



GLOBAL STRATEGY FOR THE CONSERVATION AND USE OF SORGHUM GENETIC RESOURCES

With support from



Federal Ministry
of Food
and Agriculture

Global Strategy for the conservation and use of sorghum (*Sorghum bicolor* (L.) Moench) genetic resources

Paula Bramel, Stephen Kresovich and Peter Giovannini

2022

With input from Mohammad Shahid, Sally Norton, Guirguissou Maboudou Alidou, Eyerusalem Arusi, Lawrence Aboagye, Vilas Tonapi, M. Elangoven, Vania Azevedo, Hamidou Falalou, Sushil Pandey, Destario Nyamongo, Joseph Kimani Ndungu, Peterson Wambugu, Matsikoane Sefotho, Amadou Sidibe, Remmie Hilukwa, Bal Krishna Joshi, Sunday Aladele, Isaura Martín Martínez, El Tahir Ibrahim Mohamed, Eyanawa A Akata, John W. Mulumba, Eva Zaake, Graybill Munkombwe, Thabo Tjikana, Giles Trouche, Geoffrey Morris, Juan Carlos Rossa, Paula Teres, Tiny Mpho Motlhaodi, Christopher Cockel, Santosh Deshpande, Kuldeep Singh, Onismus Chipfunde, Kenneth Opare-Obuobi, Jean-Francois Rami, Jurandir Magalhaes, Naoura Gapili, Diego Ortiz, Clarisse Pulcherie Barro Kondomba, Cyril Diatta, Harish Gandhi, David Jordon, Emma Mace, Alan Cruickshank, Sarah Hearne, Mitch Tuinstra, Gebisa Ejeta, Baina Dan-Jimo, Stembiso Mbhele, Juliano Gomes Padua, Jeewani Diddugoda, Amanuel Mahdere, Hassan Ouabbou and Melanie Harrison

COVER PHOTO

Sorghum field at sunrise. Photo: Jaboo Foto/Adobe Stock

DISCLAIMER

This report aims to provide a framework for the efficient and effective *ex situ* conservation of globally important collections of sorghum. The Crop Trust considers this document to be an important framework for guiding the allocation of its resources. However, the Crop Trust does not take responsibility for the relevance, accuracy or completeness of the information in this document and does not commit to funding any of the priorities identified. This strategy document (dated 16 September 2022) is expected to continue to evolve and will be updated as and when circumstances change or new information becomes available.

ACKNOWLEDGMENTS

This strategy is the result of a collaborative effort and has been made possible thanks to many contributors who provided information and participated in discussions. The development of this strategy would not have been possible without the input of those who completed the survey questionnaire and responded to requests for feedback or further information. In addition, the input from the participants in the workshop who took the time in their busy schedule to join the discussion and to contribute to the identification of priority actions was invaluable.

The development of this Global Crop Conservation Strategy was funded by the Government of Germany (BMEL) as part of the 3-year project led by the Crop Trust: "Breathing New Life into the Global Crop Conservation Strategies: Providing an Evidence Base for the Global System of *Ex situ* Conservation of Crop Diversity."

The Crop Trust also cooperated with the Secretariat of The International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) in the development of this document.

Annex V of this document provides a summary of a recent report: "The plants that feed the world: baseline information to underpin strategies for their conservation and use". That study was produced as a collaboration led by the Secretariat of the Plant Treaty, and involving the Alliance of Bioversity, the International Center for Tropical Agriculture (CIAT) and the Crop Trust, funded by the Norwegian Agency for Development Cooperation (NORAD, Government of Norway).

RECOMMENDED CITATION

Bramel P., Kresovich S., and Giovannini P. 2022. Global Strategy for the conservation and use of sorghum (*Sorghum bicolor* (L.) Moench) genetic resources. Global Crop Diversity Trust. Bonn, Germany.

The Crop Trust, Bonn, Germany, <https://www.croptrust.org>.



This work is licensed under a Creative Commons Attribution-NonCommercial-ShareAlike 4.0 International (CC BY-NC-SA 4.0) License. To view a copy of this license, visit <https://creativecommons.org/licenses/by-nc-sa/4.0/>

CONTENTS

EXECUTIVE SUMMARY	5
1 INTRODUCTION	7
2 BACKGROUND REVIEW	9
2.1 Economic importance	9
2.2 Crop evolution	13
2.3 Crop and landrace diversity	13
2.4 Use of genetic resources	16
2.5 Summary of the background review	18
3 STATUS OF <i>EX SITU</i> CONSERVATION – COMPOSITION	19
4 STATUS OF <i>EX SITU</i> COLLECTIONS – CONSERVATION	25
4.1 Conservation infrastructure	25
4.2 Routine conservation operations	28
4.3 Safety duplication	29
4.4 Human and financial resources	30
4.5 Risk assessment	31
4.6 Summary of the status of conservation	31
5 STATUS OF <i>EX SITU</i> COLLECTIONS – DOCUMENTATION	32
6 STATUS OF <i>EX SITU</i> COLLECTIONS – USE	35
6.1 Links between <i>ex situ</i> collections and users	36
7 STATUS OF <i>EX SITU</i> COLLECTIONS – CONSTRAINTS AND VULNERABILITIES	39
8 SORGHUM USER COMMUNITY CONSULTATION	43
9 A GLOBAL STRATEGY FOR THE <i>EX SITU</i> CONSERVATION OF SORGHUM CROP GENETIC RESOURCES	45
Priority Action 1: Global initiative to fill global gaps in conservation	47
Priority Action 2: Global initiative to secure the conservation and use of collections for future users	48
LITERATURE CITED	50
ANNEXES	56
Annex I. Respondents to the 2021 survey	56
Annex II. Number of accessions reported in the 2007 strategy report, and in 2021 in the survey or in the consolidated global database	58
Annex III. Number of accessions conserved at ICRISAT for each Sorghum race and intermediate races for each country, region, biome or altitude in the diversity tree	60
Annex IV. Expert consultation	62
Annex V. Selected metrics for sorghum and maize (as comparison)	63

蜀黍



Sorghum Saccharatum, L.

成形圖說卷之十九



Sorghum in Kenya. Photo: A. Paul-Bossuet/ICRISAT

EXECUTIVE SUMMARY

Sorghum [*Sorghum bicolor* (L.) Moench] is a widely adapted cereal crop that can be grown in diverse ecological situations in semi-arid, sub-tropical, tropical and temperate climates. It is the fifth most important grain crop internationally. Sorghum is mainly grown on marginal, rainfed land that is subject to periodic droughts. In some areas of the world, such as the United States, Mexico, Argentina, Brazil, Australia, China and Japan, it is an important feed crop with a significant value from trade. The sorghum production area has declined in most regions of the world except Africa, where it is an important crop for household food security and contributes to alleviating poverty, but also has significant cultural value. Because of national declines in the importance of production, feed use, and trade value in the more temperate regions, there is a risk that the genetic resources conserved in *ex situ* collections will be lost in countries where there is also less investment being made in sorghum research and development. In the tropics, the production of sorghum has increased with a shift to more marginal areas, where it is an important food and feed security crop in environments significantly impacted by climate change. The challenges of climate change in the traditional production areas risk genetic erosion in farmers' fields for the crop and in natural ecosystems for its wild relatives. It is also a challenge for farmers to adapt, given the poor productivity of the crop in Africa and the lack of investment into sorghum research and development. Thus, the production of sorghum globally is vulnerable, and it is facing many constraints that can only be overcome by the full use of its genetic diversity.

The cultivated crop, *Sorghum bicolor* subsp. *bicolor* has significant genetic diversity but there are also many related species that have unique traits and adaptations that could serve as a source for improvement in the future. The use of genetic resources for the improvement of sorghum production has been important in the past, and crop breeders continue to prioritize the improvement of traits such as drought tolerance, cold or heat tolerance, pest/disease resistance, and growth duration. This interest in genetic resources presents both opportunities for *ex situ* collection holders and challenges to meet the needs of end users.

Global conservation strategies aim to facilitate a transition from the current complex, fragmented and largely independent crop conservation activities to a more integrated, collaborative and cooperative global system of crop conservation. The objective of the update of the 2007 global strategy for sorghum was to consider changes in the global context in terms of the security of conservation and enhanced use of *ex situ* collections. This reassessment was used to identify priority global actions to address remaining vulnerabilities and enhance global collaboration. The update is based on a background study, a survey of 37¹ institutions on the status of conservation and use of their collections, an analysis of the current accession-level composition of sorghum collections and consultation with users.

¹37 institutions and 38 genebanks as 2 genebanks are from the same institution (ICRISAT) but located in different countries.

Overall, the survey respondents' collections harbor about 80% of the total number of accessions conserved globally. Landraces are the predominant type of accession being conserved, but a few accessions of related wild species are also conserved *ex situ*. Globally, there is evidence of significant redundancy in *ex situ* collections resulting from the history of donations, acquisitions and joint collections; for example, 20 institutions conserve 72% of the global accessions that are mainly derived from 11 countries. The 2007 strategy recognized that the high degree of duplication made it difficult to interpret the adequacy of the diversity and coverage of the accessions conserved globally. There are still significant conservation gaps in West and Central Africa as well as South Sudan that were originally identified in 2007. The assessment of the consolidated database for Central America, Central Asia, and the Caucasus indicate there are potential gaps in terms of secure conservation as well as the need for collecting in those regions. Finally, the species coverage in collections is still considered inadequate, as is ecological sampling at the national level. As we gain a much greater understanding of social and cultural diversity and genotypic/allelic diversity using genomic tools, it will be feasible to use a global approach to identify duplicates and gaps. This will build upon greater collaboration and information sharing to address a global need for a more rational, cost-effective system for the conservation of sorghum genetic resources.

Compared with national collections, the genebanks conserving global collections tend to meet the internationally recommended standards for conservation of orthodox seed to a greater degree. Many national genebanks in the centers of diversity have limitations related to inadequate facilities, equipment, staffing, regeneration sites and resources. This has led to backlogs in viability testing, regeneration and multiplication, which poses risks to long-term conservation and limits the quantity and quality of seed available for distribution. There are also constraints to routine operations, so many institutions are not using the

most efficient and secure procedures and protocols. Finally, there is an increased awareness of the need for safety duplication. Many institutions are committed to backing up their collections, but it is not a priority given the significant constraints. This is a vulnerability for the global system that needs to be addressed.

Priority needs for upgrades have been identified in routine operations, facilities, equipment and procedures. This is largely because genebanks rely on short-term project funds that are uncertain and seem to be declining. The financial support for long-term conservation and use is not a priority for many donors. The relatively lower priority of sorghum compared with other crops, both nationally and internationally, means that there are few opportunities to apply for funds to address these gaps. The lack of global action to address these collection-specific constraints is a risk for the conservation of a high proportion of the unique diversity.

In summary, the current global system of conservation for sorghum diversity is a fragmented, insecure system that is vulnerable to genetic erosion due to climate change in the more marginal semi-arid tropics, the low priority of the crop in many countries and in the private sector, and inadequate links to users. The 2007 strategy recommended several actions to address the constraints to conservation and use, but not all of them have been implemented. The two global actions identified in this 2021 update of the global strategy are built upon those recognized earlier, with additional insights from a broader range of institutes that conserve sorghum genetic resources and key users. Thus, taking lessons from the previous strategy, two priority actions are proposed for the initial implementation of the strategy. The first action is a global initiative to address redundancies and fill conservation gaps. The second action is a global initiative to secure conservation and the use of collections for future users. It is generally recognized that the global system needs to be strengthened now and these actions are urgent.



