

Sorghum and Pearl Millet Genetic Resources Utilization

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Abstract

Sorghum and pearl millet are unique in size and diversity. The largest collections contain 40,570 (U.S. sorghum collection) and 21,191 (ICRISAT pearl millet collection) accessions. Less than three percent of these accessions have been used in crop improvement. Curation—or acquisition, maintenance, characterization, and utilization—plays a role in exploitation of the genetic variation within these collections.

Cultivation of sorghum and pearl millet is increasing the use of marginal agricultural land. Future utilization will depend on increased research on abiotic and biotic stress tolerance. To facilitate exploitation of this vast germplasm, traditional and biotechnical methods must be combined to provide better understanding of the genetic variation available, which then can be used in crop enhancement. This can only be accomplished through sharing of ideas, particularly through creation of an arena where information is globally accessible.

Sorghum [*Sorghum bicolor* (L.) Moench] and millet (pearl millet [*Pennisetum glaucum* (L.) R. Br.] and several other small-seeded grasses grown as grain and fodder crops) are some of the most important cereals globally. In 1995, the FAO estimated sorghum was harvested on 43 million ha, with a production of 53 million MT, and an average yield of 1544 kg ha⁻¹. Millet was harvested on 37 million ha, producing 26 million MT, with an average yield of 1070 kg ha⁻¹ (FAOSTAT database, 1996). Despite their importance as food and feed crops, literature on their curation is limited. As demand for food

production—with fewer inputs based on a more balanced ecological scale—increases, information on more effective methods of identifying, maintaining, and using exotic germplasm within both crops is needed.

World collections are unique, not only in size, but also in diversity (Dahlberg and Spinks, 1995; Hanna and Lovell, 1995; Lawrence and Rettke, 1995; Prasada Rao et al., 1995; Wenzel, 1995). The diversity and availability of these resources has led to steady improvement in sorghum and millet. Sorghum improvement has been characterized by long-term increase of hybrid yields (Miller and Kebede, 1984; Doggett, 1988). Early work on utilization of sorghum germplasm was confined to pure line selection within cultivated landrace populations in Africa and India that

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resulted in somewhat improved cultivars, some of which continue to be widely grown. Selection within dwarf populations was then taken up, followed by exploitation of cytoplasmic male-sterility, which permitted the production of commercial hybrids. Crossing and/or backcrossing between adapted introductions and local germplasm has been used to derive improved self-pollinated varieties and parental lines (Prasada Rao et al., 1989). Sorghum yields have increased by over 30% within the last 30 years and much of this gain can be attributed to genetic diversity found within the species. Useful traits such as increased seed number, larger panicles, greater total plant weight, drought tolerance, disease resistance, greater plant height, longer maturity, greater leaf area indices, increased green leaf retention, and greater partitioning of dry matter have contributed to increased yields (Miller and Kebede, 1984).

Utilization has been primarily limited to agronomically important and, in some cases, wild sources of germplasm. For example, use of Zerazera sorghum has become widespread in the development of new, superior hybrids because of superior yield potential and grain quality (Duncan et al., 1991). Restricted utilization of extensive germplasm collections has occurred because of several characteristics inherent to the collections themselves. The size of many collections has made it difficult to adequately screen them for useful traits. Most breeders rely on a one-time, one-environment evaluation of germplasm to make selections for use in breeding programs. Passport data is limited and, in many cases, missing. Information from donor countries on use, unique

characteristics, and importance of individual accessions does not exist. Consequently, utilization of the total collection has not been realized.

