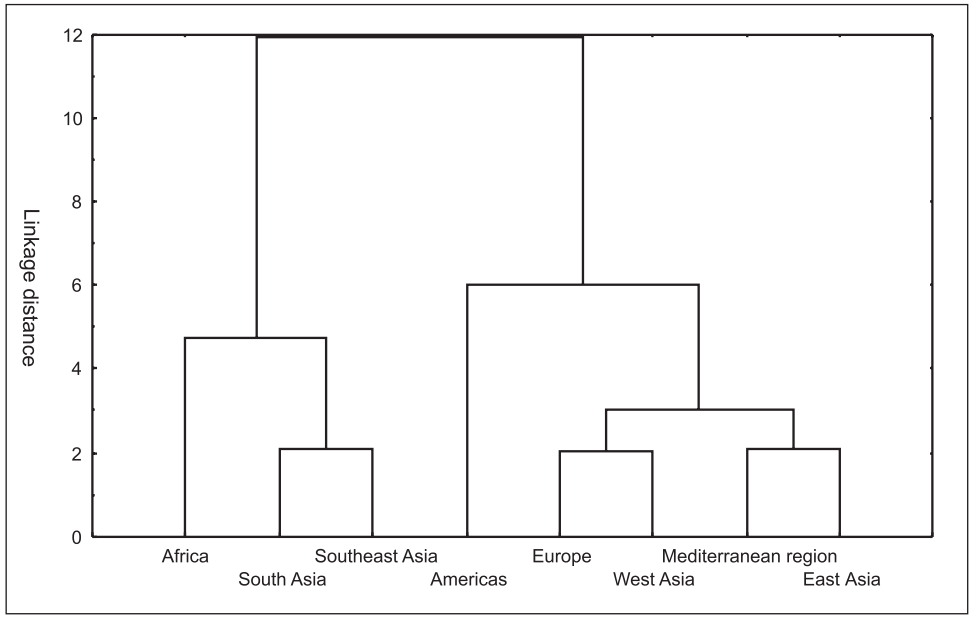

Figure 3. Dendogram of eight regions in the entire chickpea germplasm based on first three principal components (Upadhyaya et al. 2003a).

Groundnut: Using data on 38 traits from 13,342 accessions from 92 countries, Upadhyaya et al. (2002b) assessed the pattern of diversity. The accessions revealed vast diversity for pod size and shape and seed characteristics (Figure 4). The PCA revealed that clustering on first seven PC scores delineated all the regions into three clusters: North America, Middle East and East Asia in the first cluster; South America in the second cluster; and West Africa, Europe, Central Africa, South Asia, Oceania, Southern Africa, Eastern Africa, Southeast Asia, Central Asia and Caribbean in the third cluster (Figure 5). The means for agronomic traits differed significantly among regions. The variances for all the traits among regions were heterogeneous. Accessions from South America showed large range variation for morphological traits.

Figure 4. Diversity in pod/seed size and shape and seed color among groundnut germplasm.

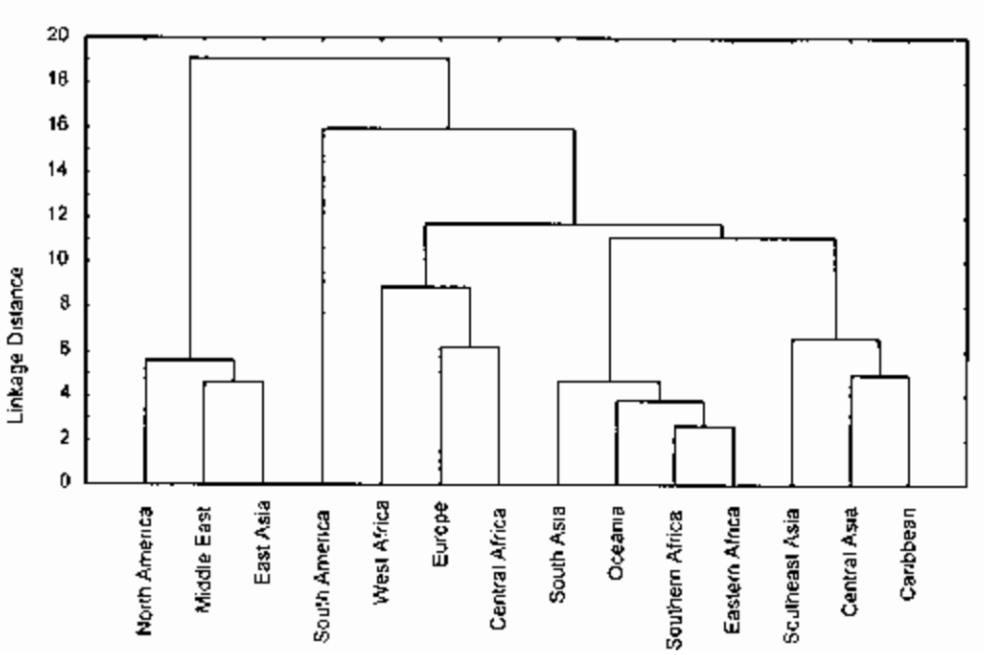

Figure 5. Dendogram of 14 regions of the entire groundnut germplasm based on scores of first seven principal components (Upadhyaya et al. 2002b).

Pigeonpea: Upadhyaya et al. (2005b) characterized 11,402 accessions from 54 countries, grouped into short (<100 days), medium (101 to 130 days), and late maturing (>130 days) types (Sharma et al. 1981) prior to evaluating for 26 morpho-agronomic traits. A vast diversity was seen for pod size and pod color (Figure 6a) and for seed size and seed color (Figure 6b) in the collection.

India is a major pigeonpea growing country. It consists of vast geographical and climatic diversity, classified into four broad groups based on geographical proximity and similarity of the climate: i) northwestern India, ii) northeastern India, iii) central India, and iv) southern India (Reddy et al. 2005). The accessions from neighboring countries were grouped with appropriate

Figure 6a. Diversity in pod size, color and number of seeds among pigeonpea germplasm.

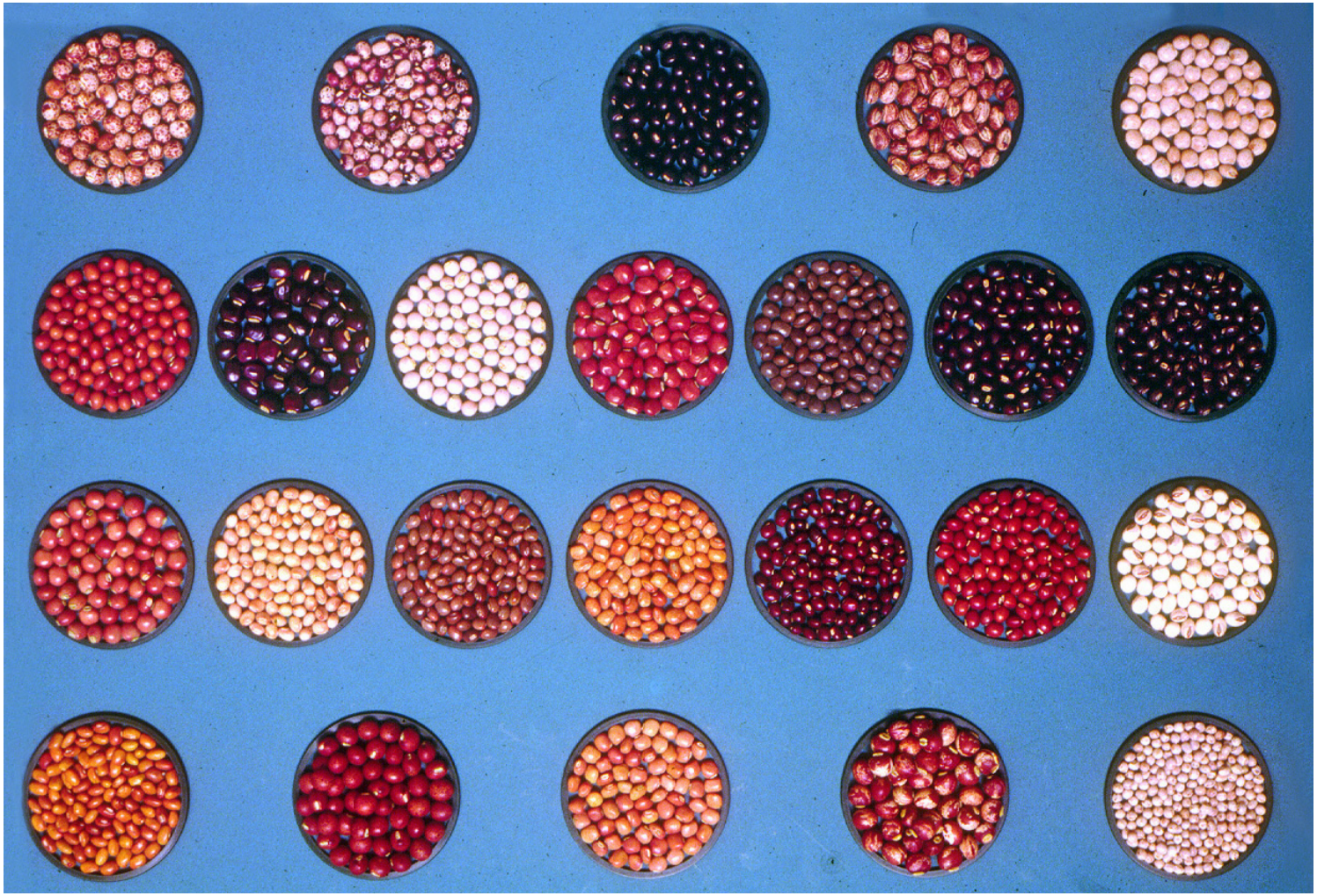

Figure 6b. Diversity in seed size, shape and color among pigeonpea germplasm.