1 INTRODUCTION

The Crop Trust is an international organization working to safeguard crop diversity for the long term by focusing on *ex situ* conservation in genebanks. Since 2006, it has worked with crop experts to develop global *ex situ* conservation strategies for key food and commodity crops. Global conservation strategies facilitate a transition from the current complex, fragmented situation of largely independent crop diversity conservation actions to a more integrated, collaborative and cooperative global conservation system. The aim of a global strategy for sorghum is to recommend evidence-based strategic actions to build such a system.

A Strategy for the Global Conservation of Sorghum Genetic Diversity (hereinafter, the 2007 strategy) was completed in 2007. The development of the strategy involved a survey of key *ex situ* collection holders on the status of conservation and use to assess the state of global conservation. This was followed by a workshop with crop experts to discuss the conclusions of the survey, make key recommendations and initiate global actions to address priorities. The primary goal of the strategy was to facilitate the development of

an efficient and effective conservation system for sorghum genetic resources, known as “The International Sorghum Germplasm Collection”. This included:

- Assessment of the composition and conservation standards of collections, and the role of global, regional, and national collection holders;
- Identification of key gaps in existing collections;
- Establishment of a model for collaboration to share responsibilities and costs for the management of key genetic resource collections;
- Identification of the key information needs for a comprehensive global database network to enhance conservation, exchange and use; and
- Identification of capacity-building needs to upgrade and enhance collections.

The results of the survey of collection holders were discussed at a consultation workshop held with key experts. The workshop identified actions that would be implemented by five task forces, with oversight by a Global Sorghum Group. The workshop recognized that the global strategy was not static and needed regular review with revision as needed. Some of the key issues identified were:

- Constraints to secure and effective conservation, such as limited safety duplication, a need for urgent regeneration, and poor storage infrastructure;
- Limited availability and sharing of accession-level information with users;
- Limited availability of accessions to users, except from a few collections, such as the International Centre for Research in the Semi-Arid Tropics (ICRISAT) and the United States Department of Agriculture - Agricultural Research Service (USDA-ARS);
- The very limited use of sorghum crops accessions conserved in genebanks in crop improvement programs (for example, in temperate environments, limited diversity within predominantly photoperiod-insensitive accessions have been evaluated); and
- A lack of effective links to users due to poor information flow between genebanks and users, limited engagement between genebanks and crop-based research institutes, and limited collaboration of genebanks with *in situ*/on-farm conservation efforts.

The 2007 strategy identified three key areas for global collaboration: The development of a global accession-level information system, a joint evaluation program, and an urgent regeneration program. Annex 5 of the 2007 strategy identified five task forces, each with a set of tasks. There has been some progress in each of the three areas. Sorghum descriptors have been revised and updated and a revision of the racial classification of sorghum has been published. There is better global sharing of passport information on accessions through Genesys, where 56 institutions

have contributed information on 118,152 accessions. A Crop Trust project focused on regeneration has resulted in 7,272 accessions being regenerated and securely conserved globally. In addition, regeneration guidelines for sorghum have been published. The success of these global activities highlights the role of the strategy in facilitating the identification of priority needs for securing the long-term conservation and use of sorghum genetic resources.

This update of the 2007 strategy is the outcome of a background study on sorghum's importance, its genetic diversity and the use of its germplasm, an assessment of various databases with accession-level information, a survey of major sorghum collection holders and consultation with experts on the future of conservation and utilization. The 2021 survey focused on the composition of *ex situ* collections and their status in terms of the security, effectiveness, and sustainability of conservation. The survey addressed the interrelationships among individual collections, based on collection histories, compositions and specific activities linking conservers. There have been follow-up consultations with genebank curators and users to develop this update, and this additional effort will lead to a stronger commitment to a truly global system in which sorghum diversity conservation and use efforts are more secure, coordinated, systematic and efficient. A key outcome of this effort is the identification of priority actions to address shortfalls in the current global conservation system. The Crop Trust and other organizations will use these priority actions to identify key investments needed to secure conservation and use for the long term.



Photo: ICRISAT

2 BACKGROUND REVIEW

2.1 Economic importance

Sorghum [*S. bicolor* (L.) Moench] is a widely adapted cereal crop that can be grown in diverse ecological environments in semi-arid, sub-tropical, tropical and temperate climates. Sorghum is the fifth most important grain crop internationally. With its extensive root system and its ability to become dormant during water stress, it is mainly grown on marginal, rain-fed land that is subject to periodic droughts. It also has some degree of tolerance to high temperatures and salinity (Bhagvatula et al. 2013; OECD 2016).

While sorghum is grown in much of the world as a feed and fodder crop, it is also a staple food for millions of people in the semi-arid regions of Africa and South Asia. Batey (2017) identified four major groups of sorghum: grain, sweet, forage and broom. The use of the four types varies considerably among different regions of the world. In the Americas, Europe and Australia, 94%–100% of production is used for feed and only about 0.4% has other uses, for example, in ethanol production. In Africa and Asia, 73%–79% of production is used as a food crop in household products such as porridge, bread, cake, couscous, and other dishes (Reddy et al. 2008). In Africa, sorghum is also used traditionally to produce local beer (Sawadogo-Lingani et al. 2021), while in Asia it is an important feed for livestock and poultry. In the more temperate regions of the world, it is used mainly for feed and for ethanol production. It is also an important forage. Sweet sorghums are used as sweeteners or fermented into ethanol. The plant and stover have other uses in Africa and Asia.

Sorghum is grown on all continents bar Antarctica. Table 2.1 lists the top ten countries accounting for about 75% of global production and consumption from 2017 to 2021 (Foreign Agricultural Service/United

States Department of Agriculture (FAS/USDA) 2021). Three countries (United States, Argentina, and Australia) consumed less than half of the sorghum they produced. Some countries did not meet their domestic consumption entirely through production, while China consumed more than three times its domestic production. The United States is the largest producer of sorghum globally, but China is the largest consumer. In fact, China imported more than 80% of the sorghum imported globally. Most countries, however, rely on their own production.

Table 2.1 Production and consumption of sorghum in 2020/21 (FAS/USDA 2021).

	Production (thousand metric tons)	Consumption (thousand metric tons)
United States	9474	2667
Nigeria	6570	6550
Ethiopia	5200	5300
Sudan	5000	4850
India	4780	4550
Mexico	4000	4100
China	3550	11600
Argentina	3400	1800
Brazil	2732	2700
Niger	1922	2000
Mali	1801	1700
Burkina Faso	1560	1700
Australia	1350	300
Cameroon	1200	1225
Bolivia	1100	1050
European Union	1003	1013
Chad	980	1000
Others	7618	7842
World Total	62237	62374

Sorghum production and productivity have changed over time. Figures 2.1a, b and c highlight the trends in the area of production, production, and productivity from 1961 to 2019. Generally, the area under production and total production have more than doubled in Africa but productivity has only increased slightly. In

Asia, the area under production and total production have declined by more than 50%, and productivity has increased at a slightly higher rate than in Africa. In these regions, most of the sorghum crop is produced by smallholder farmers with very limited inputs.

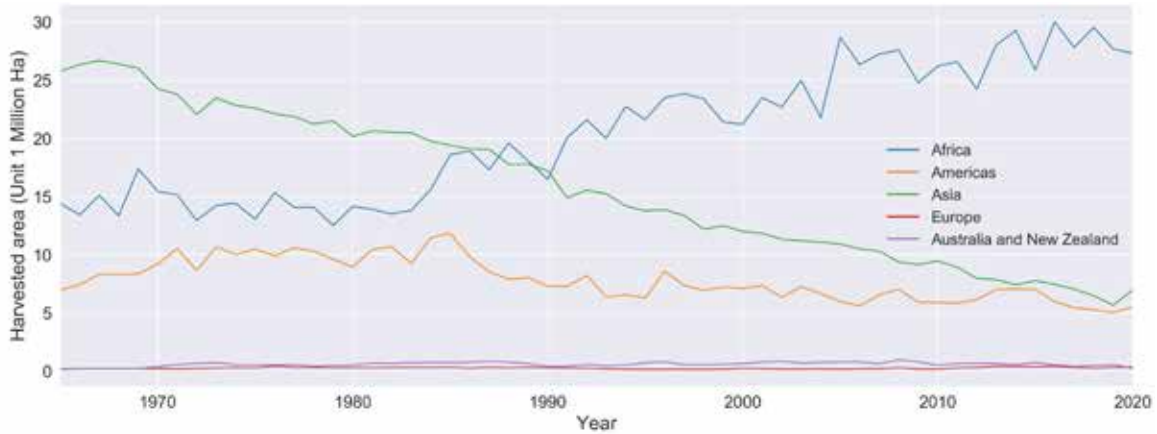


Figure 2.1a. Production area (Harvested ha) of sorghum in Africa, Asia, the Americas, Australia and Europe (Source, Food and Agriculture Organization (FAO) 2021)

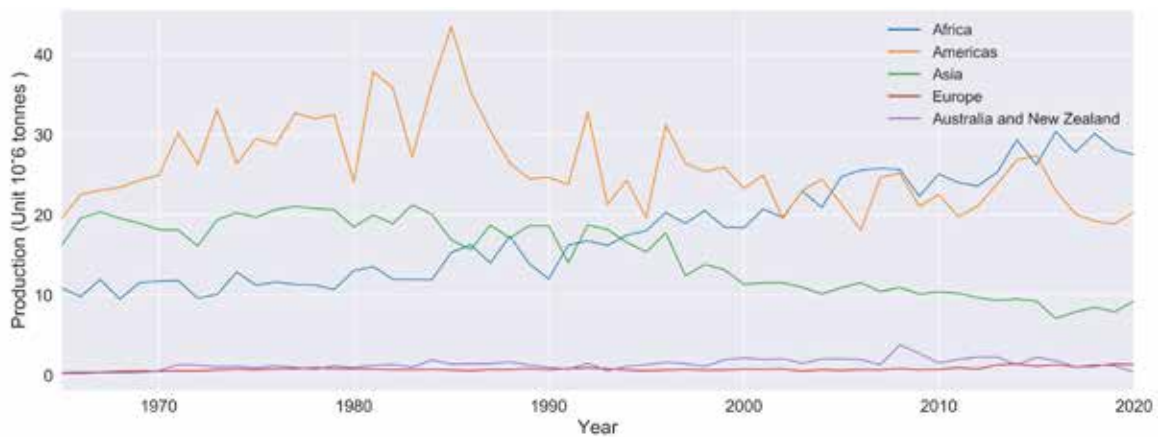


Figure 2.1b. Production (tonnes) of sorghum in Africa, Asia, the Americas, Australia and Europe in three periods: 1961 to 1980, 1981 to 2000 and 2001 to 2019. (Source, FAO 2021)

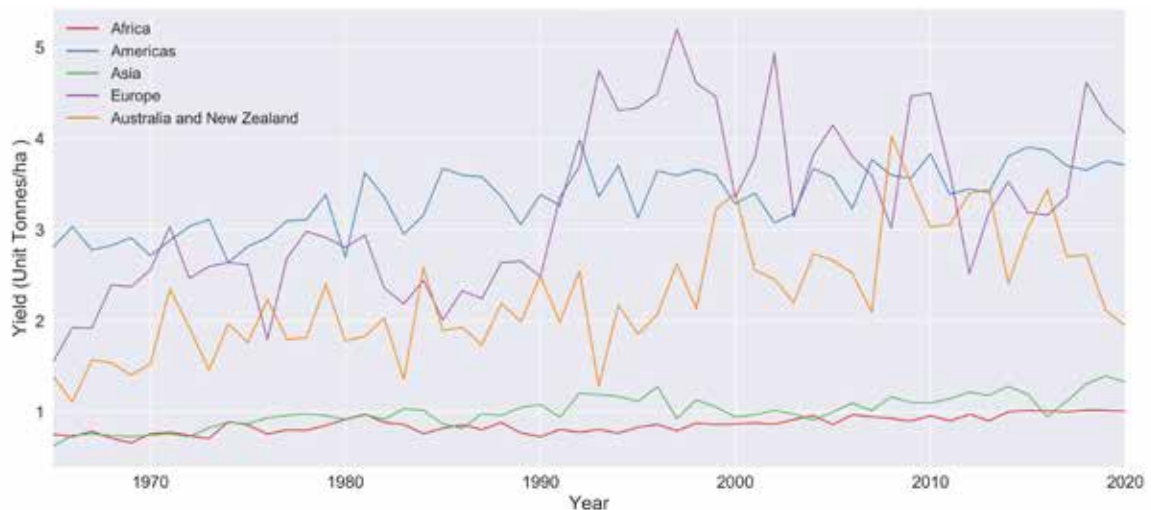


Figure 2.1c. Productivity (tons/ha) of sorghum in Africa, Asia, the Americas, Australia and Europe in three periods: 1961 to 1980, 1981 to 2000 and 2001 to 2019. (Source, FAO 2021)

The historical trends in sorghum production differ among the Americas, Australia and Europe, where the production systems are much more intensive, and there has been considerable investment into research and development to improve sorghum production. In the Americas, sorghum productivity leveled off from 1980 to 2019. In Australia and Europe, sorghum productivity has continued to increase (the overall trend as there is large variation from year to year), as has the area under production.