This is not to say that we have not been successful in making use of available exotic germplasm. Examples of the importance of germplasm utilization have been cited in sorghum (Duncan et al., 1991) and millet (Andrews and Bramel-Cox, 1993). In 1968, greenbugs (*Schizaphis graminum* Rondani) were observed on sorghum in Wall, Texas. Hackerott and Harvey, working at the Kansas State University Agricultural Research Center in Hays, Kansas, planted their available collection of germplasm and found KS-30, tunisgrass, to have resistance to the new C-biotype. Cooperation between public and private sector scientists made this germplasm quickly available, resulting in enough seed of resistant hybrids to plant 1.6 million ha in 1976. The classic example of germplasm utilization in sorghum has been the Texas A&M-USDA Sorghum Conversion Program. For a review of the program and its impact, see Duncan et al. (1991). Currently 623 converted lines have been released; 533 lines are listed in Duncan and Dahlberg (1993); 50 are listed in Rosenow et al. (1995); and 40 new lines have been released by TAES & USDA (1996).

The successful introgression of resistance to midge (*Stenodiplosis sorghicola* Coq.) and downy mildew [*Peronosclerospora sorghi* (Weston & Uppal)] C. G. Shaw] has greatly stabilized sorghum production in Australia and Argentina. Considerable opportunities remain for exploiting the collections to improve sorghum production globally. For example,

over 340 accessions of the genus sorghum belonging to sections *Chaetosorghum*, *Heterosorghum*, *Stiposorghum*, *Parasorghum*, and *Sorghum* were recently evaluated for resistance to shootfly (*Atherigona soccata* Rondani) at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) Asia Center. Seven accessions with very high levels of resistance — in some cases close to immunity — were found (Nwanze et al., 1995). Transfer of this high level of resistance to cultivated sorghum could greatly improve productivity of late-sown crops in Africa and Asia, where shootfly is a major production constraint.

The pearl millet landrace 'Iniadi' has had widespread impact on the improvement of that crop globally over the last 25 years (Andrews and Anand Kumar, 1996). Large Grain Populations (LaGraP) and the Bold Seeded Early Composite (BSEC), which have excellent grain yield, grain size, and disease resistance, have been developed from this landrace at ICRISAT Asia Center. CZP-IC 923 was developed from a cross between a smut-resistant dual-purpose variety (ICMV 82132) and a mass-selected experimental variety from BSEC (ICMV 87901). GB 8735, ICMV 221, ICTP 8203, and Okashana 1 are examples of improved open-pollinated cultivars, based largely on this landrace, that have been widely accepted by farmers. Iniadi has also been used extensively in developing hybrid parents for India and the USA. Many of the popular early-maturing pearl millet hybrids in India are based on male-sterile lines developed in Kansas from crosses involving a sample of Iniadi (PI 185642) collected from a local market in Kumasi, Ghana, in 1949. Extensive evaluations of

the potential utility of wild relatives of pearl millet in improving forage and grain cultivars over the past 20 years have taken place at the Coastal Plain Experiment Station, Tifton, Georgia, and in Francophone West Africa (Andrews and Bramel-Cox, 1993; Burton, 1995; Hanna, 1990, 1993; Hanna and Burton 1987; Marchais and Pernes, 1985; Wilson and Hanna, 1992).

Although these are impressive examples of the impact that can be achieved using exotic germplasm, the number of accessions used in crop improvement is very small given the size of collections maintained around the world. For example, the sorghum and millet collections in the United States stand at 40,477 and 1,507 respectively. At ICRISAT, the sorghum collection contains 35,643 accessions, while the millet collection, the largest in the world, contains 21,191 accessions (see Eberhart et al., 1996, for a country-wide breakdown of each collection). The Sorghum Conversion Program, which has released 623 converted lines, has tapped into less than 4% of the overall collection. Given these numbers, the question arises as to whether we have created collections that are too large and poorly characterized to effectively manage and utilize them for the benefit of global crop production.