Indian regions. For example, accessions from Pakistan and Iran were grouped with those of northwestern India, and the region was named Asia 1 (AS 1), while those from Bangladesh, Myanmar, Nepal, China and Taiwan with northeastern India (AS 2). The accessions from central India had their own exclusive group (AS 3). The accessions from Maldives and Sri Lanka were grouped with southern India (AS 4). The accessions from India for which precise geographical locations were not known were grouped under AS 5. The accessions from Indonesia, the Philippines and Thailand were grouped as AS 6. Accessions from Africa (17 countries), America (seven countries), Caribbean (12 countries), Europe (four countries), and Oceania (Australia), respectively, were grouped as AS 7, AS 8, AS 9, AS 10 and AS 11 regions.

The patterns of variation across 11 regions revealed that the semi-spreading growth habit, green stem color, indeterminate flowering, and yellow flower color were predominant among qualitative traits. Primary seed color had maximum variability and orange color followed by cream were the two most frequent seed colors in the collection. Variances for all the traits were heterogeneous among regions. The germplasm accessions from Oceania were conspicuous by short growth duration, short height, fewer branches, pods with fewer seeds, smaller seed size and lower seed yields. The accessions from Africa were of longer duration, taller, with multiseeded pods and larger seeds. The cluster analysis based on three PC scores using 12 quantitative traits revealed three clusters: cluster 1 included accessions from Oceania; cluster 2 accessions from India and adjacent countries, and cluster 3 accessions from Indonesia, Thailand, the Philippines, Europe, Africa, America and the Caribbean countries (Upadhyaya et al. 2005b).

Sorghum: Cultivated sorghum consists of five basic races: *Bicolor*, *Guinea*, *Caudatum*, *Kafir* and *Durra* (Harlan and de Wet. 1972). Natural intercrossing among these races gave rise to ten intermediate races: *Guinea-bicolor*, *Guinea-caudatum*, *Guinea-kafir*, *Guinea-durra*, *Caudatum-bicolor*, *Kafir-bicolor*, *Durra-bicolor*, *Kafir-caudatum*, *Kafir-durra* and *Durra-caudatum*. These races are characterized by differences in inflorescence morphology. Race *Bicolor* is widely distributed in Africa and Asia. *Guinea* race is predominant in West Africa, *Caudatum* throughout Central Africa, *Kafir* in the Southern African Development Community (SADC) countries and *Durra* in a belt across Africa in the dry zone immediately south of Sahara between 10^{o} and 15^{o} N, predominant in Ethiopia. These races showed immense diversity in panicles, spikelets and seeds (Figure 7a and b).

Figure 7a. Diversity in panicle (head) size, shape and grain color among sorghum germplasm.

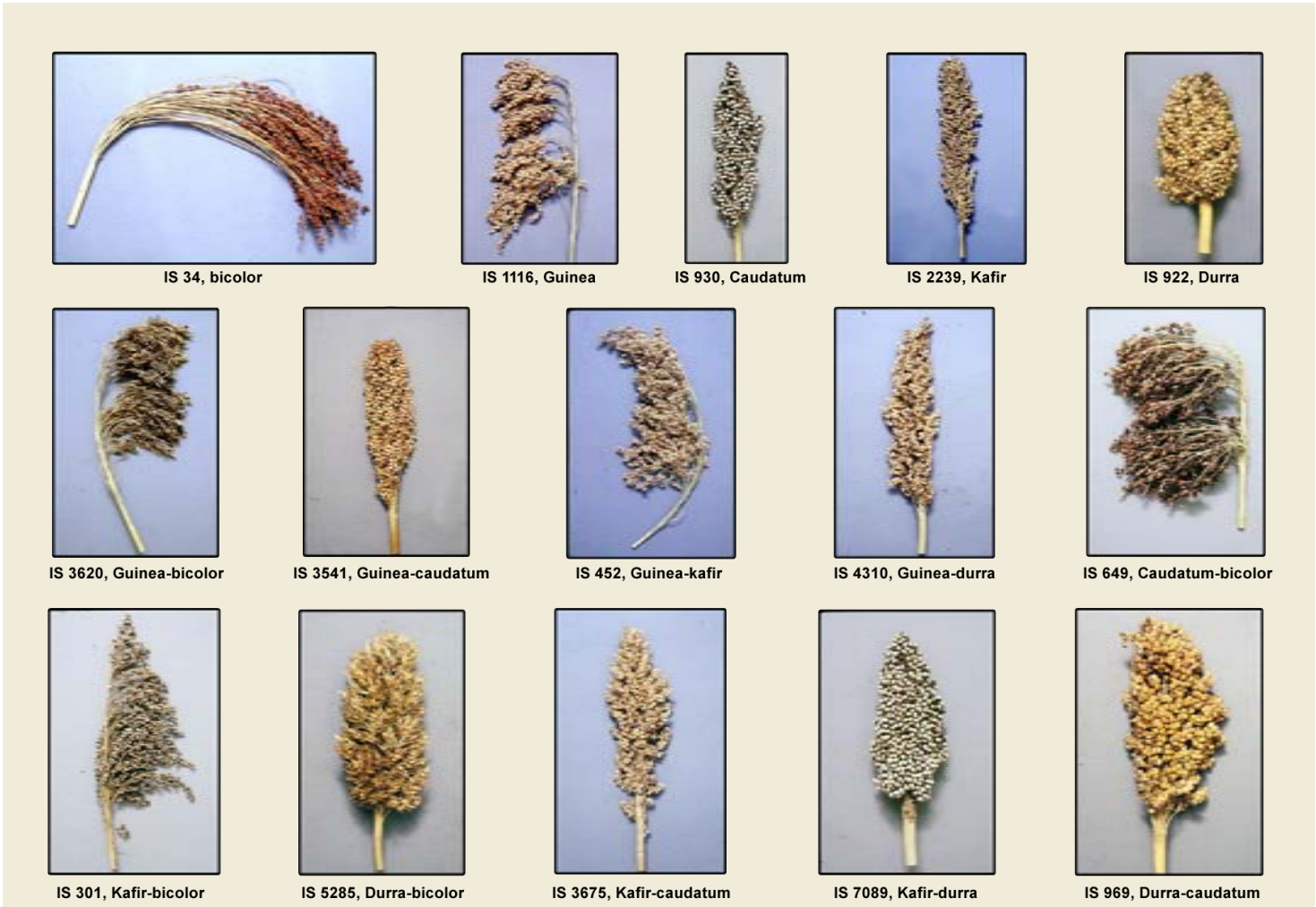

Figure 7b. Sorghum accessions representing major races and intermediate races as differentiated by variation in panicle (head) size, shape and grain color.

Diversity in 31,752 accessions of sorghum germplasm was characterized for 23 morphoagronomic traits that revealed large variability for quantitative traits. For example, accessions varied for days to flowering from 36 to 199 days, plant height from 55 to 655 cm, peduncle exsertion from 0 to 55 cm, panicle length from 2.5 to 71 cm, and 100-seed weight from 0.29 to 8.56 g (Stenhouse et al. 1997).

Pearl millet: Diversity in 21,594 pearl millet accessions from 50 countries was assessed for 23 morphoagronomic traits that revealed large variability for days to flowering (33 to 159 days), plant height (30 to 490 cm), tillers plant^{-1} (1 to 35), panicle length (5 to 135 cm), and 1000-seed weight (1.5 to 21.3 g). Figure 8 shows vast diversity in panicle size among pearl millet germplasm. The phenotypic diversity index ranged from 0.427 (tiller number) to 0.772 (endosperm structure) with a mean of 0.528 (Upadhyaya et al. 2007b).

Finger millet: When phenotypic diversity was characterized for 19 morphoagronomic traits on 5,059 accessions, the panicle forms and seeds showed vast diversity (Figure 9). Green was the most frequent plant color followed by purple and violet. Of the three growth habit classes, erect was predominant, followed by decumbent and prostrate growth habits. Four grain colors were observed: light brown was most common, followed by reddish

Figure 8. Diversity in panicle (head) size, shape and color among pearl millet germplasm.