Mundia et al. (2019) assessed the history, current constraints and opportunities for sorghum production based on an extensive literature review. They aimed to identify the primary drivers and develop insights into the production dynamics in India, China, United States, Mexico, Nigeria and Burkina Faso. They identified ten key factors that affected sorghum production in countries with vulnerable populations that depend upon sorghum: climate change, agricultural inputs, population/economic growth, sorghum genetic diversity, agricultural resource scarcity, other crop demands, price, non-food demands, cultural influence and armed conflict. The impacts of the ten factors and their interrelationships were compared for the six countries. The most important factors globally were improved agricultural inputs, population/economic growth, and climate change. All the other factors, especially genetic diversity, culture and conflict, affected specific localities, countries, or regions. The assessment concluded that policy intervention should be targeted to populations in at-risk areas, because sorghum production is most variable in areas with a lower capacity to adapt to climate change. Possible interventions included facilitated seed exchange, the development of new varieties, and crop insurance plans. Monitoring sorghum production in these localities could be used as an indicator for the need to address malnutrition and famine if the crop fails.

Hyman et al. (2016) considered the role of sorghum, among other cereals, in 18 farming systems where dryland cereal and legumes were produced in significantly large areas and where more than 60% of the poor live globally. Sorghum makes up more than 20% of the agricultural area in three farming systems in sub-Saharan Africa: (1) the cereal-root crop mixed system, where it is the dominant cereal; (2) the agropastoral sorghum-millet system; and (3) the pastoral system. Sorghum is the dominant cereal in the dry rain-fed system in South Asia. The agropastoral sorghum-millet system, the pastoral system, and the dry rain-fed system are all characterized by extensive production with low productivity. Sorghum is the dominant crop in four of the eight farming systems with the poorest people. The authors determined the productivity of sorghum, as well as other dryland cereals such as pearl millet and small mil-

lets. They found the yield of sorghum was equal to or lower than that of millets in the farming system in sub-Saharan Africa and South Asia. The farming system where sorghum dominates is characterized by high drought and high temperature stress, as well as acid soil, low soil nutrient availability, and low water holding capacity. Hyman et al. (2016) concluded that sorghum is the main dryland cereal in the dominant farming systems where people live in poverty with a low nutritional status. These cropping systems are significantly affected by abiotic stresses and are being impacted by climate change with increased temperatures and prevalence of drought. Some farming systems would benefit from greater research and development investment to improve the production and nutritional value of sorghum and further develop markets for the crop.

Orr et al. (2020) conducted a synthesis of unpublished literature from ICRISAT that included studies on adoption of varieties, crop production practices, and processing technologies as well as value-chain development and impacts. The study modeled four scenarios: a "baseline" model, with income and population growth set to medium with no impact of climate change; an "optimistic" model with low population growth, high income growth and no climate change impact; an "increased productivity" model where the yield growth rate for sorghum was 25% above the baseline; and a "climate change" model that included both higher temperatures and lower rainfall. Using these models, Orr et al. (2020) assessed the investment potential for research and development as well as commercialization in East and Southern Africa.

The business case for investment into research and development was clear, with a growing demand for sorghum driven by high population growth and increased production that was projected to triple by 2050. This increased production would reduce poverty and increase household food security in areas where sorghum is grown, with higher yields and shorter periods of hunger, because most of the varieties have a shorter growth duration than that of traditional varieties. They are also more resilient to climate change, so there would be a high return on investment in research and development. This was not the situation projected for commercialization, where there was evidence for a "subsistence production trap" for many of the sorghum value chains. Sorghum has a higher price than maize, which limits its substitution for livestock feed and the flour value chain. To address this, the yield for sorghum would need to increase and the price would need to drop. This would affect specific smaller value chains, such as clear beer, but not the more substantial value chains. Generally, the authors concluded that commercialization will not drive adoption of new varieties or improved produc-

tion practices, so the business case for investment is lower.

Zereyesus and Dalton (2017) also found high returns on investment in sorghum research and development, with increased productivity and consumer benefits in the semi-arid and arid regions of the world. Their meta-analysis of 59 studies conducted between 1958 and 2015 concluded that the return on sorghum research and development ranged from 58% to 81% per year, and was socially profitable because public investments provided the research funds. The return on investment was higher when the impact was quantified for more local areas, rather than at the national or international levels. Technological innovation had greater returns when it focused on narrow adaptation to specific agro-ecological conditions. The highest rates of return were in the United States, where the

economic environment and costs of research were more favorable.

Bhagavatula et al. (2013) reported that sorghum production in Asia declined steadily from 1980 to 2009 at about 3% per year. The greatest declines were in India and China. The production area declined by 4.5% per year in the rainy season sorghum production area in India, but by only 1% per year in the post-rainy season sorghum production area. In this area, other crops are not competitive when grown under residual moisture and stover is a high-value product during the dry season. The study concluded that the importance of sorghum as a staple food had declined from the 1980s until 2009/10 in all the agro-ecologies in India. However, its importance is now slowly starting to increase mainly due to its alternative use as a feed grain, for alcohol production, and in processed foods.

Table 2.2 Species in the *Sorghum* genus.

Species	Section	Genepool	Distribution
<i>Sorghum bicolor</i> (L.) Moench subsp. <i>bicolor</i>	Eu-sorghum	Primary	Africa
<i>Sorghum bicolor</i> (L.) Moench nothosubsp. <i>drummondii</i> (Steud.) de Wet ex Davidse	Eu-sorghum	Primary	Africa
<i>Sorghum bicolor</i> (L.) Moench subsp. <i>verticilliflorum</i> (Steud.) de Wet ex Wiersema & J. Dahlb.	Eu-sorghum	Primary	Africa
<i>Sorghum propinquum</i> (Kunth) Hitchc.	Eu-sorghum	Primary	Southeast Asia and Indian subcontinent
<i>Sorghum halepense</i> (L.) Pers.	Eu-sorghum	Secondary	Southern Eurasia and India
<i>Sorghum</i> × <i>alrum</i> Parodi	Eu-sorghum	Secondary	Southeast Asia and Indian subcontinent
<i>Sorghum purpureosericeum</i> (Hochst. ex A. Rich.) Schweinf. & Asch.	Parasorghum	Tertiary	India, Sahel, east, and west tropical Africa
<i>Sorghum versicolor</i> Andersson	Parasorghum	Tertiary	East and Southern Africa
<i>Sorghum grande</i> Lazarides	Parasorghum	Tertiary	Australia
<i>Sorghum leiocladum</i> (Hack.) C. E. Hubb.	Parasorghum	Tertiary	Australia
<i>Sorghum matarakense</i> E. D. Garber & Snyder	Parasorghum	Tertiary	Australia
<i>Sorghum nitidum</i> (Vahl) Pers.	Parasorghum	Tertiary	Australia, New Guinea, Southeast and East Asia
<i>Sorghum timorense</i> (Kunth) Büse	Parasorghum	Tertiary	Australia and Timor
<i>Sorghum amplum</i> Lazarides	Stiposorghum	Tertiary	Australia
<i>Sorghum angustum</i> S. T. Blake	Stiposorghum	Tertiary	Australia
<i>Sorghum brachypodum</i> Lazarides	Stiposorghum	Tertiary	Australia
<i>Sorghum bulbosum</i> Lazarides	Stiposorghum	Tertiary	Australia
<i>Sorghum ecarinatum</i> Lazarides	Stiposorghum	Tertiary	Australia
<i>Sorghum exstans</i> Lazarides	Stiposorghum	Tertiary	Australia
<i>Sorghum interjectum</i> Lazarides	Stiposorghum	Tertiary	Australia
<i>Sorghum intrans</i> F. Muell. ex Benth.	Stiposorghum	Tertiary	Australia
<i>Sorghum plumosum</i> (R. Br.) P. Beauv.	Stiposorghum	Tertiary	Australia
<i>Sorghum stipoides</i> (Ewart & Jean White) C. A. Gardner & C. E. Hubb.	Stiposorghum	Tertiary	Australia
<i>Sorghum laxiflorum</i> F. M. Bailey	Heterosorghum	Tertiary	Australia and New Guinea
<i>Sorghum macrospermum</i> E. D. Garber	Chaetosorghum	Tertiary	Australia
<i>Sorghum trichocladum</i> (Rupr. ex Hack.) Kuntze		Tertiary	Mexico, Guatemala, Honduras

These alternative uses account for more 50% of the crop. However, sorghum productivity is still low, especially in rain-fed conditions, where there is a need for greater yield stability with increased pest and disease resistance. There is also a need to develop varieties with improved traits for alternative uses, and to focus on products other than grain and stover.

In summary, sorghum is an important cereal for international trade as well as domestic consumption in many countries. It is an important crop for reducing poverty and increasing household food security in sub-Saharan Africa and South Asia. It is also an important cereal crop in agro-ecologies where farmers still depend upon local varieties, thereby conserving significant genetic diversity of this crop. However, investment into the conservation and use of genetic resources is critical to ensure that crop productivity continues to improve in these increasingly marginal agro-ecologies.

2.2 Crop evolution

Sorghum is a domesticated crop that is taxonomically classified in the kingdom Plantae, division Magnoliophyta, class Liliopsida, order Cyperales, family Poaceae, tribe Andropogoneae, subtribe Sorghinae, and genus *Sorghum*. Ananda et al. (2020) extensively reviewed the history and status of classification of the *Sorghum* genus. There are several different views of the number of species and their classification into sections, but according to the USDA (2021), there are 25 accepted *Sorghum* species with three subspecies for the cultivated *S. bicolor* (Table 2.2). There are five sections within the *Sorghum* genus, but only those in the Eu-sorghum section are within the primary and secondary gene pools for the crop. Within the secondary gene pool, *Sorghum x almum* is a hybrid between *Sorghum halapense* and *S. bicolor*. Most of the species within the tertiary gene pool are found only in Australia. Only two species, *Sorghum purpureosericeum* and *Sorghum versicolor*, are distributed in Africa.

Ananda et al. (2020) reviewed the evidence for the cross-compatibility of cultivated sorghum with its wild relatives in various gene pools. The three subspecies of the domesticated species, *S. bicolor*, are fully inter-fertile and they also grow sympatrically with local landraces in Africa. Several studies have demonstrated gene flow between the crop and its wild relatives in Kenya, Ethiopia, Niger, Cameroon and Western Africa (Tesso et al. 2008; Barnaud et al. 2009; Mutegi et al. 2010; Mutegi et al. 2011; Sagnard et al. 2011; Mutegi et al. 2012; Okeno et al. 2012; Fernandez et al. 2014). Thus, there is a close relationship between cultivated sorghum and its progenitor, subsp. *verticilliflorum*, as well its weedy relatives in its area of origin.