One approach to addressing this question is to critically evaluate the utilization or "curation" of major agricultural collections. The overall goal of preserving genetic resources in an agricultural setting is the future safety of food and fiber production world-wide. This requires a long-term strategy based on the overall curation of each crop. A curator is defined by Webster (1979) as "one that has the care

and superintendence of something.” The role of curation and curators of plants has traditionally been associated with herbariums, natural history collections, and/or botanical gardens. In fact, most writing dealing with preservation and curation of plants has concentrated on natural history collections or botanical gardens (Callery, 1995; Dessauer et al., 1990; Hawks, 1990; Hicks and Hicks, 1978; Howie, 1986; Spongberg, 1984). *Conservation Biology: A Training Manual for Biological Diversity and Genetic Resources* (1992) explored much of the theoretical background that encompasses curation from the standpoint of collecting, maintaining, and evaluating collections. Though a training manual for plant biodiversity, many of the principles are relevant to us within an agricultural context. The primary tasks of curation can be divided into four categories: acquisition, maintenance, characterization and evaluation, and utilization (Committee on Managing Global Genetic Resources, 1991).

Acquisition

Acquisition of germplasm has been a strong point within the sorghum and millet programs. Both ICRISAT and the U.S. National Plant Germplasm System (NPGS) have developed large germplasm collections from around the world (Eberhart et al., 1996). Unfortunately, in both collections, passport data available online is limited to date collected, collector, pedigree, country, state/province, location, and secondary identification. The lack of meaningful passport data makes the evaluation of accessions based on geographical diversity difficult. Oliveira et al. (1996) pointed out that geographical origin was found to be correlated with relat-

edness and that in some cases, the region of origin was a more significant factor than race in establishing how variation is partitioned.

Descriptors for Sorghum [*Sorghum bicolor* (L.) Moench] by IBPGR and ICRI-SAT (1993) lists over 50 variables critical to valid and informative passport data. Complete and thorough data is required for planning acquisition strategies. Even without full passport data and limited morphological traits, molecular techniques can provide useful information for further collection needs. Calculations of genetic distances will identify divergent subpopulations that could harbor valuable genetic variations not apparent in current holdings.

Genetic conservation, and therefore germplasm utilization, depends on effective sampling techniques used in the original collection. Snaydon (1992) observed that “collections may be made (a) to conserve, as accurately as possible, a particular population perhaps in danger of extinction; (b) to conserve, as accurately as possible, the overall pattern of genetic variation in a particular species, perhaps again in danger of extinction; (c) to conserve, or perhaps maintain temporarily, a wide range of useful variation for a breeding program; (d) to conserve, or maintain temporarily, variation in some specific attribute (e.g. cold tolerance or disease resistance) for a breeding programme.” In the case of sorghum and millet, we strive to conserve the overall pattern of genetic variation for future use in evaluation and enhancement. To ensure that future collections are made to maximize genetic diversity, collection strategies should be coordinated through their curators, and

strategies should be based on sound scientific theory (Snaydon, 1992; Usher, 1992).

Two areas of need for acquisition in both millet and sorghum are in genetic stocks and wild species or relatives. Genetic stocks are becoming increasingly important in crop improvement. The use of molecular approaches has emphasized studies of gene loci that control traits described in germplasm accessions and for which breeders select. Although genetic and cytogenetic stocks have been used in many ways, including cultivar development, their main use in sorghum and millet has been for research. Studies have been conducted on their inheritance, allelism, linkage, penetrance, and introgression, but their direct use in breeding programs has been limited. Most breeders have chosen to use the original germplasm accession or derived line as a source of an allele of interest. In other species, notably tomato, genetic stocks have been used for more practical purposes (Tomato Genetic Stock Center Task Force, 1988), because, in part, a wider array of stocks is available, they are more thoroughly described, and the potential user community is large and diverse.

With the availability of molecular approaches in sorghum and millet improvement, genetic and cytogenetic stocks should play a more important role. Indeed, the requests for genetic stocks have increased considerably during the last few years. Sorghum and millet scientific communities need to make the acquisition of genetic stock germplasm a priority for future enhancement and research.