Figure 9. Diversity in panicle and seed characteristics among finger millet germplasm.

brown, dark brown and white. The accessions also differed for lodging. Plant foliage in about 3% of accessions remained fully green until maturity – a valuable fodder trait. Cultivated and wild races are differentiated by glume characteristics. Most of the two wild races (*Africana* and *Spontanea*) had prominent glumes; while prominent, non-prominent or medium glume types were found in cultivated races.

Foxtail millet: Taxonomically, it comprised of two subspecies, *Setaria italica* and *S. viridis*, with diploid chromosome number 2n=18. *S. viridis* is the progenitor of cultivated type, *S. italica*. It mainly differs from the cultivated type by its grain shattering habit and non-synchronous plant maturity (Prasada Rao et al. 1987). Three recognized races are *Moharia*, *Maxima* and *Indica*. The phenotypic diversity in 1,535 accessions from 26 countries was determined for 24 traits. The accessions ranged from single-stemmed to highly tillered plants and drooping panicles. The average plant height ranged from 1 to 2 m, panicle length from 1 to 39 cm, and panicle diameter from 1.5 to 3.0 cm. In contrast, some accessions from China were single-stemmed tall plants. The leaves on such accessions were 30 to 35 cm long and 1.5 to 3.0 cm wide. Panicle length and width, respectively, varied from 12 to 15 cm and 4 to 6 cm. Light cream colored seeds have 100-seed weight of 2-3 g. Figure 10 shows large diversity in panicle size, shape and seed color.

Figure 10. Diversity in panicle shape, size and seed color among foxtail millet germplasm.

Approaches to establish core and mini core collections

Large scale evaluation of the germplasm collection is feasible only for traits which can be scored easily and do not show interaction of genotype (G) and environment (E). However, for applied plant breeding research, evaluation often requires replicated field evaluation as the traits of economic importance (such as yield and yield components) often display large GxE interaction. Thus, the collection needs to be sampled to get the size of the collections to a manageable level for meaningful evaluation.

Frankel and Brown (1984) suggested that greater use of germplasm in crop improvement is possible if a small collection representing diversity of well characterized accessions is made available to researchers. Frankel (1984) coined the term “core collection” to sample representative variability from the entire collection. A core collection contains a subset of accessions from the entire collection that captures most of available diversity in the species (Brown 1989a). The core collection thus formed can be evaluated extensively and the information derived could be used to guide more efficient utilization of the entire collection (Brown 1989b). The guiding principles to constitute a core collection are:

- The entire collection is a large collection (from the stand point of management and making a choice for use in research) with a taxonomic entity
- The core collection has a reduced size
- The core is a representative sample of the entire collection
- Like the entire collection, core too is a diverse set of germplasm.

A good core collection does not require that every part of the entire collection be equally represented. Nor does it require the absolute maximum possible diversity; otherwise the core would be biased towards large numbers of distant wild relatives. Rather the diversity should be as high as possible; where “possible” entails consistency with the core being a representative genetic resource collection of practical utility to researchers (Brown and Spillane 1999). The four steps involved in constituting the core are:

i. **Defining the collection to be represented and deciding size of the core:** The core collection should be comprehensive so that it may serve diverse users and purposes. The data on taxonomy, passport and characterization should be assembled and verified. The size of the core should be about 10% of the entire collection and should retain at least 70% of the alleles present in the entire collection (Brown 1989a).

ii. **Classifying the accessions into groups:** This can be done hierarchically using taxonomic, geographic and characterization data, grouping the collection into smaller subgroups within groups. Generally, about 10% of accessions are retained from each subgroup.

iii. **Selecting accessions for core:** Having divided the whole collection into groups, the next step is deciding number and choice of accessions, which should be based on considerations such as group size, within group genetic diversity, or the accessions with special merit and utility.

iv. **Managing the core collection:** The final stage is managing the core accessions themselves. They may be regenerated, held separately from the parent collection and further evaluated for diversity assessment, or screening for specific purposes.

The degree of the genetic similarity or commonality among accessions is useful in determining groups within the entire collection. The hierarchy of grouping begins with the groupings suggested by taxonomy (subspecies and races) followed by assigning accessions to major geographic groups (country, state), climate, or agroecological regions. The clustering within the broad geographic group could be done to sort accessions into clusters. The number of accessions selected from each cluster will depend on the strategy used.

The core collection could be of several types: global core collection, regional core collection or even trait-specific core collection.

Global core collection: The international agricultural research centers have wider responsibility to conserve germplasm from all geographical regions and countries globally. A core collection developed from these global germplasm collections could be termed as global core collection.

Regional core collection: Ecological environments influence adaptation of germplasm accessions. For example, groundnut is cultivated in over 113 countries, but it is an important crop in 25 countries (>1000 tons production) in the Asian continent. The core developed from the accessions involving

accessions from these countries might be more beneficial to users in Asia than a global core collection. However, we must realize that we don't have access to large variability in the regional core, compared to the global core collection.

Trait-specific core collection: Some research programs might have special focus on developing a trait-specific core collection, for example, early maturity, seed characteristics and stress responsiveness. Hence, such core collections are likely to be more useful than those constructed based on all traits. However, it is realistic to make trait-specific core collections from the entire collection data only for those traits that show high heritability and are least affected by GxE interaction.

Developing and validating core and mini core collections

Standard procedure as described below has been used to develop and validate the core collection at ICRISAT. The entire collection was first stratified by country of origin. The accessions from smaller and adjacent countries with similar agro-climates were grouped together. The data was standardized using the range of each variable to eliminate scale differences (Milligan and Cooper 1985). The standardized data was subjected to hierarchical cluster algorithm of Ward (1963) at an R^2 (squared multiple correlation) value of 0.75, using SAS (SAS Institute 2009), that optimizes an objective function because it minimizes the sums of squares within groups and maximizes the sums of squares among groups. The agglomerative procedure starts with *n* groups (ie, one observation in one group; maximum among group sum of squares), and proceeds by merging observations in groups so that the between-groups sum of squares increases and within-groups sum of squares decreases. In certain cases the within-groups sum of squares will remain the same. From each cluster, ~10% of the accessions were randomly selected for inclusion into the core collection. At least one accession was included even from those clusters that had less than 10 accessions. To test the validity of the core collection, the means of the entire collection and core collection were compared using Newman-Keuls procedure (Newman 1939, Keuls 1952). The homogeneity of variances of the entire collection and the core collection was tested with the Levene's test (Levene 1960) and χ^2 was used to test homogeneity of frequency distribution of traits between the entire collection and the core collection. To know whether the phenotypic associations, which may be under genetic control, were conserved in the core collection, the phenotypic correlations among different traits in the entire collection and the core collection were estimated independently.

Core and mini core collections in chickpea, groundnut, pigeonpea, sorghum, pearl millet and small millets

Core collection: Using passport information and characterization and evaluation data generated over a period of time, ICRISAT scientists have developed global core collections in

chickpea (http://www.icrisat.org/what-we-do/crops/Chickpea/Chickpea/GR_Chickpea.htm),
groundnut (http://www.icrisat.org/what-we-do/crops/GroundNut/Project1/Core/Start.htm),
pigeonpea (http://www.icrisat.org /what-we-do/crops/PigeonPea/CoreCollections.htm),
pearl millet (http://www.icrisat.org/what-we-do/crops/PearlMillet/Pearlmillet/coreMillet.htm),
sorghum (http://www.icrisat.org/what-we-do/crops/sorghum/Project1/sorghumcore.htm),
finger millet (http://www.icrisat.org /what-we-do/crops/crops-smallmillets/Finger_millet_Core_Collection.htm), and
foxtail millet (http://www.icrisat.org /what-we-do/crops/crops-smallmillets/Foxtail_millet_Core_Collection.htm) (Table 3).

Chickpea: The core collection consists of 1,956 accessions, constituted from 16,991 accessions (Upadhyaya et al. 2001a). It comprises 1,579 (80.7%) accessions from Asia, 200 (10.2%) accessions from Africa, 87 (4.5%) accessions from the Americas, and 60 (3.1%) accessions from Europe. Southwest Asia and the Mediterranean regions, which are the two centers of primary diversity, accounted for 588 (30.1%) and 53 (2.7%) accessions in the core collection, respectively.

The other core collection reported in chickpea consists of 505 accessions from 3,350 chickpea lines maintained at Western Regional Plant Introduction Station, Pullman, USA (Hannan et al. 1994).

Groundnut: The core collection consists of 1,704 accessions, constituted from 14,310 accessions from 92 countries (Upadhyaya et al. 2003). This

Table 3. Core and mini core collections developed for ICRISAT mandate crops.