Ananda et al. (2020) also summarized the evidence for crossability and transfer of traits from *Sorghum pro-pinquum* in the primary gene pool and *S. halapense* in the secondary gene pool. *S. x almum* is a natural inter-specific cross between these two gene pools. Ohadi et al. (2017) reviewed attempts to cross cultivated sorghum and its wild relatives, especially those in the tertiary gene pool. Ananda et al. (2020) concluded that the species in the tertiary gene pool had many traits that could improve adaptation to specific ecological environments. Kuhlman et al. (2010) described the use of the *iap* gene from *S. bicolor* in the development of hybrids with *Sorghum macrospermum* in the tertiary gene pool.

Sorghum was domesticated in the Ethiopia-Sudan region of Northeast Africa (de Wet, 1978) from subsp. *verticilliflorum*, while secondary centers of origin are found in India and China. A single domestication event occurred in the center of domestication and the racial diversity found globally has arisen from migration and dispersal. The only exception is the possible independent domestication of the race guinea subrace *margaritiflorum* (Deu et al. 2006; Figueiredo et al. 2008), but this is still unclear.

After its domestication in East Africa, sorghum dispersed across much of sub-Saharan Africa. Studies by the OECD (2016) and Maunder (2000) illustrated the origins and movement of the five races of sorghum within Africa, to the Indian sub-continent and China, and the return of race *durra* to East Africa. This movement was related to human migration and trade to India, China and the Americas.

Dahlberg (2000), de Wet (1978) and de Wet and Harlan (1971) described the four races of subsp. *verticilliflorum* and their distribution in sub-Saharan Africa. These four races have been recognized as ecotypes rather than races due to their morphological and ecological similarities, but they do have clear distinct geographical niches. Dahlberg and Rosenow (2018) described the major races of sorghum based upon spikelet and panicle morphology.

2.3 Crop and landrace diversity

Doggett (1988) hypothesized that the diversity of sorghum landraces, varieties and races has resulted from human migration, disruptive selection, geographic distance, gene flow from the wild subspecies to the cultivated varieties and cross-pollination. Westengen et al. (2014) evaluated the farming–language co-dispersal hypothesis in relation to geographic patterns in the distribution of sorghum genetic diversity and its association with ethnolinguistic groups. Social and cultural factors were identified as the main drivers of the pattern of sorghum diversity in Africa.

Table 2.3 Reports on phenotypic and genotypic diversity among collections of local landraces.

Report	Samples and locality	Diversity measures
Westengen et al. (2014)	20 seed lots collected from granaries and fields in 2010 and 2013 from Lafon villages in the southeastern part of South Sudan as well as 1983 <i>ex situ</i> collection.	19 simple sequence repeat (SSR) markers
A dugna (2014)	20 plants per eight landrace populations from Wello, Gibe River valley, and Metekel zone in Ethiopia	Seven phenotypic traits and 12 SSR markers
Rabbi et al. (2010)	1104 accessions, grouped into 46 samples from individual farmers from two contrasting agro-ecologies in eastern Sudan and western Kenya	16 SSR markers
Mutegi et al. (2011)	329 cultivated and 110 sorghum seed samples collected from farmers' fields in the four main sorghum production regions in Kenya and from the National Genebank of Kenya	24 SSR markers
Ngugi and Onyango (2012)	139 accessions of landraces from various sorghum growing regions in Kenya	11 SSR markers
Deu et al. (2008)	484 varieties collected from 79 villages distributed across Niger	28 SSR markers
Naoura et al. (2019)	56 cultivars of dry season sorghum collected at three important zones of production in Southern Chad	21 quantitative traits and 11 qualitative traits
Missihoun et al. (2015)	61 accessions collected in 13 villages in four districts in North west Benin	20 SSR markers
Dossou-Aminon et al. (2015)	142 accessions of sorghum landraces collected from three departments in Northern Benin	10 qualitative and 14 quantitative traits
Girma et al. (2020)	2010 accessions from the Ethiopian Biodiversity Institute (EBI) collection that represented a major sorghum production environment with different stresses, local production systems and local uses.	16 morphological traits, 6 quantitative traits, and genotyping with GBS
Amelework et al. (2013)	200 landraces collected from seven lowland districts in Ethiopia	30 SSR markers
Djè et al. (2004)	Two farmers' field sites in Northwestern Morocco	Five SSR markers
Danquah et al. (2019)	Seven cultivars and 34 accession collected from Northern Ghana	22 SSR markers
Mujaju and Chakauya (2008)	47 landraces collected from farmers in two districts in Zimbabwe	24 morphological traits
Mofokeng et al. (2014)	103 accessions that included 69 landraces from six provinces and two breeding programs in South Africa	30 SSR markers
Labeyrie et al. (2014)	290 samples collected from three ethnic groups in a study site on the Eastern slope of Mount Kenya	22 SSR markers
Burow et al. (2012)	159 landrace accession collected originally from main sorghum production area in the Northeast and other cold regions of China	41 SSR markers
Barro-Kondombo et al. (2010)	124 landraces collected from 10 villages in three regions of Burkina Faso	28 morphological traits and 29 SSR markers
Nikiema et al. (2020)	120 accessions that included 92 collected from farmers a wide range of agro-ecologies mainly in Central Burkina Faso	28 SSR markers
Ng'uni et al. (2011)	27 landraces representing two agro-ecological zones in Zambia	10 SSR markers
Bucheyeki et al. (2009)	40 landraces collected from South and Central Tanzania and two from Zambia	14 morphological traits
Tovignan et al. (2015)	84 accession, mainly Senegalese landraces	22 morphological traits, including biomass and stem sugar quantification
Ghebru et al. (2002)	28 accessions from Eritrea, both lowland and highland collections	15 SSR markers
Elongavan et al. (2009)	674 accessions collected from seven states in India	Economic, culinary, and adaptation traits from farmers
Grenier et al. (2004)	2017 accession from Sudan conserved at ICRISAT	Nine quantitative and 10 qualitative traits
Maina et al. (2018)	520 accessions from Niger conserved at USDA-NPGS	144,216 single nucleotide polymorphisms (SNP)
Faye et al. (2019)	421 accessions from Senegal conserved at USDA-NPGS	213,916 SNP
Cuevas and Prom (2020)	318 accession from Sudan conserved at USDA-NPGS	183,144 SNP
Girma et al. (2019)	1425 accessions from Ethiopia conserved at EBI	72,190 SNP
Olatoye et al. (2018)	607 accessions from Nigeria conserved at USDA-NPGS	>400,000 SNP
Faye et al. (2021)	756 accessions from the national breeding programs of Senegal, Mali, Burkina and Togo	156,191 SNP

All the other factors were contingent on social and cultural factors. They also considered the origin and resilience of local genetic diversity. Westengen et al. (2014) postulated that the local genetic diversity is an example of a successful social-ecological adaptation by farmers to climatic changes that occurred in the past in sub-Saharan Africa, because the drought tolerance of sorghum enabled cultivators to successfully migrate to new areas.

The explosion of genomic resources for sorghum has led to global assessments of their diversity and genetic basis. This information forms a useful basis for linking conservation and utilization. At the “meta” level, key studies include: Casa et al. (2008); Billot et al. (2013); Morris et al. (2013); Mace et al. (2013); Lasky et al. (2015); and Yu et al. (2016). The strategies and data sets in those studies shed light on the levels of diversity within and among species and provide tools for the discovery and genetic dissection of key agronomic and compositional traits.

In addition, over the last 20 years there have been several reports on the degree and distribution of phenotypic and genotypic diversity at the “micro” level among and within landraces or farmers’ varieties (Table 2.3). Many of these studies considered the assessment of diversity as a very important step in the development of a national collection conserving traditional varieties *ex situ*, and in increasing the use of such materials in the development of improved varieties that meet the needs of local producers and consumers. Most of these studies concluded there was a high degree of genetic diversity among local varieties. The varieties were grouped or clustered by race classification, geographic or agro-ecological adaptation, culinary use or ethnicity of the farmers, among other criteria. There was considerable variation among varieties within geographical zones or other groupings. This variation was considered to result from seed exchange among farmers, or to some degree of cross-pollination when multiple varieties are cultivated together in farmers’ fields. The various studies demonstrated the importance of landraces to subsistence farmers, who maintain and use a significant amount of diversity across a wide range of agro-ecologies globally.

There are limited studies on diversity amongst local varieties grown within an agro-ecological environment that cuts across national borders. Nikiema et al. (2020) reported that the clustering and distribution of diversity amongst collections from farmers in central Burkina Faso was similar to that reported for Niger and Mali, which have similar agro-ecology and probably share some of the same varieties. A similar result was reported by Bucheyeki et al. (2009) for landraces from Southern and Central Tanzania and Zambia.

Thus, it is important to consider cross-border collaborations in diversity assessments.

Other studies assessed the risk of the loss of sorghum diversity. To monitor temporal dynamics of genetic diversity, Bezançon et al. (2009) and Deu et al. (2010) compared diversity between collections made in 1976 and collections in the same villages in 2003. Generally, both studies found no major loss of genetic diversity in the previous 26 years, but found evidence of differences in the evolution of allelic richness and gene diversity due to differences in socio-economic factors across the regions. This evolution can also be dependent upon the farmers’ cultural identity. Deu et al. (2010) concluded that these assessments of temporal changes required more local data on socio-economic factors, especially seed exchange.

Labeyrie et al. (2014) assessed genetic diversity among varieties obtained from farmers in three ethnic groups at a single site in Eastern Kenya. They found that social boundaries associated with ethnolinguistic diversity influenced the distribution of varieties and their spatial distribution. This effect was only seen for landraces, and not improved varieties. They concluded that crop diversity patterns result from the interactions among genotype, environment and social boundaries, especially in subsistence farming systems where crops continue to evolve. Social boundaries limit seed exchange and the diffusion of plant materials.

Leclerc and d’Eeckenbrugge (2012) described the important role of social components in crop evolution and the maintenance and use of diversity. They concluded that crop diversity organization is a result of the three-way interaction among genotype, environment and social differentiation factors. de Wet (1978) recognized that racial evolution in cultivated sorghum was closely associated with ethnological, ecological and geographic isolation. These factors have resulted in morphological differentiation shaped by differential selection and restricted seed exchange. In their review of crop diversity assessments, Leclerc and d’Eeckenbrugge (2012) concluded there was a lack of recognition of social identity in sampling strategies and in the interpretation of results. Thus, the genotype × environment interaction is taken into account where regions are geographically based but sociological aspects are not considered. Leclerc and d’Eeckenbrugge (2012) pointed out the contradictions found in many of the studies listed in Table 2.3, which considered fields, farmers’ production practices, landrace identity, and seed systems, but not social structure, in the sampling design. Many of those studies were not able to interpret patterns of diversity or to guide *in situ* or *ex situ* conservation.

Westengen et al. (2014) concluded that a strong, culturally based seed system was important for the maintenance of landraces. Within-population diversity is maintained through the traditional practice of mixing seeds from the whole community and some degree of outcrossing. Despite drought, conflict and relocation of villages, the local seed system has been resilient, with no evidence of significant genetic erosion. Thus, building upon the local seed system and landraces needs to be considered in research and development for sorghum in the future, especially with the challenges of climate change.