Collection and preservation of wild relatives has been a major weakness in our acquisition policy. Currently, less than 1.5% of either the ICRISAT or the NPGS collections contain wild relatives. The collections' deficiencies in representation of wild relatives become more critical as native habitats come under increasing pressure from human and livestock populations, thus threatening some wild species — or at least local populations of them — with extinction. Both ICRISAT and Australian scientists have recognized the need to strengthen this area of germplasm acquisition and major collection trips are scheduled. The U.S. wild sorghum collection is being reevaluated for authenticity, and status of this collection should be available by the end of 1996. Australian scientists have undertaken a collection of indigenous sorghum (Lawrence and Corfield, 1995), which has been sent to both ICRISAT and NPGS for inclusion in their respective programs. The first set received by ICRISAT contained wild sorghum species belonging to the sections *Parasorghum*, *Stiposorghum*, *Heterosorghum*, and *Chaetosorghum* (Prasada Rao et al., 1995). These are being studied at ICRISAT Asia Center for taxonomic classification and species identification.

Maintenance

Sites for preservation and maintenance of the largest sorghum and millet accessions are located at: ICRISAT, Andhra Pradesh, India; the National Seed Storage Laboratory, Fort Collins, Colorado, U.S.; and the USDA-ARS Plant Genetic Resources Conservation Unit (PGRCU), Griffin, Georgia, U.S. Several countries also maintain their own collections within

their national collections. Major growouts and regenerations take place at the ICRI-SAT Center in India and at the USDA-ARS Tropical Agriculture Research Station, Mayagüez, Puerto Rico.

The number of plants required to maintain genetic variability within a sorghum or millet accession has not been determined scientifically. In self-pollinated crops, the population structure can be variable, depending on the percentage of outcrossing. Burton (1951) reported that wild-grass sorghum may outcross between 18 and 30% while Jones and Sieglinger (1951) indicated that cultivated sorghum may outcross between 5 and 10%. With no outcrossing, landrace collections will be primarily a mixture of pure lines. Theoretically, sorghum accessions collected from small plots in farmers' fields could contain a mixture of pure lines of cultivated, wild \times cultivated, and wild sorghum. In this case, the number of plants to be regenerated becomes a function of maintaining as many pure lines within the accession as possible. Ideally, a sorghum accession should be separated into its separate pure lines; realistically, however, this is not feasible. Therefore, maintenance of an accession must be divided into: 1) saving an equal number of seeds from each plant harvested from the first increase during the quarantine growout, and 2) bulking the accession to be used in distribution. Returning a balanced sample of the first increase for long-term storage will help preserve rare genes.

In cross-pollinated crops such as pearl millet, population structure can be more complex, depending on the percentage of selfing that takes place (Crossa et al., 1994). Ideally, an accession would be

based on nearly 200 plants and would be regenerated by random mating, in isolation, a balanced bulk of the descendants. This strategy is almost never practical, except in the case of released open-pollinated cultivars where regeneration and breeder seed multiplication can occur simultaneously. Regenerating an accession by harvesting open-pollinated panicles from non-isolated plants is not acceptable, as most seeds will be hybrids of unknown male parentage. Intercrossing by hand is the next best option for maintaining the original population structure. Although laborious, the risk of cross-contamination between accessions is low. Selfing to produce S_1 seed has been recommended by Burton (1979) as a method for increasing seed of pearl millet accessions for distribution and evaluation. This is less laborious than intercrossing, and has a lower risk of cross-contamination. It has the added advantage of producing a population with a known genetic structure. However, many pearl millet accessions are not adapted to selfing and set little or no seed when panicles are bagged. Because of this, the ICRISAT pearl millet collection is maintained by cluster-bagging, in which several panicles of a given accession are enclosed in a single large selfing bag. The seed harvested has an unknown genetic structure, being composed of a mixture of selves and crosses within each bag used in multiplying seed of the accession. Seed from accessions that have been maintained in this manner should be random-mated several times, or crossed to a tester, to overcome inbreeding depression, before being assessed for traits related to grain and stover yield. Trait-specific gene pools, formed by random-mating many accessions, have been developed as an alternative strategy for

more efficiently maintaining and distributing pearl millet germplasm (Rai et al., 1997).