Crop	Accessions	Traits	Subset developed	Accessions in subset	Reference
Sorghum	33,100	7	Core collection	3,475	Prasada Rao and Ramanatha Rao 1995
	22,473	2*	Core collection	2,246	Grenier et al. 2001a,b
		21	Mini core collection	242	Upadhyaya et al. 2009b
Pearl millet	16,063	11	Core collection	1,600	Bhattacharjee et al. 2007
	20,766	12	Core collection	2,094	Upadhyaya et al. 2009a
		18	Mini core collection	238	ICRISAT unpublished data
Chickpea	16,991	13	Core collection	1,956	Upadhyaya et al. 2001a
		22	Mini core collection	211	Upadhyaya and Ortiz 2001
Pigeonpea	12,153	14	Core collection	1,290	Reddy et al. 2005
		34	Mini core collection	146	Upadhyaya et al. 2006e
Groundnut	14,310	14	Core collection	1,704	Upadhyaya et al. 2003
		31	Mini core collection	184	Upadhyaya et al. 2002a
		15	Asian core collection	504	Upadhyaya et al. 2001b
Finger millet	5,940	14	Core collection	622	Upadhyaya et al 2006c
Foxtail millet	1,474	12	Core collection	155	Upadhyaya et al. 2008

* Photoperiod response as measured by flowering and plant height was used to group the accessions and 19 traits used to validate core.

core collection comprises 784 (46.0%) accessions of var. *hypogaea,* 584 (34.3%) accessions of var. *vulgaris,* 299 (17.5%) accessions of var. *fastigiata,* 27 accessions (1.6%) of var. *peruviana,* 6 accessions (0.4%) of var. *aequatoriana,* and 4 accessions (0.2%) of var. *hirsuta.* Except for *aequatoriana* (15 accessions) and *hirsuta* (20 accessions), the representation of botanical varieties in the core collection corresponded with their contribution to the entire collection.

The other core collection reported in groundnut consists of 831 accessions selected from 7,432 accessions maintained at Griffin, Georgia, USA (Holbrook et al. 1993). More recently, Dwivedi et al. (2008) developed a core collection specific to Valencia type groundnut.

Pigeonpea: The core collection consists of 1,290 accessions, constituted from 12,153 accessions from 56 countries (Reddy et al. 2005), predominantly indeterminate types (1,210 accessions), but also included 69 determinate and 11 semi-determinate types, representing diversity from 11 geographic regions of pigeonpea cultivation (see section: Assessing diversity in germplasm). It also included 10 accessions of vegetable type pigeonpea, characterized by multi-seeded, large, green pods/seeds with sweet taste, mostly grown in Africa.

Sorghum: Grenier et al. (2001a, b) used a number of sampling strategies to constitute three core collections from the collection of 22,473 sorghum germplasm: 2,247 accessions in core C and 2,247 accessions each in core P and core L. For developing these core subsets, the 22,473 accessions were stratified into 60 groups as a result of 15 basic and intermediate races and four photoperiod sensitivity groups. Then, from the frequency distribution of landraces within the race-latitudinal groups (60 groups) and the eight photoperiod classifications (four each for flowering date and plant height), a K-means clustering procedure was performed using a priori number of four clusters. Cluster-1 contained 1,160 accessions (photoperiod insensitive), cluster-2 contained 1,062 accessions (mildly photoperiod sensitive), cluster-3 contained 10,630 accessions (photoperiod sensitive), and cluster-4 contained 9,621 accessions (highly photoperiod sensitive). The C strategy sampled at random a constant number (562) of accessions from each cluster irrespective of its size. The P strategy sampled at random 10% of the accessions within each cluster (ie, 116, 106, 1,063 and 962 accessions). The L strategy sampled at random proportionally from the logarithm of the number of accessions within each cluster (ie, 488, 482, 642 and 635 accessions).

Other core collections reported in sorghum consists of 3,475 accessions selected from 33,100 accessions (Prasada Rao and Ramanatha Rao 1995) and 3,011 accessions selected from 40,000 accessions (Dahlberg et al. 2004). However, we at ICRISAT use a landrace core collection of 2,247 accessions (Grenier et al. 2001a, b) for all practical purposes.

Pearl millet: The original core collection consists of 1,600 accessions, constituted from 16,063 accessions from 25 countries (Bhattacharjee et al. 2007). The composition of the core collection reflected the predominance of accessions from India and North-West Africa, both representing dry semi-arid tropical ecology, capturing 399 accessions from North-West Africa and 522 accessions from India (the secondary center of diversity). This core collection was further augmented by adding 501 accessions representing 4,717 accessions assembled and characterized between 1998 and 2008 (Upadhyaya et al. 2009a). The augmented core collection consists of 2,094 accessions (five duplicate and 2 male sterile accessions were deleted from the original core).

Finger millet: The core collection consists of 622 accessions, constituted from 5,940 accessions from 23 countries (Upadhyaya et al. 2006c). In this core, Africa region was represented by 365 accessions (59%), Asia by 223 accessions (36%), Americas by 5 accessions (0.8%), and Europe by 7 accessions (1%). Biologically, race *Vulgaris* was epresented by 61%, *Plana* by 16%, *Compacta* by 12%, *Elongata* by 8% and *Africana* by 3%.

Foxtail millet: The core collection consists of 155 accessions, constituted from 1,474 accessions from 23 countries (Upadhyaya et al. 2008). Included in the set are 102 accessions of race *Indica* [subrace *Erecta* (2), *Glabra* (16), *Nana* (81), *Profuse* (3)], 24 accessions of race *Maxima* [subrace *Assamense* (1), *Compacta* (20), *Spongiosa* (3)], and 29 accessions of race *Moharia* [subrace *Aristata* (11), *Fusiformis* (1), *Glabra* (17)].

When the core collections were compared for mean and variances, range and frequency distribution, Shanon-Weaver diversity (H`) index (Shannon and Weaver 1949), or preservation of coadaptive gene complexes, all these parameters were non-significant for most of the traits, thus revealing that adequate variability has been sampled, while constituting the core collection in each crop.

Mini core collection

Most often, the germplasm collections at International Agricultural Research Center (IARC) genebanks are very large in size. For example, the CIMMYT genebank has more than 94,000 wheat accessions, while the IRRI genebank over 108,000 rice accessions; hence the size of core collection will be about 10,000 accessions, which is difficult for evaluation and use by crop breeders. To overcome the size of large core collection, Upadhyaya and Ortiz (2001) postulated the mini core concept and devised a seminal two-stage strategy for selecting mini core collections with minimum loss of variability. They suggested using the core collection as a basis for developing a mini core collection, which consists of ~10% accessions of the core collection (~1% of the entire collection). The first stage in constituting a mini core collection involves developing a representative core collection (about 10%) from the entire collection using the available information on origin, characterization and evaluation data. The second stage involves evaluation of the core collection for various morphological, agronomic and grain quality traits, and selecting a further set of about 10% accessions from the core collection. At both the stages, standard clustering procedures were used to create groups of similar accessions (Figure 11). Following this strategy, mini core collections have been constituted in

chickpea (http://www.icrisat.org /what-we-do/crops/ChickPea/Chickpeaminicore.htm),
groundnut (http://www.icrisat.org /what-we-do/crops/GroundNut/Project1/gnmncore.htm),
pigeonpea (http://www.icrisat.org /what-we-do/crops/PigeonPea/Pigeonpeaminicore.htm),
sorghum (http://www.icrisat.org /what-we-do/crops/sorghum/Project1/Sorghumminicore.htm), and
pearl millet (http://www.icrisat.org /what-we-do/crops/PearlMillet/Project1/Pearlmilletminicore.htm) (Table 3). Validation studies of these mini core collections with core collections revealed that these mini core collections represented adequate diversity for most of the traits detected in core collections.

Chickpea: The mini core collection consists of 211 accessions selected from 1,956 core collection accessions. The composition of mini core reflected the predominance of accessions from Asia (82%) and Africa (12%), with only 2-3% from America and Europe. Biologically desi (75%) and kabuli (21%) seed types were predominant, with fairly less representation of pea-shaped (4%) seed types. This corresponds well with the proportion of