2.4 Use of genetic resources

Sorghum is a tropically adapted cereal that has extensively widened its range of production environments during its evolution. This has resulted in a significant focus on the use of genetic resources in the history of crop improvement of sorghum (Rosenow and Dahlberg, 2000; Qingshan and Dahlberg, 2001; Reddy et al. 2008). In the United States, only a few parents were introduced from Africa. In the early years of sorghum improvement, this resulted in a bottleneck that was to be addressed with the development of the Sorghum Conversion Program in 1963 (Stephens et al. 1967). The program aimed to make more tropically adapted genetic resources available to breeders, with the requisite dwarf height for mechanical harvesting and photoperiod insensitivity. This resulted in new, diverse sources of biotic and abiotic stress tolerance being globally available (Rosenow and Dahlberg, 2000). Klein et al. (2008) reported that the genetic basis of sorghum hybrids in the United States has broadened with greater use of newly introduced germplasm. The Sorghum Conversion Program significantly contributed to this. The degree of recovery of the exotic parent with backcrossing in the conversion process was not as complete as predicted but it has increased the amount of genetic diversity available to breeders in the temperate regions of the world.

The importance of genetic resources for the future improvement of sorghum was also recognized with the establishment of *ex situ* collections, such as that at ICRISAT in India. Reddy et al. (2008) summarized the evaluation and utilization of accessions from the genebank for a variety of traits by ICRISAT, and the use of this diversity to develop improved cultivars, inbred parents for hybrids and advanced lines. They also reviewed the evaluation and use of genetic resources by the national program in India. Qingshan and Dahlberg (2001) reviewed the history of collections of sorghum in China, as well as the evaluation and use of germplasm in crop improvement programs with a particular focus on using locally adapted accessions. Duncan et al. (1991) and Rosenow and Dahlberg (2000) reviewed the use of genetic resources for the

improvement of parent lines to create hybrids in the United States. In all these reviews, there are excellent examples of the successful use of genetic resources to improve sorghum production, and to address significant constraints such as drought, diseases, and insect pests.

While there has been considerable focus on sorghum genetic resources in the past, this has not resulted in the extensive use of accessions in collections. Some barriers include the size and complexity of collections, and the lack of information on accessions. This has led to the development of subsets, both trait-specific and representative (core and mini-cores). The first sorghum core collection with associated genomic information for subsequent genetic studies was established by Casa et al. (2008). To date, this reference has been cited over 300 times in the literature. These types of diversity subsets have been constructed to allow users to identify useful diversity or to identify further sources of diversity in the larger collection with similar traits, origins or alleles. In addition, with the availability of molecular data, the genetic basis for many of the desired traits can be determined.

Upadhyaya et al. (2016a) and Upadhyaya and Vetriventhan (2018) reviewed the development of core or representative subsets by ICRISAT, USDA, and others. Billot et al. (2013) described the composition of the Global Compositive Germplasm Collection (GCGC) with 3384 cultivated and wild accessions that were genotyped to establish a reference set of 383 accessions with 78.3% of the overall allelic variation. The GCGC reference set and the mini-cores established by ICRISAT and USDA for their collections have been characterized, evaluated for many traits, used as association panels and used in breeding. Prasad et al. (2021) reviewed the evaluation of drought and heat tolerance in sorghum and breeding to improve these traits. Specific accessions with various traits have been reported by Upadhyaya et al. (2016a), Upadhyaya and Vetriventhan (2018) and Prasad et al. (2021).

Upadhyaya and Vetriventhan (2018) and Ananda et al. (2020) reviewed the conservation, evaluation and use of the wild relatives of sorghum. Both reviews included a list of wild species that had been identified with traits of interest to breeders and the status of their use. Both studies concluded there was significant useful variation within the wild relatives, especially those in the tertiary genepool. However, these are currently underrepresented in *ex situ* collections and not adequately protected *in situ* reserves, so there needs to be more emphasis on securing their conservation for the future.

Ananda et al. (2020) reviewed research on the barriers to using wild species for the improvement of

cultivated *S. bicolor*. Mainly, these barriers are the result of pre- and post-zygotic reproductive barriers or pollen-pistil incompatibility. Kuhlman et al. (2010) developed a *S. bicolor* line homozygous for the *iap* (inhibition of alien pollen) gene, resulting in reduced incompatibility so that pollen can grow successfully. This allows for the production of hybrids when this line is crossed with species in the tertiary gene pool. Ohadi et al. (2017) discussed the use of this gene to transfer traits into cultivated sorghum.

There have been several extensive reviews of the genomic resources available for genetic studies and breeding to better link phenotype and genotype. Such resources include diversity panels, reference genomes, and multiparent mapping populations, such as nested association mapping, multi-parent advanced generation inter-cross, and mutagenized populations (Upadhyaya et al. 2016; Boyles et al. 2019; Hao et al. 2021; Xin et al. 2021). Boyles et al. (2019) described the development of these genomic resources in detail and identified the sources of the germplasm. They concluded that, because many of these populations and the corresponding data are held by individual researchers or organizations, they are vulnerable to being lost if there are changes in staff or research direction. Thus, more attention needs to be paid to securely conserving the seeds of these resources and making them more accessible. Curation and warehousing of key data are also important for any future use, but these need to be better coordinated so both the data and the germplasm lines can be accessed from a central location. Hao et al. (2021) concluded that there is a need for agreed standards for the management, interpretation and sharing of data. This will allow rational use without redundant or wasted effort and will increase knowledge by strengthening the community of researchers and including data from all relevant studies.

Hao et al. (2021) also reviewed the use of genomic tools to study diverse genetic resources, such as the studies of Mace et al. (2013), Morris et al. (2013), and Zhang et al. (2018). All of those studies used genomic tools to dissect the genetic basis of complex traits and population structure. The use of regional diversity panels has been reported in Maina et al. (2018), Faye et al. (2019), Girma et al. (2019), Cuevas et al. (2017), and Cuevas and Prom (2020). Hao et al. (2021) summarized the evidence for domestication events and candidate genes for complex agronomic traits in sorghum obtained in genomic studies, genome-wide association studies, quantitative trait loci (QTL) analyses, and transcriptome analyses. They presented a table summarizing the major QTL or genes related to important agronomic and adaptive traits in sorghum. Hao et al. (2021) proposed a breeding scheme for sorghum using these genomic resources and genetic selection to

develop elite lines from populations developed from wild relatives, landraces and improved lines. They listed four key components of the breeding scheme: diagnosis of the impact of domestication and diversification, description of genetic and genomic variation, pre-breeding through genomic selection, and the use of genomic-assisted introgression. They summarized how these components have been used in breeding so far but concluded that this modern approach to sorghum breeding is in its infancy.

Jannink (2010) predicted that genome-wide selection would enable shorter breeding cycles and greater early generation gain prior to the more expensive step of phenotyping, but it would also result in the loss of genetic variance, less accurate genomic selection and a low selection plateau. Thus, there is a need to balance selection gain with maintaining diversity. Nguyen and Norton (2020) suggested that a breeding approach using high throughput phenotyping (HTP) tools together with genomic selection would result in better genetic gains with a reduced loss of allelic diversity. They extensively reviewed the use of HTP tools for characterization and evaluation to generate internationally agreed crop descriptors to exploit genebank collections for conservation and breeding. They concluded that the application of HTP in genebanks would reduce the cost and time of operations, and increase the consistency and accuracy of characterization. It would make characterizations more comprehensive and reduce the lag time before making information available to users. For breeders, this would increase opportunities to accurately identify the desired accessions and increase gains from pre-breeding or breeding. They also concluded that the application of HTP tools for phenotyping during regeneration would allow for better monitoring of the genetic integrity of accessions. This would reduce genetic erosion over time, and ensure that end users and archivers know exactly which materials they are dealing with.

Nyugen and Norton (2020) reviewed use of HTP tools in genebanks and identified some of the key challenges. These included the costs of equipment and operations, as well as data analysis, curation and storage. There are technical challenges in data capture, quality assurance and analysis. Robust data are important for the integrity of the collection, as well as for metadata applications. Long-term data stewardship is also important. Along with the passport data, phenotypic and genotypic data should be made available to end users. Nyugen and Norton (2020) proposed a strategic phenomics approach and described its application at the Australian Grain Genebank (AGG) in Horsham, Victoria, Australia. They concluded there is a need for coordinated national and international efforts to ensure that phenotypic data are comparable

across genebanks, with an agreed protocol for sharing and exchanging data with unique identifiers, such as DOI's, via global portals such as Genesys.

While there are many new opportunities to increase the use of accessions from *ex situ* collections in the future, there are still significant barriers that contribute to the limited use of genebank accessions in breeding. Gollin (2020) concluded this has led to the use of a broad range of diverse accessions only for genomics, gene discovery, or more basic scientific research. If breeders are interested in genetic gain in their improvement program, they should utilize improved germplasm. Galluzzi et al. (2020) reported on a survey of breeders in 19 countries across a wide diversity of crops, including sorghum. The survey asked about their perception of changes in the climate of their target environments, and how this affected their breeding objectives as well as the use of specific types of genetic resources. The survey also asked whether regulatory, financial, technical, and other issues influenced how they used various types of genetic resources. Both breeders and farmers in the survey perceived changes in the climate of the environment mainly related to rainfall patterns, the frequency of drought and timing of the seasons. Consequently, the priorities for breeding were pest/disease resistance, drought tolerance, shorter growth cycles and tolerance to hot and cold temperatures.

Gollin et al. (2000) pointed out that breeders view the use of landraces (and wild relatives) as costly and time consuming, with an increased risk of introducing undesirable characteristics. Galluzzi et al. (2020) found that, faced with the challenges of climate change, breeders had significantly increased their use of advanced/elite lines, but not landraces or wild relatives. They only ventured to explore landrace diversity when faced with more complex challenges. They used mainly *ex situ* accessions from their own collection or institution (35%) or Consultative Group on International Agricultural Research (CGIAR) genebanks (23%), followed by those from national genebanks (9.3%), farmers' fields or natural areas (10.3%) and community genebanks (5.3%). Breeders obtained wild species and advanced/elite lines from different sources, but mainly from collections outside the country, while landraces were mainly sourced from collections in the country. Breeders indicated that the lack of tools for using germplasm was the most significant issue. For example, 68% indicated they had limited access to molecular tools and 24% said they lacked infrastructure for phenotyping, trials and characterization. Only 6% of the breeders surveyed indicated that the availability of genetic material or associated information was a critical limitation. The prominence of CGIAR as a provider of germplasm has decreased. This is probably

due to the large number of transfers that have already occurred. Based on the survey results, Galluzzi et al. (2020) concluded that the lack of supportive policies and/or administrative environment was more of a barrier to the use of germplasm than technical capacity. This needs to be addressed with greater national and international collaboration.

2.5 Summary of the background review

Sorghum is an important cereal crop, especially for subsistence farmers in South Asia and Sub-Saharan Africa. In some other areas of the world, such as the United States, Mexico, Argentina, Brazil, Australia, China and Japan, it is an important feed crop with a significant value for trade. The areas of production for sorghum have declined in most regions of the world except Africa, where it is vital for household food security, contributes to poverty alleviation and has major cultural value.

The cultivated crop, *S. bicolor* subsp. *bicolor*, has significant genetic diversity. The wild and weedy subspecies are another source of additional, potentially useful allelic diversity. There are also many related species with unique traits and adaptations that can serve as resources for genetic improvement. The diversity within landraces is extensive and is a product of differences in genetic origin, environments and social systems. There is limited indication of genetic erosion of landraces in the field over time. The use of genetic resources to improve sorghum production has been important in the past, and will be essential for addressing the crop's many challenges, such as climate change, and opportunities, such as new uses. Sorghum breeders prioritize improving traits related to climate change, for example, drought tolerance, cold or heat tolerance, pest/disease resistance, and shorter growth duration. This has resulted in increased use of genetic resources such as elite lines from other breeding or research programs, landraces from local farmers, and wild relatives. This increased interest in using genetic resources presents future opportunities for *ex situ* collection holders, but also challenges.