Genetic markers can play a crucial role in monitoring heterogeneity and heterozygosity as accessions are regenerated. Their use will provide guidelines in the refinement of regeneration strategies to ensure the long term maintenance of genetic diversity. Molecular markers will also assist identification of duplicate accessions, a problem within large collections that has never been fully addressed.

Accessions are probably most vulnerable to genetic drift or loss due to mishandling, labeling problems, growouts and regenerations, and storage. Therefore, proper maintenance of collections is critical in preserving the integrity of each accession. Both ICRISAT and the USDA have established guidelines for properly maintaining and regenerating accessions (Dahlberg, 1995; Prasada Rao et al., 1995; Roberts, 1992). Improper handling of the collection at this stage can minimize the potential utility of the germplasm and potentially lose valuable genes needed for future enhancement.

Characterization and Evaluation

Estimates of genotypic and phenotypic variation allow for the inference of genetic structures of individual germplasm accessions. This structure provides the framework in which utilization takes place. Phenotypic variation has been the primary evaluation tool utilized in millet and sorghum, and inference based on phenotypic variability has distinct advantages over that based on genetic variability. It is relatively easy to measure in the field and

often provides assessment of a sample of many genetic loci (Huenneke et al., 1992).

Several collections have been evaluated for phenotypic or morphological traits (Table 1). Descriptor lists for evaluation purposes are available from ICRISAT and the USDA (Dahlberg and Spinks, 1995). Sorghum accessions have been identified with resistance to aluminum toxicity, shoot fly, stem borer (*Chilo partellus* Swinhoe), *Striga*, midge (*Stenodiplosis sorghicola* Coq.), rust (*Puccinea purpurea* Cooke), and downy mildew. Sources of twin seededness, cytoplasmic male-sterile systems, brown mid-rib, and other traits also have been identified (see both ICRISAT and USDA databases).

ICRISAT is developing improved screening systems in pearl millet to evaluate tolerance or resistance to witchweed [*Striga hermonthica* (Del.) Benth], head miner (*Heliocheilus albipunctella* de Joannis), stem borer (*Coniesta ignefusalis* Hampson), and several other biotic constraints. Pearl millet germplasm evaluation has identified sources of increased grain yield potential, cytogenic male-sterile systems (Hanna, 1990, 1993), disease resistance to rust (*Puccinia* sp.) and *Pyricularia* leaf blast (Hanna and Burton, 1987; Singh, 1990; Wilson and Hanna, 1992), and apomixis in several species and wild relatives (Hanna, 1995). Sources of resistance to important panicle diseases such as downy mildew [*Sclerospora graminicola* (Sacc.) Schroet], smut [*Moeziomyces penicillariae* (Bref.) Vanky] and ergot (*Claviceps fusiformis* Lov.) also have been identified (Thakur and King, 1988a, 1988b; Singh et al., 1993).

Table 1. Approximate number off accessions evaluated for abiotic and biotic stresses within the U.S. National Plant Germplasm System for sorghum (updated and modified from Duncan et al. 1995).