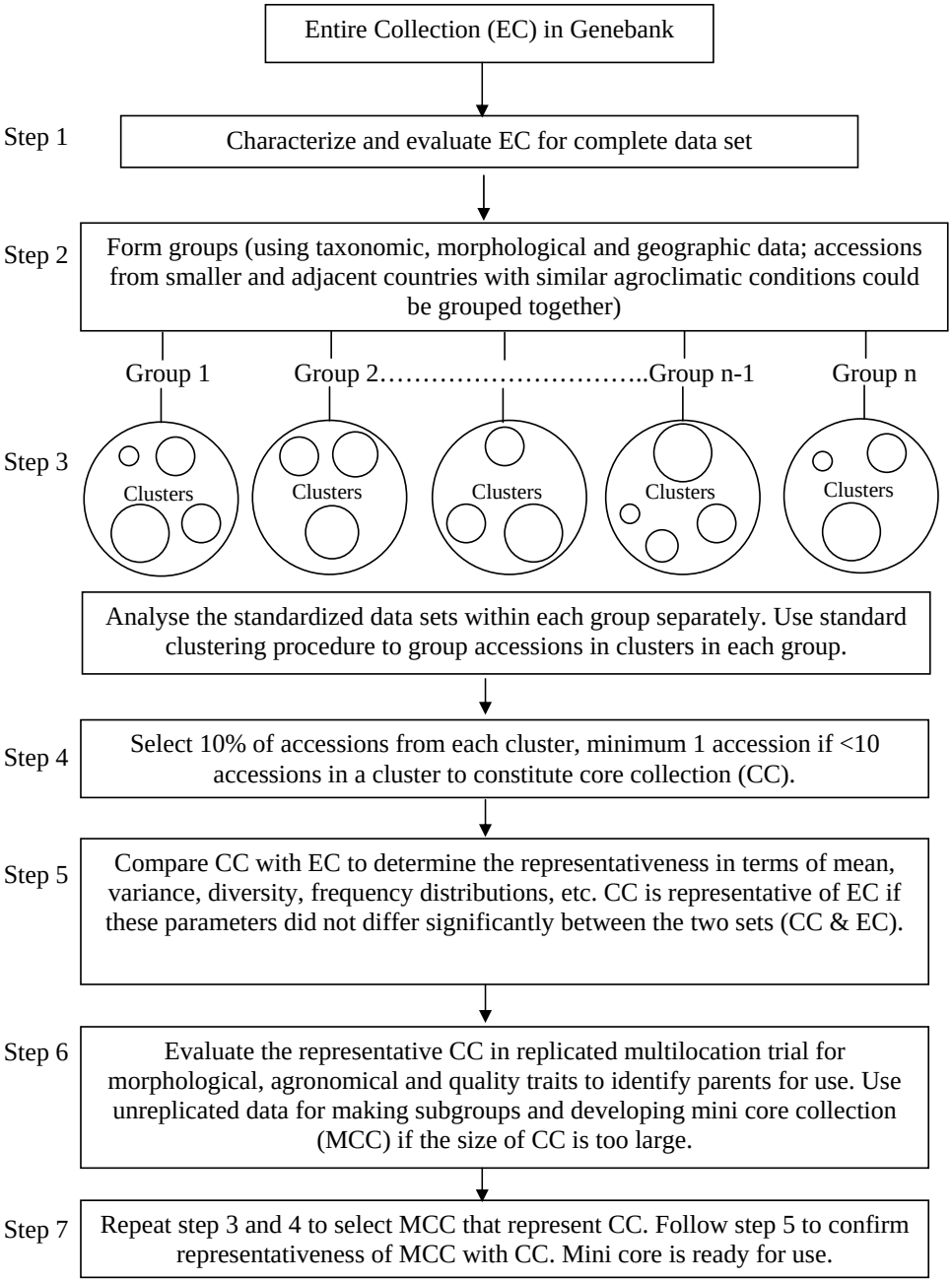

Figure 11. Flow diagram to establish core and mini core collections in a crop species.

representation of accessions (both geographically and biologically) in the core collection.

Groundnut: The mini core collection consists of 184 accessions selected from 1,704 core collection accessions. This mini core represented all the six botanical varieties, with fairly high representation from *hypogaea* (46%), *vulgaris* (31%) and *fastigiata* (20%) types, which corresponded well with representation of *hypogaea* (46%), *vulgaris* (36%) and *fastigiata* (16%) types in the core collection. Geographically, the accessions from Asia (33%), America (33%) and Africa (23%) were predominant. South America, where groundnut originated, is represented by 16% of the accessions.

Pigeonpea: The mini core collection consists of 146 accessions selected from 1,290 core collection accessions. The composition of this mini core collection reflected the predominance of accessions from southern India, Sri Lanka and Maldives. Other regions represented include northwestern India, Pakistan, Iran, Bangladesh, Myanmar, Nepal, China, Taiwan, northeastern India and Central India. Likewise ~8% of the accessions were from southern and eastern Africa while ~3% each were from western and central Africa.

Sorghum: The mini core collection consists of 242 accessions selected from 2,246 core collection accessions representing 58 countries. Accessions in this mini core represented geographic regions (10) and biological races (five races and 10 intermediate races). Further, *caudatum*, *durra* and *guinea* among races and *caudatum-bicolor* and *guinea-caudatum* among intermediate races were dominant in both the core and mini core.

Pearl millet: The mini core collection consists of 238 accessions selected from 2,094 core collection accessions representing 46 countries. The composition of this mini core reflected the predominance of accessions from India and North-West Africa, both representing dry semi-arid tropical ecology. This mini core collection captured 90% range variation of the core collection.

These core and mini core collections are dynamic and should be augmented as and when information on additional sets of germplasm (not previously included in the formation of core/mini core collection) become available.

Research is in progress to develop mini core collections in finger millet and foxtail millet.

Identifying new sources of variation for crop improvement using core and mini core collections

Agronomic traits, including yield: The core and mini core collections have provided several new sources of variation for use in crop improvement programs. For example, using days to 50% flowering, pods per plant, seed yield and 100-seed weight as a selection criterion, Upadhyaya et al. (2007a) identified 19 desi, 15 kabuli and five pea-shaped seed types as most promising accessions for early maturity, seed size and grain yield from chickpea core. The desi types produced 8.5% more seed yield with 32% larger seeds than control cv. Annigeri, while the kabuli types yielded at par with control cv. L550, but had 84% larger seeds. Several pigeonpea accessions with early maturity, greater harvest index and shelling percentage, and high grain yield were identified (ICRISAT Archival Report 2008). The groundnut core showed variation for several morphological and agronomic traits. The *hypogaea* group showed significantly greater mean pod length, pod width, seed length, seed width, yield per plant, and 100-seed weight; whereas the *fastigiata* group had greater plant height, leaflet length, leaflet width and shelling percentage (Upadhyaya 2003b). Interestingly, the evaluation of groundnut core was more rewarding as the scientists identified rich diversity among accessions for early maturity (Upadhyaya et al. 2006d), and in the Asia region core for high pod yield, greater shelling percentage and larger 100-seed weight (Upadhyaya et al. 2005a). Pearl millet accessions with high green fodder yield, more productive tillers plant^{-1}, high spikelet density earhead^{-1}, higher grain yield and large-seed size were identified. The researchers were also able to identify sorghum accessions with high grain and/or fodder yield, extra-early flowering, more basal tillers, panicles with variable exsertion and head shape, and high soluble sugar content in stalk (for use in biofuel). Likewise, accessions with high grain and/or fodder yield, early maturity, more basal tillers, and long inflorescence types were identified in finger millet and/or foxtail millet (ICRISAT Archival Report 2008).

The mini core collections have also been extensively evaluated by national programs for identifying lines with beneficial traits. For example, Indian program scientists identified 13 kabuli accessions with large seed size. Using the groundnut mini core, Chinese scientists identified four accessions with high oleic/linoleic acid ratio, five accessions each with high shelling percentage and large seeds. Similarly, researchers from Thailand and Vietnam identified five accessions each with large seed size and high shelling percentage.

Drought tolerance: Root length and root length density (RLD) have been recognized as important traits for improving chickpea productivity under progressively receding soil moisture conditions. Kashiwagi et al. (2005) detected large genetic variation in the chickpea mini core collection for RLD and for the ratio of plant dry weight to root length density, and identified nine accessions that had the largest RLD and the deepest root system in comparison to previously identified drought tolerant accession ICC 4958 (Figure 12). Moreover, the chickpea landraces from the Mediterranean and the West Asian region showed a significantly larger RLD than those from the South Asian region. In addition, landraces from Central Asia (former Soviet Union), characterized by arid agro-climatic conditions, also showed relatively larger RLD. Thus, information on the genetic variability for root traits provides valuable baseline knowledge for further progress in the selection and breeding for drought avoidance root traits in chickpea.

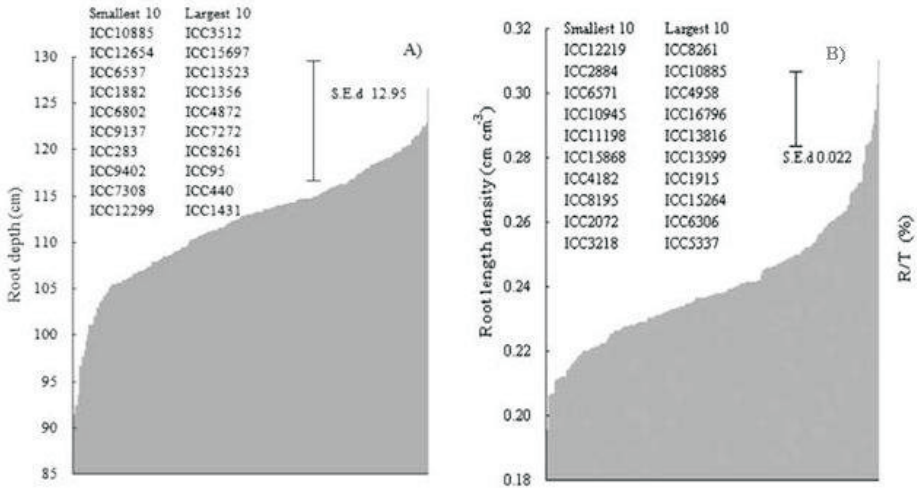

Fig. 12. Distribution of the means of 211 chickpea mini core germplasm and five cultivars for (A) root depth and (B) root length density (RLD) across seasons at 35 days after sowing (Kashiwagi et al. 2005).