The greater application of genomics and HTP (Shakoor et al. 2015; Shakoor et al. 2017; Wang et al. 2018) will benefit both end users and genebanks. However, it will challenge the capabilities of genebank curators, their data management systems, and global collaborations in the curation and sharing of data. It will require much stronger links among genebanks, between genebanks and end users, and among end users, nationally and internationally. These challenges were considered in the 2007 strategy, but only from the view of the genebanks, and without the benefits of the technological advances during the last 15 years.



3 STATUS OF *EX SITU* CONSERVATION – COMPOSITION

A very important input into the global conservation strategy is the survey of current collection holders to determine the status of *ex situ* conservation and use of genetic resources. The 2007 strategy listed 122 sorghum collections conserving 194,250 accessions. The collections were prioritized based on their size and likely contribution to the global diversity of landraces and wild relatives. A survey was sent to 57 high-priority *ex situ* collections and 19 of them responded. At a subsequent consultation workshop, experts considered “major collections” as those with a significant sampling of diversity that is readily accessible with accession-level passport, characterization and evaluation data. They considered the ICRISAT and USDA collections as major collections. They considered 21 other collections as important, especially those in the primary and secondary centers of diversity, or specialized collections, such as the broomcorn sorghum collection in Serbia.

In 2021, the 135 institutions that currently conserve sorghum were again prioritized and 58 were identi-

fied for a follow-up survey. A priority genebank had to meet at least one of the following criteria:

- More than 500 accessions reported in FAO-World Information and Early Warning System (WEIWS) and/or Genesys;
- Conserves significant local diversity or specialized accessions; or
- Was recognized as a major or important collection in the 2007 strategy.

The questionnaire differed from the 2007 survey, with a greater focus on the composition of the collection, the status of various routine conservation activities and use of the conserved genetic resources. We received responses from 38 institutions (see Annex 1 for contact details).

Annex II lists the number of accessions conserved in different genebanks *ex situ* reported in the 2007 survey and/or the 2021 survey, FAO-WIEWS, and Genesys. Several collection holders did not respond to the survey or provide information to FAO-WIEWS

or Genesys. The most significant were the Chinese Academy for Agricultural Sciences, the N. I. Vavilov Institute of Plant Genetic Resources (Russia), the Institute of Field and Vegetable Crops (Serbia), and the national genebanks of Rwanda, Yemen and Guatemala. The genebanks in Japan, Hungary, Bulgaria and Pakistan did not respond to the survey, but have added accession-level information to FAO-WIEWS. Eleven institutions responded to the survey in 2021, but not the survey in 2007. When the numbers of conserved accessions were compared between 2007 and 2021, four institutions had a significant reduction in the number of conserved accessions. One institute reported that the number given in 2007 was incorrect, because they did not have a sorghum collection at that time. In addition, five institutions reported a significant reduction in the number of accessions conserved in 2021 versus 2007 based on data in the FAO-WIEWS/Genesys consolidated database. Some losses may have been due to various challenges faced by the genebanks. This will be explored in more detail in the strategy as we consider the vulnerability of the global system to genetic erosion.

Overall, the 2021 Survey respondents conserve about 84% of the global accessions, with very good participation. The only exception was Europe, where only three institutions conserving 20% of accessions from that region responded (Table 3.1). There are many

small collections in Europe that account for only 5% of the global total. Some important collections in Europe conserve a broad base of diversity and some specialized collections. In the other three regions, the survey respondents conserved from 80% to nearly 100% of the accessions in their respective regions.

According to the survey results, few accessions of wild species are conserved *ex situ*, especially the wild and weedy subspecies of *S. bicolor* in Africa (Table 3.2). Landraces are the main type of accession conserved globally. The largest proportions of accessions conserved in Africa and Asia-Pacific are farmers' varieties or landraces that have been collected in the country of the institution. A large number of landraces acquired from outside the country is also conserved in Asia-Pacific. Compared with other regions, America conserves more released varieties, breeding lines and unclassified materials.

Given the extent of conservation of farmers' varieties acquired from other collections and research materials, there could be significant redundancies in the global system. In the consolidated database, 73% of the accessions have information on the country of origin. In most cases, that is the country of collection or breeding, but sometimes it is the country of the donor. This is especially the case for accessions from the United States, India (ICRISAT) and Australia.

Table 3.1 Regional distribution of institutions, number of conserved accessions listed in consolidated FAO-WIEWS/Genesys database, and number of accessions conserved by 2021 Survey respondents.

Global regions	Consolidated FAO-WIEWS/Genesys database		2021 Survey respondents	
	No. of countries	No. of accessions	No. of countries	No. of accessions
Africa and Middle East	47	53024 (20%)	26	52705 (24%)
Europe	41	13880 (5%)	2	2586 (1%)
Asia Pacific	21	133652 (52%)	5	107255 (49%)
America	26	59039 (23%)	4	55133 (25%)
Grand total	135	259595	37	217679

Table 3.2 Regional distribution of number of accessions classified as of landraces collected in the country, landraces acquired from outside the country, old cultivars and released varieties, Research or breeding advanced lines, populations or genetic stocks, *S. bicolor* subsp. *verticilliflorum* and *drummondii*, wild relatives or other *Sorghum* species, and not classified conserved by 2021 Survey respondents.

Global regions	Landraces collected in country	Landraces acquired from outside country	Old cultivars and released varieties	Research or breeding advanced lines, populations or genetic stocks	<i>S. bicolor</i> subsp. <i>verticilliflorum</i> and <i>drummondii</i>	Wild relatives or other <i>Sorghum</i> species	Not classified
Africa and Middle East	30172	10526	716	2384	495	169	3585
Europe	61	1118	50	1059	32	241	25
Asia-Pacific	44354	37276	808	13125	657	413	10622
America	110	2576	2473	19437	338	120	30079
Grand total	74697	51496	4047	36005	1522	943	44311

Despite this shortcoming, accession-level information allows for the assessment of potential redundancies and gaps based on the geographical origin of accessions. Twenty institutions conserve accessions originating from eight to 108 countries. Some of these (ICRISAT, International Center for Biosaline Agriculture (ICBA), South African Development Community (SADC) Regional Genebank and International Livestock Research Institute (ILRI)) are international or regional collections. Two institutions conserve very small collections. Table 3.3 lists the 14 institutions that conserve geographically diverse collections, all of which are national collections. The National Bureau of Plant Genetic Resources (NBPGR) in India, The Kenya Agricultural and Livestock Research Institute- Genetic Resources Research Institute (KALRO-GRRI), and the national genebank in Brazil conserve collections wherein more than 60% of accessions are from their own country. Eighteen internationally diverse collections conserve about 45% of the global accessions. These 18 genebanks conserve 100% the accessions conserved globally from 58 countries but less than 25% of the accessions for 15 countries are conserved globally by these genebanks. These 18 diverse collections are a key component of the global system, and further analysis would allow for a much better understanding of global duplications.

There is also evidence of a high degree of duplication for accessions from a limited number of countries. Eleven countries are the most highly represented in the global system as sources of accessions, and account for about 40% of accessions conserved globally (Table

Table 3.3 Number of accessions with country of origin designated, the number of countries of origin, and the proportion of accessions that derived from the country of the institute.

Institution	Number of accessions with country of origin designated	Number of countries of origin	Proportion of accessions that derive from country of institute
USA016	38404	108	13.1%
AUS165	5731	79	20.8%
UZB006	662	48	5.0%
HUN003	612	38	17.5%
GBR004	235	26	0.4%
BGR001	333	33	6.6%
DEU146	336	29	2.4%
CZE122	60	14	3.3%
ROM002	49	16	38.8%
BLR026	152	13	34.2%
UKR005	197	29	56.9%
IND001	16845	47	65.7%
KEN212	5257	18	76.1%
BRA003	2649	8	62.1%

3.4). The number of accessions from India includes those at ICRISAT, which is listed as the origin for about 30% of the accessions from India. Some countries, such as the United States and Australia, were not included in this analysis because they are more likely to be the source of accessions through acquisition. This assessment demonstrates the potential redundancies in the global system, considering that many collections have been made jointly with another collection holder, the accessions collected were conserved by both, and then distributed to others.

An assessment of the geographical source of accessions revealed significant gaps. Table 3.5 summarizes the number of accessions conserved globally, the number of institutions conserving, and the proportion conserved nationally for 25 of the countries whose institutes responded to the survey. For example, few accessions from Eritrea are conserved outside Eritrea. There are seven countries where more than 50% of global accessions are only conserved nationally. This could be a significant risk if these collections are not safety duplicated.

The survey respondents were asked to carry out a self-assessment of the degree of 'uniqueness' of the accessions they conserve (Figure 3.1). The categories included fully unique, more than 50% unique, and less than 50% unique. Very few respondents classified the wild relatives, breeding materials, and old cultivars as fully unique but about half rated the landraces in their countries as unique. In general, the respondents in the survey considered that there was duplication in their collections.

Many accessions from Ethiopia are conserved globally, and about 45% are conserved nationally by the Ethiopian Biodiversity Institute (EBI) (Table 3.5). Figure

Table 3.4 Eleven most frequent source countries of sorghum accessions, number of accessions conserved globally and number of institutions conserving these accessions.

Origin	No. of accessions conserved globally	No. of institutions conserving
India	24722	18
Sudan	20269	16
Ethiopia	22168	15
Kenya	6795	11
Mali	6321	15
Zimbabwe	6265	11
Nigeria	5697	12
Uganda	4486	12
Tanzania	2989	13
South Africa	2857	14
China	2216	15
Total	104785	

3.2 shows the location of accessions conserved by EBI (black dots) and those conserved by other genebanks (white dots) (pers. comm. Nora Castaneda-Alvarez, 2019). There is significant overlap for these accessions overall, but there are localities of Ethiopia where the only accessions conserved globally are at the EBI and a few localities where accessions are only conserved outside Ethiopia. There are also localities where the accessions are conserved only by local farmers. A global gap assessment would allow for much better targeting of collecting and safety back-ups.

Another example is the GRRII in Kenya, which conserves about 60% of the global accessions from that country (Table 3.4) (pers. comm. Nora Castaneda-Alvarez, 2019). As shown in Figure 3.3, there is significant overlap between the accessions held globally and those held in the national collection, especially accessions from the southwest and the central areas of Kenya. There are also many localities where their accessions are conserved only in the national genebank, and these should be targeted for safety back-up. There are still localities where the genetic resources are conserved only by the local farmers or in natural areas. Again, this demonstrates the value of a global gap assessment to consider all the accessions conserved by all collection holders.

While some gaps in the global collection are because of the low number of accessions from particular countries, some are due to the insecure status of conservation. Even in countries with a high degree of redundancy globally, there are gaps in localities nationally. In the 2007 strategy, it was recognized that the high degree of duplication made it difficult to determine the adequacy of coverage within the diversity conserved globally. This was due to the poor availability of passport data in many collections and the number of accessions commonly conserved in the country of

Table 3.5 Number of accessions conserved globally from a country, total number of institutions conserving accessions sourced from that country, and proportion of the global accessions conserved in the country of origin.