Characteristic	Causal organism	Approx. # of accessions evaluated	% of total collection
Al toxicity		8955	22.1
Mn toxicity		5910	14.6
Lodging		1186	2.9
Chinch bug	<i>Blissus leucopterus</i> (Say)	1000 [†]	2.5
Fall Armyworm	<i>Spodoptera frugiperda</i> (J.E. Smith)	8503	21.0
Yellow sugarcane aphid	<i>Sipha flava</i> (Forbes)	5564	13.7
Greenbug (E, I)	<i>Schizaphis graminum</i> (Rondani)	19,000 [†]	46.9
Midge	<i>Stenodiplosis sorghicola</i> (Coquillett)	10,000 [†]	24.7
Head smut	<i>Sporisorium reilianum</i>	10,000 [†]	24.7
Anthracnose	<i>Colletotrichum graminicola</i> (Cesati) Wilson	357	0.9
<i>Striga</i>	<i>S. Hermonthica</i> , <i>S. Asiatica</i> , <i>S. densiflora</i>	5000 [†]	12.4
Downy mildew	<i>Peronosclerospora sorghi</i> (Weston & Uppal) C.G. Shaw	6214	15.4
Rust	<i>Puccinia purpurea</i> Cooke	877	2.2
Charcoal rot	<i>Macrophomina phaseolina</i> (Maulb.) Ashby	5000	12.4
Maize dwarf mosaic virus	Aphid-vectored Poty virus	500	1.2
Grain mold complex	<i>Fusarium</i> , <i>Curvularia</i> , <i>Aschocyta</i>	1000 ¹	2.5

[†]These are approximations and totals are not currently available on GRIN.

Although these evaluations have identified several important sources of genes, assessment based on phenotypic variability is limited. It often is difficult to determine whether phenotypic variability is due to genetic or environmental effects, particularly when screenings are done only once at a single location. In contrast, molecular markers allow for assessment based on gene, genotype, and genome, and provide a more accurate and detailed outline of the genetic diversity within an accession. Molecular markers also provide a way to measure genetic variability in the absence of environmental influences. Markers must, however, be heritable, discriminate between accessions, populations, and taxa, easy (cost effec-

tive) to measure and evaluate, and provide reliable, repeatable results (Hillis and Moritz, 1990).

Future evaluations will require merging of traditional phenotypic screening with molecular markers to ensure a more complete and informative evaluation. One area in which merging of morphological and molecular data should be used is in designating core collections. Core collections are a subset of the total collection that can be effectively evaluated in times of particular need. Ideally they are rationalized, refined and structured around a small, well-defined and representative 'core' (Brown, 1988). Thus, a core represents the genetic diversity of a

crop and its relatives with minimal repetitiveness (Frankel, 1984). Development of core collections and the concept of their use has gained acceptance globally (Hodgkins et al., 1995; Knüpffer and van Hintum, 1995). Using geographic and taxonomic diversity and traditional evaluation, a representative core sorghum collection was set up at ICRISAT containing about 10% of the total collection (Prasada Rao and Ramanatha Rao, 1995). Using both traditional morphological evaluations and molecular markers, a more effective core subset can be developed which will optimize sources of genetic variation.

Utilization

Dudal (1976) points out that drought, shallow soil, and mineral deficiencies or toxicities account for 75% of the agricultural limitations from the soil (Table 2). Sorghum and millet have historically encountered higher levels of abiotic stress than other primary crops. They are primarily relegated to marginal land, accounting for roughly 80% yield loss in U.S. sorghum due to climatic/nutritional factors (Table 3, Kramer and Boyer, 1995). In the near future, sorghum and millet will remain the primary crops of poor soils and agricultural conditions. Therefore, utilization and improvement of yield stability will depend on increased research efforts on abiotic stress tolerance to drought, temperature, and adverse soil composition. Greater use of local landraces in crosses with agronomically elite material will be needed to combine higher grain yield with resistance/tolerance to locally important biotic and abiotic stresses (Andrews and Bramel-Cox, 1993). Improved selection methods of ac-

Table 2. Area of total world land surface subject to environmental limitation of various types (Dudal, 1976).

Environmental limitation	Area of world soil subject to limitation (%)
Drought	27.9
Shallow soil	24.2
Mineral (excess vs. deficiency)	22.5
Flood	12.2
Miscellaneous	3.1
None	10.1
Total	100.0
Temperature*	14.8

*Note area affected by unfavorable temperatures overlaps with other classifications and is shown separately.

cessions that enhance combining ability for grain and biomass yield, along with better information on heterotic patterns between germplasm accessions is essential to increase sorghum and millet acreage worldwide.