Accessions tolerant to drought, as measured by SPAD Chlorophyll meter reading (SCMR) and specific leaf area (SLA), have also been identified in the groundnut mini core collection, and these include 18 accessions (Upadhyaya 2005).

Salinity tolerance: Vadez et al. (2007) reported six-fold variation in the chickpea mini core for seed yield under salinity (80 mM NaCl; pot screening), with 12 accessions yielding more than a previously released saline tolerant chickpea cultivar, CSG 8962. The three highly salinity tolerant accessions in their study were ICC 1431, ICC 5003 and ICC 15610. Screening of groundnut and pigeonpea mini core collections resulted in identification of many accessions that performed well under saline conditions (1.9 L of 80 mM NaCl per 7.5 kg Vertisol) (Srivastava et al. 2006, 2007; ICRISAT Archival Report 2008).

Low temperature tolerance: The groundnut core collection was tested for tolerance to low temperature at germination (12^0C). Several accessions with capacity to germinate at lower temperature have been identified, with many of them maturing and/or yielding similar or greater than the best control cultivar (Upadhyaya et al. 2009c). Some of the best performing accessions for pod yield include ICGs 12625, 13284, 2039, 13513 and 1824 in rainy season, ICGs 12553, 12625, 7898, 10595, 6148, 6022, 7013, 7884, 7905 and 4992 in postrainy season, and ICGs 12625, 7898, 11130, 6148, 7013, 6022, 7905, 7884 and 4992 in both the seasons.

Resistance to diseases: Host plant resistance is the major component in crop improvement to minimize the losses due to diseases. When the chickpea mini core collection was evaluated for biotic stresses, Pande et al. (2006) detected high level of resistance to fusarium wilt (FW) in 46 accessions while 3 showed moderate resistance to ascochyta blight (AB), 55 to botrytis gray mold (BGM), and 6 to dry root rot (DRR). They also identified a few accessions with multiple resistances: ICC 11284 resistant to AB and BGM; ICC 11764 and ICC 12328 resistant to BGM and DRR; ICC# 1710, 2242, 2277 and 13441 resistant to DRR and FW; and 11 accessions resistant to BGM and FW (Table 4). Tolerance to root-knot nematode, early leaf spot, pepper spot, tomato spotted wilt virus and many soilborne fungal diseases, including pre-harvest aflatoxin contamination were identified in groundnut core and mini core collections (Isleib et al. 1995; Anderson et al. 1996; Holbrook et al. 1998, 2000; Franke et al. 1999; Damicone et al. 2003). A few sorghum accessions resistant to grain mold have also been identified.

Table 4. New sources of variation reported after evaluating chickpea mini core (Pande et al. 2006).

Diseases	Accession (ICC no.)	Origin	Seed type	100-seed weight (g)	Growth duration
AB+BGM	11284	Russia & CIS	Desi	16.1	Medium
BGM+DRR	11764	Chile	Kabuli	28.8	Late
	12328	Cyprus	Kabuli	27.5	Medium
BGM+FW	2990	Iran	Desi	17.8	Late
	4533	India	Desi	18.2	Late
	6279	India	Desi	24.9	Early
	7554	Iran	Desi	22.6	Early
	7819	Iran	Desi	24.1	Late
	9848	Afghanistan	Pea-shaped	15.5	Late
	12028	Mexico	Desi	22.0	Medium
	12155	Bangladesh	Desi	13.0	Early
	13219	Iran	Desi	15.0	Early
	13599	Iran	Desi	22.4	Late
	13816	Russia & CIS	Kabuli	29.0	Late
FW+DRR	1710	India	Desi	11.6	Medium
	2242	India	Desi	11.5	Late
	2277	Iran	Kabuli	24.0	Medium
	13441	Iran	Kabuli	16.7	Late

AB = Ascochyta blight, BGM = Botrytis grey mold, DRR = Dry root rot, FW = Fusarium wilt

ICRISAT's research on development of mini core collections and their evaluation for finding new sources of variation have been recognized worldwide because of the usefulness of the concept. There is a huge demand from the national programs to receive mini core subsets for evaluation and use in crop improvement programs. ICRISAT has supplied 19 sets of core and 84 sets of mini core collections to researchers in 20 countries (Canada, China, India, Japan, Malawi, Mexico, Nigeria, Thailand, UAE, USA, France, Uganda, Tanzania, Senegal, Mali, Germany, Niger, Syria, Kenya and Vietnam) and scientists have reported finding useful variation for grain yield, grain quality and resistance/tolerance to stresses. For example, four

large-seeded kabuli (ICCs 12033, 14203, 14187 and 14199) and six desi and kabuli types (ICCs 5879, 7255, 8350, 10393, 10885 and 13125) are being used in chickpea improvement in India (Kaul et al. 2005, Johnson et al. 2007).

Likewise, groundnut and pigeonpea mini core collections provided useful variation for use in crop improvement in many countries. For example, groundnut accessions ICG 8760 and ICG 3787 resistant to rust and late leaf spot in India (Kusuma et al. 2007); 11 groundnut accessions with high quality oil and 14 accessions resistant to bacterial wilt in China; five large-seeded groundnut accessions each in China and Thailand; and five groundnut accessions for high shelling percentage each in China, Thailand and Vietnam (ICRISAT Archival Report 2008). Several pigeonpea mini core accessions exhibited rich diversity for agronomic traits that researchers selected for use in pigeonpea breeding in India (Singh et al. 2007). Preliminary evaluation of pigeonpea mini core further revealed that some of these accessions are adapted to nutrient-poor soil conditions (Rao and Shahid 2007).

Conclusion

Core collections, consisting of ~10% accessions but representing over 80% variability present in the entire collection, have been established in chickpea (1,956 accessions), groundnut (1,704 accessions), pigeonpea (1,290 accessions), pearl millet (2,094 accessions), sorghum (2,247 accessions), finger millet (622 accessions) and foxtail millet (155).

To overcome large size of the core collections, mini core collections (representing ~10% of core or ~1% of entire collection) in chickpea (211 accessions), groundnut (184 accessions), pigeonpea (146 accessions), pearl millet (238 accessions) and sorghum (242 accessions) have been developed to enhance use of germplasm in crop improvement programs. Research is in progress to form mini core collections in finger millet and foxtail millet.

Researchers found that the mini core collections enabled them to undertake intensive screening and evaluation, which led to identifying new sources of variation for various traits including resistance to biotic and abiotic stresses and agronomic traits, more effectively.

Optimal and convenient size of mini core collections have led to increased demand for germplasm use by researchers as witnessed by increasing demand for supplying mini core collections for evaluation by NARS (84 mini core sets in 13 countries).

Feedback from researchers in national programs revealed that mini core collections are the most convenient for evaluation and identification of sources of variation for beneficial traits such as early maturity, resistance to diseases, large seed size and high grain yield.

Developing core and mini core collections have enhanced the capacity of germplasm curators for their effective regeneration and conservation strategies.

The mini core concept, developed by ICRISAT, has been well recognized by researchers worldwide to enhance use of germplasm in crop improvement programs.

Limited seed of mini core collections are available to scientists globally for research and training.

References

Anderson WF, Holbrook CC and **Culbreath AK.** 1996. Screening the peanut core collection for resistance to tomato spotted wilt virus. Peanut Sci. 23:57-61.

Bhattacharjee R, Khairwal IS, Bramel PJ and **Reddy KN.** 2007. Establishment of a pearl millet [*Pennisetum glaucum* (L) R. Br.] core collection based on geographical distribution and quantitative traits. Euphytica 155:35-45.

Brown AHD. 1989a. Core collections: a practical approach to genetic resources management. Genome 31:818-824.

Brown AHD. 1989b. The case for core collections. Pages 136-155 *in* The use of plant genetic resources (Brown AHD, Frankel OH, Marshall DR and Williams JT, eds.). Cambridge, UK: Cambridge Univ. Press.

Brown AHD and **Spillane C.** 1999. Implementing core collections-principles, procedures, progress, problems and promise. Pages 1-9 *in* Core Collections for Today and Tomorrow (Johanson RC and Hodgkin T, eds.). Rome, Italy: IPGRI.

Cantrell RP, Christopher R, Dowswell CR and **Paliwal RL.** 1996. Maize in the third world. Boulder, USA: Westview Press. 268 pp.

Dahlberg JA, Burkee JJ and **Rosenow DT.** 2004. Development of a sorghum core collection: Refinement and evaluation of a subset from Sudan. Econ. Bot. 58:556-567.

Dalrymple DG. 1986. Development and spread of high-yielding wheat varieties in developing countries, 7th edition. Washington DC: US Agency for International Development.

Damicone JP, Jackson KE, Dashiell KE, Melouk HA and **Holbrook CC.** 2003. Reaction of the peanut core to sclerotinia blight and pepper spot. http://www.apres.okstate.edu/old%20proceedings/APRES%202003%20Proceedings%20vol%2035.pdf#search='APRES%202003. Proc. Amer. Peanut Res. and Educ. Soc. 35:55.