Country	Number of accessions conserved globally	No. of other institutions conserving accession from that country	Proportion held by institute in country of origin
Eritrea	724	1	99.7%
Spain	79	2	77.2%
Sri Lanka	110	4	73.6%
Nepal	83	4	72.3%
Niger	5671	6	60.7%
Kenya	6795	10	58.9%
Senegal	1539	9	51.4%
Lesotho	856	5	47.4%
Ethiopia	22168	14	45.1%
Ghana	757	7	44.8%
India	24722	16	44.7%
Morocco	89	9	41.6%
Mali	6321	14	40.9%
Botswana	1197	8	40.4%
Nigeria	5697	11	39.8%
Namibia	535	4	35.5%
Sudan	20269	15	35.5%
Burkina Faso	3778	8	34.9%
Zambia	2924	6	32.8%
Zimbabwe	6265	10	32.4%
Chad	526	4	26.4%
Uganda	4486	11	21.2%
South Africa	2857	13	19.4%
Benin	509	2	16.9%
Togo	1016	2	15.4%

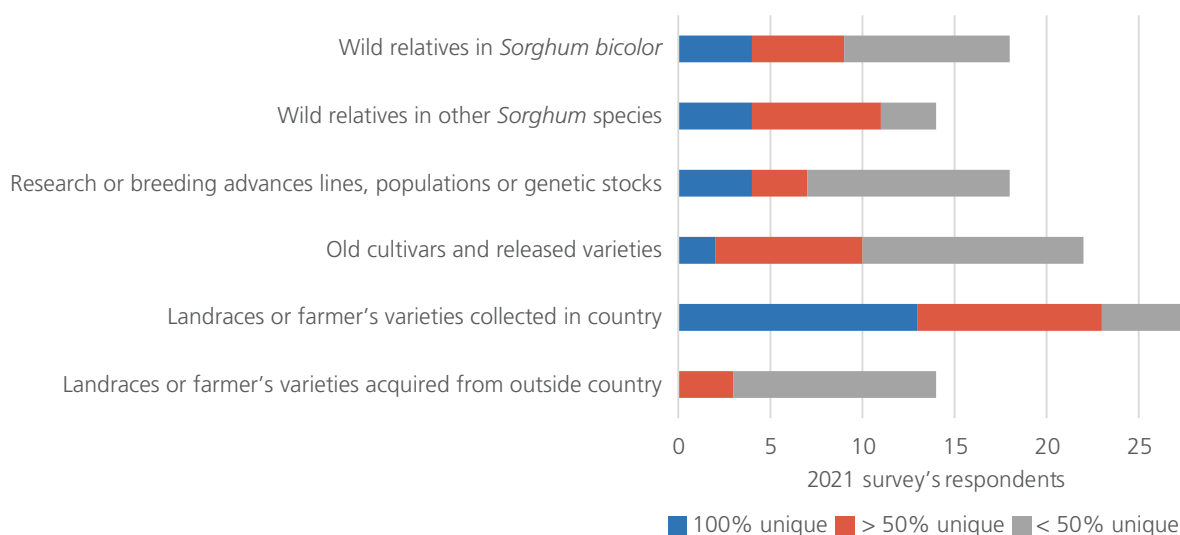


Figure 3.1 Self-assessment of 'uniqueness' of accession by institutions in the survey.

origin, the USDA collections and ICRISAT. This was still an issue in 2021. In 2007, the expert workshop concluded that it was important to assess the level of duplication among major collections based on analyses of passport data. Although this was identified as a priority action for the global system, it has not yet been done. The 2007 strategy also identified gaps based on expert knowledge. These were² Liberia, Ivory Coast, Guinea, DRC, Ghana, Nigeria and along the Niger River inland delta, as well as Central America, Central Asia and the Caucasus, Dafar in Sudan and South Sudan. Wild species coverage was also viewed as inadequate.

The 2021 survey asked about any assessment of redundancies and gaps in the past 20 years. Some institutes have assessed their collection for redundancy. The Indian Institute of Millets Research (IIMR) in India found that 15%–20% of their collection was also conserved by the NBPGR and ICRISAT, based on passport data. The NBPGR also used passport data to assess duplication with the ICRISAT collection. El Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA) in Spain used Genesys to assess duplication in their collection. The Australian Grains Genebank (AGG) in Australia is planning to use passport data and genomic data to detect duplicates in their collection. In Burkina Faso, variety names were used to assess duplication. Several respondents recognized that there was duplication with other collections and viewed these as safety duplicates.

Some respondents have identified gaps in their collections and have made efforts to address them with collecting, especially ICRISAT and national genebanks in Africa. ICRISAT, IIMR and the NBPGR in India as well as genebanks in some African countries identified gaps using Geographic Information Systems (GIS),

²Order in list does not reflect the size or importance of the gap.

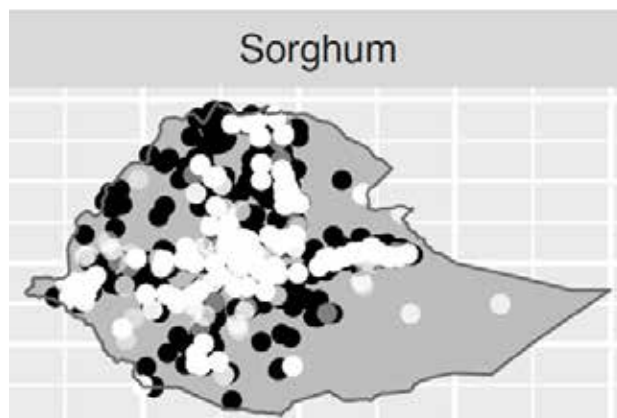


Figure 3.2 Distribution of accessions collected in Ethiopia and conserved by the EBI (black dots) and by other genebanks outside Ethiopia (white dots).

and are now filling them. Some countries including Nepal, India and South Africa reported that they did not know of any geographical gaps nationally, mainly because of a lack of any formal assessment. In other cases, gaps were identified on the basis of expert knowledge, morphological characterizations, stakeholder consultations, specific traits identified by users and the distribution of local production. Some of the gaps can be filled by collecting and others by acquisition. When the gaps identified in the 2021 survey were compared with those identified in 2007, many in West and Central Africa and South Sudan are yet to be filled. Based on an assessment of the consolidated database, there are also significant gaps remaining in many other areas of the world, including Central America, Central Asia, and the Caucasus. Finally, species coverage is seen as inadequate, as well as ecological sampling at the national level.

A “[diversity tree](#)” has been developed for sorghum. The structure of the tree was based on published information and consultations with experts (Genesys 2021). This analysis was conducted to assess the racial diversity of *S. bicolor* subsp. *bicolor* in the ICRISAT collection (Annex III) and to identify gaps in the collection. ICRISAT has the second largest collection of sorghum globally, and this international collection holds diversity from most of the important regions of the world. The gaps identified in Annex III are consistent with ICRISAT’s own assessment of gaps in their collection, as described below.

Upadhyaya and Vetriventhan (2018) reviewed the application of gap analysis to the ICRISAT sorghum collection for South Asia (Upadhyaya et al. 2016b), East Africa (Upadhyaya et al. 2017a), and West and Central Africa (Upadhyaya et al. 2017b). These studies used accession-level passport and characterization

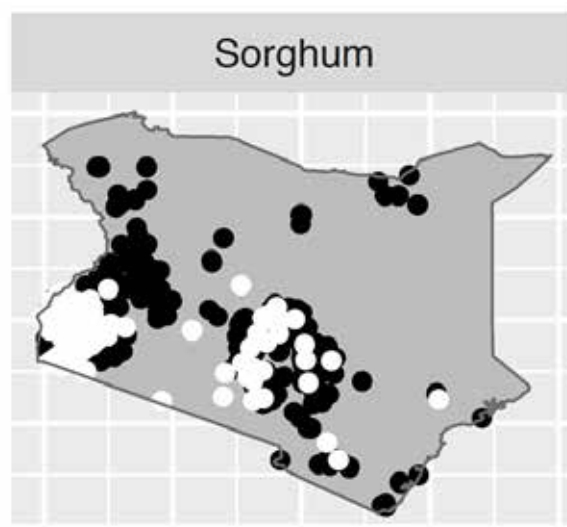


Figure 3.3 Distribution of accessions collected in Kenya and conserved by the GRRII (black dots) or by genebanks outside Kenya (white dots).

data to assess the distribution of diversity within the target region. The general approach used to identify gaps was to: target localities where no accessions were being conserved; determine the degree of representation in other localities and target those with very limited sampling; use characterization data to identify localities with the greatest wild species richness or morphological diversity; and to use ecological modeling to identify geographical areas likely harboring unique ecotypes or populations.

A key constraint to assessing gaps using this approach was discussed by Westengen et al. (2014) and Leclerc and d'Eeckenbrugge (2012). In the studies reviewed by Upadhyaya and Vetriventhan (2018), it was assumed that the main factor determining diversity in sorghum populations was geographical distance and ecological adaptation. However, Westengen et al. (2014) found that the structure of cultivated sorghum diversity in Africa was most strongly associated with social and cultural factors, while geographical distance, ecological adaptation, and even morphological traits were contingent on social structure. This was discussed in detail by Leclerc and d'Eeckenbrugge (2012). Thus, an assessment of gaps in individual collections using limited subsets, even if there are adequate data for

geographical or morphological structures, may be insufficient to assess the adequacy of global coverage of diversity and significant conservation gaps, either *ex situ* or *in situ*. The assessment of conservation priorities for the wild *Sorghum* species reported in Myrans et al. (2020) used geographical and ecological factors where they were likely the main factors responsible for population structure. They identified taxa that were a high and medium priority for *ex situ* and *in situ* conservation.

The composition of an individual collection is a product of its history and past objectives. Upadhyaya et al. (2017b) reviewed the history of the accessions from West and Central Africa in the ICRISAT collection. Most of the accessions were donations from 24 institutions and only about 20% were from collection missions. Gollin (2020) concluded that an *ex situ* conservation strategy focusing on conserving everything needs to be reconsidered to meet the needs of conservation and use in the future. As we gain a better understanding of genotypic and allelic diversity through enhanced genomic tools and more accurately estimate social and cultural diversity, it will be feasible to use a global approach for the identification of duplications and gaps in collections.

4 STATUS OF *EX SITU* COLLECTIONS – CONSERVATION

S. bicolor has orthodox seeds that are tolerant to drying to a low moisture content and to storage for very long periods at low temperatures if their quality and initial viability are high. Some other *Sorghum* species, however, have low seed set and seeds that do not tolerate such storage conditions well. Such species may need to be maintained in field collections. The routine operations for the conservation of sorghum are similar to those specified for genebanks in general by Hay and Seršen (2021) and Engels and Ebert (2021b). A key input into the development of the global strategy is an assessment of the efficiency, effectiveness and security of conservation of current *ex situ* collections. Therefore, the survey sent to collection holders included questions related to the routine operations being conducted, the type and state of their facilities, the type of any conservation research and the security of conservation.

4.1 Conservation infrastructure

Most genebanks conserve accessions in active collections, base collections or both. Active collections are typically conserved for a medium term at 2°C to 4°C, while base collections are under long-term conservation at lower temperatures, mainly –18°C to –20°C. Thus, one of the key infrastructure needs are cold-storage units. Hay and Senshen (2021) suggested using medium-term storage as a cost-effective way to conserve seed intended for distribution, while materials that are accessed less frequently can be stored long term. Nine of the institutions in the survey conserved accessions only in long-term storage, while seven only

had medium-term storage. Four of the institutions had to store seed at ambient temperature because they had no access to reliable cold storage. According to the FAO (2014), seeds stored at ambient temperature maintain viability for 8 years or so, but the temperature needs to be kept as cool and stable as possible. If not, then seeds stored at ambient temperature will require frequent regeneration to maintain their viability.

The efficiency and security of routine conservation operations depends on trained staff with adequate facilities, equipment, key consumables like packaging, and adequate procedures and processes. The institutes surveyed classified the types of storage facilities used for long-, medium-, and short-term conservation (Figure 4.1). Cold storage units were used for both long-term and medium-term conservation, but individual freezers were more frequently used for long-term conservation. The FAO (2014) indicates that storage conditions need to be more stringent for the most original samples and safety duplicates. The warmer temperatures used for medium-term storage are appropriate for samples that will be distributed, multiplied, and characterized. A small number of institutions reported the use of air conditioning to maintain a stable temperature in the storage room, and sometimes a dehumidifier to control the moisture content. Unfortunately, a small number of institutes stored seed at ambient temperatures. These lower-standard storage units would not be considered secure for long-term storage but could be adequate for some purposes.