Breeders view utilization as the ability to place a specific gene(s) or special trait(s) in adapted cultivars. Utilization encompasses the capability to move identified genes into superior lines or cultivars that provide farmers with improved yield, disease resistance, tolerance to abiotic and biotic stress, and improved quality. Traditional breeding programs will continue to benefit from rapid identification and insertion of genes into elite material. Biotechnology offers many tools by which this process may be enhanced. Transgenic plants offer the potential for fast genetic solutions to serious problems. Insertion of Bt genes, incompatibility genes to prevent outcrossing with Johnsongrass (*Sorghum halepense*), and protein genes to enhance the nutritional value of sorghum and millet are just some of the examples in which both crops could benefit from biotechnology and genetic

Table 3. Record yields, average yields, and yield losses for major U.S. Crops in kg ha⁻¹ (Kramer and Boyer, 1995).

Crop	Record yield	Average yield	Average losses			
			Disease	Insect	Weeds	Climatic/nutritional
Maize	19,300	4,600	836	836	697	12,300
Wheat	14,500	1,880	387	166	332	11,700
Soybean	7,390	1,610	342	73	415	4,950
Sorghum	20,100	2,830	369	369	533	16,000
Oat	10,600	1,720	623	119	504	7,630
Barley	11,400	2,050	416	149	356	8,430
Potato	94,100	28,200	8,370	6,170	1,322	50,000
Sugar beet	121,000	52,600	10,650	7,990	5,330	54,400
Mean % of record yield	100.0	21.5	5.1	3.0	3.5	66.9

transformation (Bennetzen, 1995; Kononowicz et al., 1995). Marker-assisted selection (Lande, 1992; Oh et al., 1994) could potentially halve the development time of improved cultivars and greatly assist the conversion of photoperiod-sensitive accessions to day-neutral forms.

Future Vision for Sorghum and Pearl Millet Genetic Resources Utilization

Without an effective, long-term curation strategy based on input from crop curators and other scientists, efficient use of germplasm resources currently available will continue to be limited. Plant breeders will continue to make use of genetic resources as a pool from which to identify specific sources of resistance to diseases, insects, and parasitic weeds. Curatorial needs will be broader: identity—the determination that an accession is catalogued correctly, is true to type, and maintained properly; relationships—the degree of relatedness to individual accessions or groups of accessions within a collection; structure—the partitioning of variation among individuals, accessions, populations, and species; and location—

the presence of a desired gene or gene complex in a specific accession, as well as the mapped site of a desired DNA sequence on a particular chromosome in an individual or cloned DNA segment. The greater utilization of both sorghum and millet germplasm can be realized only through a strategic, forward looking plan that integrates the roles of scientists, breeders, and curators with traditional and biotechnological tools. Such a plan will provide a more complete and thorough understanding of available accessions in our collections and future acquisitions.

Sorghum and millet genetic resource utilization, as defined by curators and overseers of international and national collections, involves the integration of several disciplines. Curators strive to provide collections that are of the greatest use for scientists throughout the world. This encompasses the integration of acquisition, maintenance, evaluation and characterization, and utilization. Curators must provide collections that are easily accessible and readily available, with current and thorough information. They must strive to increase utilization of millet and sorghum germplasm through enhanced

scientific and management strategies. This integration can be accomplished through strategic planning of traditional methods of curation, such as field evaluations, data acquisition, and maintenance, with the integration of biotechnology. Core subsets for each crop will be an important part of this service. Integration of these technologies will fundamentally change how we utilize large collections by identifying new and useful genes and transferring these genes into superior, adapted cultivars.

Acknowledgment

The authors would like to thank Dr. Keith Schertz for his contribution to the genetic stocks section and Dr. K. E. Prasada Rao for his helpful suggestions on the manuscript.

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