Dwivedi SL, Puppala N, Upadhyaya HD, Manivannan N and **Singh S.** 2008. Developing a core collection of peanut specific to Valencia market type. Crop Sci. 48:625-632.

FAO. 1998. The state of ex-situ conservation. Pages 83-136 *in* The state of the World's Plant Genetic Resources for Food and Agriculture. Rome: FAO.

Franke MD, Bennemen TB and **Holbrook CC.** 1999. Identification of resistance to Rhizoctonia limb rot in a core collection of peanut germplasm. Plant Dis. 83:944-948.

Frankel OH. 1984. Genetic perspective of germplasm conservation. Pages 161-170 *in* Genetic manipulations: impact on man and society (Arber W, Limensee K, Peacock WJ and Stralinger P, eds.). Cambridge, UK: Cambridge University Press.

Frankel OH and **Brown AHD.** 1984. Plant genetic resources today: a critical appraisal. Pages 249-257 *in* Crop Genetic Resources: Conservation and Evaluation (Holden JHW and Williams JT, eds.). London: George Allen and Unwin LTD.

Grenier C, Bramel PJ and **Hamon P.** 2001a. Core collection of the genetic resources of sorghum: 1. Stratification based on eco-geographical data. Crop Sci. 41:234-240.

Grenier C, Hamon P and **Bramel-Cox PJ.** 2001b. Core collection of sorghum: II. Comparison of three random sampling strategies. Crop Sci. 41:241-246.

Hannan RM, Kaiser WJ and **Muehlbauer FJ.** 1994. Development and utilization of the USDA chickpea germplasm core collection. Page 217 *in* Agronomy Abstracts 1994. Madison, WI: ASA.

Harlan JR and **de Wet JMJ.** 1972. A simple classification of cultivated sorghum. Crop Sci. 12:172-176.

Holbrook CC, Anderson WF and **Pittman RN.** 1993. Selection of a core collection from the U.S. Germplasm collection of peanut. Crop Sci. 33:859-861.

Holbrook CC, Bruniard J, Moore KM and **Knauft DA.** 1998. Evaluation of the peanut core collection for oil content. Page 159 *in* Agronomy Abstracts 1998. Madison, WI: ASA.

Holbrook CC, Stephenson MG and **Johnson AW.** 2000. Level and geographical distribution of resistance to *Meloidogyne arenaria* in the US peanut germplasm collection. Crop Sci. 40:1168-1171.

IBPGR. 1985a. Descriptors for Finger Millet. Rome: International Board for Plant Genetic Resources Secretariat. 20 pp.

IBPGR. 1985b. Descriptors for *Setaria italica* and *S. pumila*. Rome: International Board for Plant Genetic Resources Secretariat. 18 pp.

IBPGR and **ICRISAT.** 1992. Descriptors for groundnut. Rome, Italy: International Board for Plant Genetic Resources (IBPGR) and Patancheru 502 324, Andhra Pradesh, India: International Crops Research Institute for the Semi-Arid Tropics (ICRISAT). 124 pp.

IBPGR and **ICRISAT.** 1993a. Descriptors for Pigeonpea [*Cajanus cajan* (L.) Millsp.]. Rome, Italy International Board for Plant Genetic Resources (IBPGR) and Patancheru 502 324, Andhra Pradesh, India: International Crops Research Institute for the Semi-Arid Tropics (ICRISAT). 31 pp.

IBPGR and **ICRISAT.** 1993b. Descriptors for pearl millet [*Pennisetum glaucum* (L.) R. Br.]. Rome, Italy: International Board for Plant Genetic Resources (IBPGR) and Patancheru 502 324, Andhra Pradesh, India: International Crops Research Institute for the Semi-Arid Tropics (ICRISAT). 43 pp.

IBPGR and **ICRISAT.** 1993c. Descriptors for sorghum [*Sorghum bicolor* (L.) Moench]. Rome, Italy: International Board for Plant Genetic Resources (IBPGR) and Patancheru 502 324, Andhra Pradesh, India: International Crops Research Institute for the Semi-Arid Tropics (ICRISAT). 38 pp.

IBPGR, ICRISAT and **ICARDA.** 1993. Descriptors for Chickpea (*Cicer arietinum* L.). Rome, Italy: International Board for Plant Genetic Resources (IBPGR), Patancheru 502 324, Andhra Pradesh, India: International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) and Aleppo, Syria: International Center for Agricultural Research in the Dry Areas. 31pp.

ICRISAT Archival Report 2008. http://intranet/ddg/Admin%20Pages2009/Documents/Archival_2008.pdf.

Isleib TG, Beute MK, Rice PW and **Hollowell JE.** 1995. Screening the core collection for resistance to Cylindrocladium black rot and early leaf spot. Proc. Am. Peanut Res. Educ. Soc. 27:25.

Johnson PL, Sharma RN, Nair SK, Pandey RL and **Kashyap OP.** 2007. Study of genetic diversity in chickpea under rainfed situation. Page 199 *in* Abstracts: National Symposium on Legumes for Ecological Sustainability – Emerging Challenges and Opportunities. Kanpur, India: IIPR.

Kashiwagi J, Krishnamurthy L, Upadhyaya HD, Krishna H, Chandra S, Vincent Vadez and **Serraj R.** 2005. Genetic variability of drought-avoidance root traits in the mini-core germplasm collection of chickpea (*Cicer arietinum* L.). Euphytica 146:213-222.

Kaul J, Kumar S and **Gurha SN.** 2005. Evaluation of exotic germplasm of kabuli chickpea. Indian J. Plant Genet. Resour. 18:201-204.

Keuls M. 1952. The use of the “Studentized range” in connection with an analysis of variance. Euphytica 1:112-122.

Knauft DA and **Gorbet DW.** 1989. Genetic diversity among peanut cultivars. Crop Sci. 29:1417-1422.

Kumar S, Gupta S, Chandra S and **Singh BB.** 2004. How wide is genetic base of pulse crops? Pages 211-221 *in* Pulses in New Perspective. Proceedings of the National Symposium on Crop Diversification and Natural Resources Management (Ali M, Singh BB, Shiv Kumar and Vishwa Dhar, eds.). 20-22 December 2003. Kanpur: Indian Society of Pulses Research and Development, Indian Institute of Pulses Research.

Kusuma VP, Yugandhar G, Ajay BC, Gowda MVC and **Upadhyaya HD.** 2007. Identification of sources of multiple disease resistance in groundnut (*Arachis hypogaea* L.) mini core. Pages 31-32 *in* ISOR National Seminar, 29-31 January 2007, Directorate of Oilseeds Research, Rajendranagar, Hyderabad, India.

Levene H. 1960. Robust tests for equality of variances. Pages 278-292 *in* Contributions to probability and statistics: Essays in honour of Harold Hotelling (Oklin I, ed.). Stanford: University Press.

Milligan GW and **Cooper M.** 1985. An examination of procedures for determining the number of clusters in a data set. Psychometrika 50:159-179.

Newman D. 1939. The distribution of range in samples from a normal population expressed in terms of an independent estimate of standard deviation. Biometrika 31:20-30.

Pande S, Kishore GK, Upadhyaya HD and **Rao JN.** 2006. Identification of multiple diseases resistance in mini core collection of chickpea. Plant Dis. 90:1214-1218.

Prasada Rao KE, de Wet JMJ, Brink DE and **Mengesha MH.** 1987. Intraspecific variation and systematics of cultivated *Setaria italica*, foxtail millet (*Poaceae*). Economic Bot. 41:108-116.

Prasada Rao KE and **Ramanatha Rao.** 1995. The use of characterization data in developing a core collection of sorghum. Pages 109–115 *in* Core collection of plant genetic resources (Hodgkin T, Brown AHD, van Hintum Th JL and Morales BAV, eds.). Chichester, UK: A Wiley-Sayee Publication.

Rao NK and **Shahid M.** 2007. Desert farming: continued quest for new crops. Biosalinity News 2007:2. Dubai, UAE: International Center for Biosaline Agriculture.

Reddy LJ, Upadhyaya HD, Gowda CLL and **Singh S.** 2005. Development of core collection in pigeonpea [*Cajanus cajan* (L.) Millsp.] using geographic and qualitative morphological descriptors. Genet. Resour. Crop Evo. 52:1049-1056.

SAS Institute Inc. 2009. SAS Online Doc (R) 9.2. Cary, NC: SAS Institute, Inc. (http://www.sas.com).

Shannon CE and **Weaver W.** 1949. The mathematical theory of communication. Urbana: Univ. Illinois Press.

Sharma D, Reddy LJ, Green JM and **Jain KC.** 1981. International adaptation of pigeonpea. Pages 71-81 *in* Proc. Int. workshop on pigeonpea. (Nene YL, ed.). Vol 1, 15-19 December 1980. Patancheru 502 324, Andhra Pradesh, India: International Crops Research Institute for the Semi-Arid Tropics.

Singh F, Majumder ND, Kant R and **Kumar G.** 2007. Germplasm resources in pigeonpea – A scope for their utilization. Page 197 *in* Abstracts: National Symposium on Legumes for Ecological Sustainability – Emerging Challenges and Opportunities. Kanpur, India: IIPR.

Srivastava N, Vadez V, Krishnamurthy L, Saxena KB, Nigam SN and **Rupkala A.** 2007. Standardization of a screening technique for salinity tolerance in groundnut (*Arachis hypogaea (L.)*) and pigeonpea (*Cajanus cajan (L.) Millsp.*). Indian J. Crop Sci. 2:209-214.

Srivastava N, Vadez V, Upadhyaya HD and **Saxena KB.** 2006. Screening for intra and interspecific variability for salinity tolerance in pigeonpea (*Cajanus cajan*) and its wild species. J. SAT Agric. Res. 2:1-12.

Stenhouse JW, Prasada Rao KE, Reddy VG and **Rao SA.** 1997. Sorghum. Pages 292-308 *in* Biodiversity in Trust (Fuccillo L, Sears L and Stapleton P, eds.). UK: Cambridge University Press.

Upadhyaya HD. 2003a. Geographical patterns of variation for morphological and agronomic characters in the chickpea germplasm collection. Euphytica 132:343-352.

Upadhyaya HD. 2003b. Phenotypic diversity in groundnut (*Arachis hypogaea* L.) core collection assessed by morphological and agronomic evaluations. Genet. Resour. Crop Evol. 50:539-550.

Upadhyaya HD. 2005. Variability for drought resistance related traits in the mini core collection of peanut. Crop Sci. 45:1432-1440.

Upadhyaya HD, Bramel PJ and **Sube Singh.** 2001a. Development of a chickpea core sub set using geographic distribution and quantitative traits. Crop Sci. 41:206-210.

Upadhyaya HD, Ortiz R, Bramel PJ and **Sube Singh.** 2001b. Development of groundnut core collection from Asian region. Abstract of poster. Pages 43-44 *in* Diamond Jubilee Symposium, Hundred Years of Post-Mendelian Genetics and Plant Breeding - Retrospect and Prospects, Poster Abstracts, 6-9 November 2001 (Kharkwal MC and Mehra RB, eds.). New Delhi, India: Indian Society of Genetics and Plant Breeding.

Upadhyaya HD, Bramel PJ, Ortiz R and **Sube Singh.** 2002a. Developing a mini core of peanut for utilization of genetic resources. Crop Sci. 42:2150-2156.

Upadhyaya HD, Bramel PJ, Ortiz R and **Singh S.** 2002b. Geographical patterns of diversity for morphological and agronomic traits in the groundnut germplasm collection. Euphytica 128:191-204.

Upadhyaya HD, Dwivedi SL, Gowda CLL and **Singh S.** 2007a. Identification of diverse germplasm lines for agronomic traits in a chickpea (*Cicer arietinum* L.) core collection for use in crop improvement. Field Crops Res. 100:320-326.

Upadhyaya HD, Reddy KN and **Gowda CLL.** 2007b. Pearl millet germplasm at ICRISAT genebank – status and impact. J. SAT Agric. Res. 3:1-5.

Upadhyaya HD, Furman BJ, Dwivedi SL, Udupa SM, Gowda CLL, Baum M, Crouch JH, Buhariwalla HK and **Sube Singh.** 2006a. Development of a composite collection for mining germplasm possessing allelic variation for beneficial traits in chickpea. Plant Genet. Resour: Characterization and utilization 4:13-19.

Upadhyaya HD, Gowda CLL, Buhariwalla HK and **Crouch JH.** 2006b. Efficient use of crop germplasm resources: identifying useful germplasm for crop improvement through core and mini core collections and molecular marker approaches. Plant Genet. Resour: Characterization and utilization 4:25-35.

Upadhyaya HD, Gowda CLL, Pundir RPS, Reddy VG and **Singh S.** 2006c. Development of core subset of finger millet germplasm using geographical origin and data on 14 quantitative traits. Genetic Resour. Crop Evol. 53:679-685.

Upadhyaya HD, Reddy LJ, Gowda CLL and **Singh S.** 2006d. Identification of diverse groundnut germplasm: Sources of early-maturity in a core collection. Field Crops Res. 97:261-267.

Upadhyaya HD, Reddy LJ, Gowda CLL, Reddy KN and **Sube Singh.** 2006e. Development of a Mini Core subset for Enhanced and Diversified utilization of Pigeonpea Germplasm Resources. Crop Sci. 46:2127-2132.

Upadhyaya HD, Mallikarjuna Swamy BP, Goudar PVK, Kullaiswamy BY and **Singh S.** 2005a. Identification of diverse groundnut germplasm through multienvironment evaluation of a core collection for Asia. Field Crops Res. 93:293-299.

Upadhyaya HD, Pundir RPS, Gowda CLL, Reddy KN and **Singh S.** 2005b. Geographical patterns of diversity for qualitative and quantitative traits in the pigeonpea germplasm collection. Plant Genet. Resour: Characterization and utilization 3:331-352.

Upadhyaya HD and **Ortiz R.** 2001. A mini core collection for capturing diversity and promoting utilization of chickpea genetic resources in crop improvement. Theor. Appl. Genet. 102:1292-1298.

Upadhyaya HD, Ortiz R, Bramel PJ and **Singh S.** 2003. Development of a groundnut core collection using taxonomical, geographical and morphological descriptors. Genet. Resour. Crop Evol. 50:139-148.

Upadhyaya HD, Pundir RPS, Gowda CLL, Reddy VG and **Singh S.** 2008. Establishing a core collection of foxtail millet to enhance utilization of germplasm of an underutilized crop. Plant Genet. Resour: Characterization and utilization 7:177-184.

Upadhyaya HD, Gowda CLL, Reddy KN and **Singh S.** 2009a. Augmenting the pearl millet core collection for enhancing germplasm utilization in crop improvement. Crop Sci. 49:573-580.

Upadhyaya HD, Pundir RPS, Dwivedi SL, Gowda CLL, Gopal Reddy V and **Sube Singh.** 2009b. Developing a mini core collection of sorghum for diversified utilization of germplasm. Crop Sci. 49:1769-1780.

Upadhyaya HD, Reddy LJ, Gowda CLL and **Singh S.** 2009c. Phenotypic diversity in cold-tolerant peanut (*Arachis hypogaea* L.) germplasm. Euphytica 165:279-291.

Vadez V, Krishnamurthy L, Serraj R, Gaur PM, Upadhyaya HD, Hoisington DA, Varshney RK, Turner NC and **Siddique KHM.** 2007. Large variation in salinity tolerance in chickpea is explained by differences in sensitivity at reproductive stage. Field Crops Res. 104:123-129.

Vavilov NI. 1951. The origin, variation, immunity and breeding of cultivated plants. Chronica Botanica 13:1-366.

Vellve R. 1992. Saving the seeds: genetic diversity and European agriculture. London: Earthscan Publication.

Ward J. 1963. Hierarchical grouping to optimize an objective function. J. Am. Stat. Assoc. 38:236-244.

About ICRISAT

ICRISAT
Science with a human face

The International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) is a non-profit, non-political organization that does innovative agricultural research and capacity building for sustainable development with a wide array of partners across the globe. ICRISAT's mission is to help empower 600 million poor people to overcome hunger, poverty and a degraded environment in the dry tropics through better agriculture. ICRISAT is supported by the Consultative Group on International Agricultural Research (CGIAR).

Contact Information

ICRISAT-Patancheru (Headquarters)
Patancheru 502 324
Andhra Pradesh, India
Tel +91 40 30713071
Fax +91 40 30713074
icrisat@cgiar.org

ICRISAT-Liaison Office
CG Centers Block
NASC Complex
Dev Prakash Shastri Marg
New Delhi 110 012, India
Tel +91 11 32472306 to 08
Fax +91 11 25841294

ICRISAT-Nairobi (Regional hub ESA)
PO Box 39063, Nairobi, Kenya
Tel +254 20 7224550
Fax +254 20 7224001
icrisat-nairobi@cgiar.org

ICRISAT-Niamey (Regional hub WCA)
BP 12404, Niamey, Niger (Via Paris)
Tel +227 20722529, 20722725
Fax +227 20734329
icrisatsc@cgiar.org

ICRISAT-Bamako
BP 320
Bamako, Mali
Tel +223 20 223375
Fax +223 20 228683
icrisat-w-mali@cgiar.org

ICRISAT-Bulawayo
Matopos Research Station
PO Box 776,
Bulawayo, Zimbabwe
Tel +263 83 8311 to 15
Fax +263 83 8253, 8307
icrisatzw@cgiar.org

ICRISAT-Lilongwe
Chitedze Agricultural Research Station
PO Box 1096
Lilongwe, Malawi
Tel +265 1 707297, 071, 067, 057
Fax +265 1 707298
icrisat-malawi@cgiar.org

ICRISAT-Maputo
c/o IIAM, Av. das FPLM No 2698
Caixa Postal 1906
Maputo, Mozambique
Tel +258 21 461657
Fax +258 21 461581
icrisatmoz@panintra.com

www.icrisat.org

ISBN 978-92-9066-519-9 Order code IBE 078 227-09