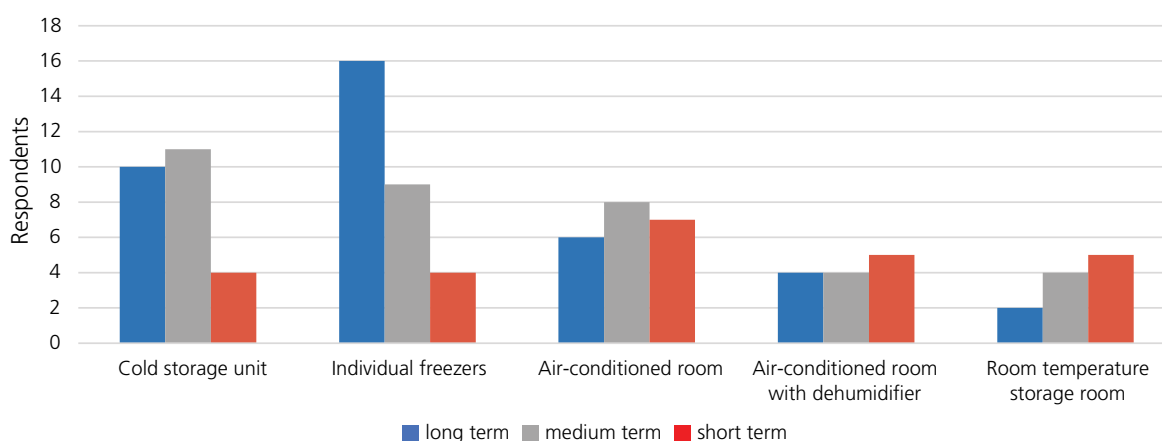


Figure 4.1 Types of storage used for sorghum seed conservation (n=28 respondents).

According to the survey, most of the respondents used sealed aluminum packs with or without vacuum packing for long-term conservation (Figure 4.2). The FAO (2014) international standards for genebanks indicate that airtight packaging is necessary for long-term conservation to minimize losses in seed viability. Non-airtight packaging should only be used for medium-term conservation, where the seeds are accessed for distribution fairly frequently. The use of aluminum packs indicate that the seeds are being appropriately stored if the packs are of sufficient thickness and strength (multiple-layer material). A smaller number of institutes also reported the use of aluminum cans, plastic containers, and glass containers to store seeds. For short-term seed storage, the genebanks mainly used cloth bags and paper envelopes or bags. Thus, many of the collection holders are not storing seed securely for the longer term.

The FAO (2014) genebank standards suggest that monitoring devices should be used to track temperature and relative humidity over time inside the storage unit, with an external readout so that the unit can remain closed. The results then need to be reviewed regularly to identify any issues, such as excessive fluctuations. All the genebanks surveyed had monitoring of the seed storage units, although six achieved this *via* daily visits by staff. Three genebanks monitored internal temperature but did not review these

data daily. While 18 of the genebanks had internal monitors in freezer or cold storage units, fewer had external monitoring of the temperature, especially for the long-term storage units (Figure 4.3). Fewer of the respondents monitored relative humidity than monitored temperature.

The FAO (2014) reported that, compared with no refrigerated storage, refrigerated storage with fluctuating temperatures and relative humidity is more detrimental to seed viability in the long term. Thus, it recommends a back-up power supply to ensure a constant temperature and relative humidity. Fifteen of the genebanks reported that they had back-up generators to secure seed storage units, while 13 had no such back-up. For many of these respondents, the back-up generator was at least adequate but there were constraints, such as the lack of funds for maintenance, repair, and replacement, and the lack of an automatic on/off system.

The international genebank standards highlight the need for adequate security to monitor and protect the collection. The main approach reported by respondents was daily visits by genebank or security staff. These visits were adequate if they were frequent, and logs were kept. There also need to be adequate protocols to ensure rapid rectification of any issues encountered. This was not explored in the survey, however.

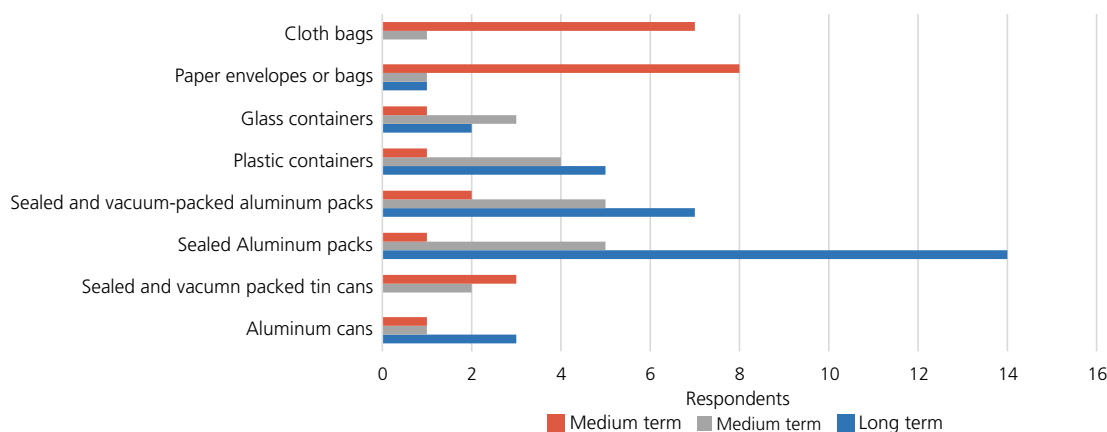


Figure 4.2 Number of genebanks storing seed in different type of containers for long-, medium-, and short-term storage (n=28 respondents).

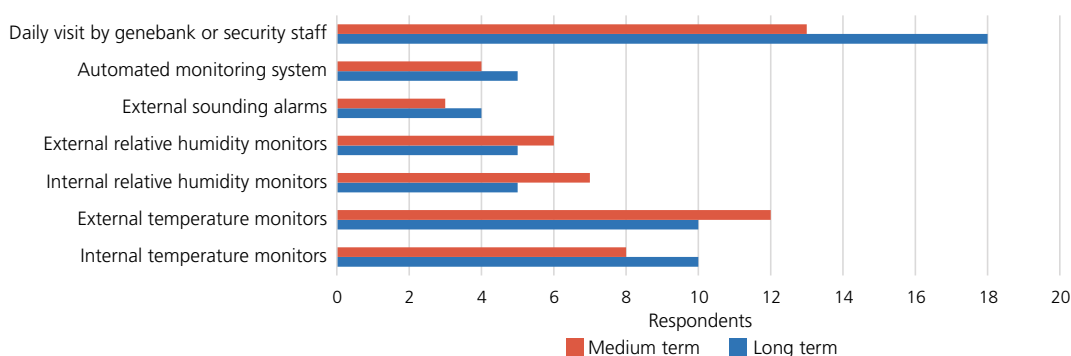


Figure 4.3 Number of genebanks using different approaches to monitor long- and medium-term seed storage units (n=28 respondents).

About one-fifth (21%) of the genebanks used an automated system for monitoring security, temperature, and relative humidity, but that number should increase as the technology becomes more available and affordable.

Another risk for genebanks is the impact of inadequate infrastructure and equipment as well as the lack of appropriate facilities for routine operations. The 28 respondents were subdivided into those that maintained global collections (*n*=6) and those that had a national focus (*n*=22). Only one of the global genebanks rated their facilities and equipment as inadequate, while more than one-third of the national genebanks rated their equipment and facilities as inadequate (Table 4.1). For genebanks in both categories, the age of the facilities and equipment varied from 6 to 40 years, and some indicated there were ongoing efforts to renovate facilities and replace equipment. For those who had constraints, the main issues were a lack of adequate funds to upgrade or replace facilities and equipment, unpredictable electricity supply and/or inadequate space in the genebank and essential laboratories.

In the future, genebanks will increasingly need to consider the carbon footprint associated with the power used to conserve their collections securely. The shift to alternative energy sources, such as solar, could

reduce the carbon footprint, as could investment into more energy efficient equipment for new or replacement purchases. Three of the respondents had already shifted to solar power for the genebank or a specific facility in the genebank. More than half of the institutions indicated that energy efficiency was a criterion when sourcing equipment.

The genebanks were also asked about access to specific types of facilities, equipment or field space to allow them to meet international standards for routine operations and secure conservation (Figure 4.4). In general, a high proportion of the global genebanks had adequate access to facilities, staff and equipment. Given the importance of proper drying for long-term conservation of sorghum seeds, it is worrying that only half of the national institutions had a low-temperature seed dryer. Appropriate work areas for the different seed handling operations is also important for seed quality, but this was reported to be lacking in 30% of the institutions, both national and global. While access to laboratories and facilities for seed viability testing was 75%–100% for both groups, a much smaller percentage had access to facilities and staff for seed health testing. These responses indicate that many of the national genebanks lack the space, facilities, and equipment to meet international standards for conserving orthodox seeds.

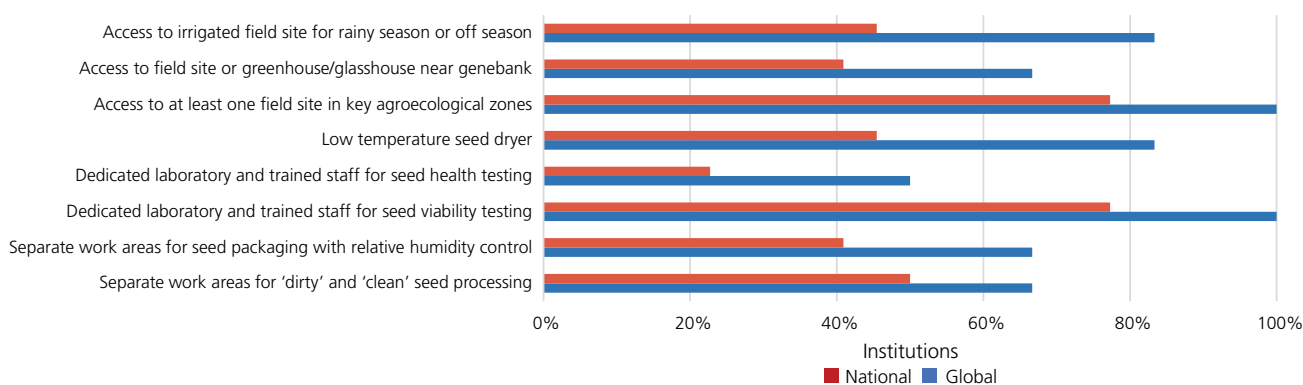


Figure 4.4 Proportion of institutions with global and national collections with specific facilities, equipment or access to space (*n*=28 respondents).

Table 4.1 Number of respondents that rated their facilities and equipment as excellent, adequate, or inadequate.

	Genebank buildings and facilities	Storage facilities	Laboratory facilities	Laboratory equipment	Field equipment	Generator
Global						
Excellent	4	2	2	2	3	3
Adequate	1	3	2	3	1	2
Inadequate	1	1	1	1	1	1
National						
Excellent	2	2	2	2	2	1
Adequate	10	10	10	9	7	6
Inadequate	8	8	7	7	7	8

Secure and successful regeneration requires access to appropriate sites and facilities. While all of the global genebanks had access to appropriate sites for regeneration, about 60%–80% did not have access to facilities such as greenhouses, glasshouses, or polytunnels that could be used to regenerate accessions with very low seed viability, with few stored seeds, or with seeds or plants that were difficult to grow. A high proportion of the national institutions had inadequate access to sites for seed regeneration.

4.2 Routine conservation operations

The survey asked about the number of accessions being conserved long-term or medium-term at the genebanks. Specific questions asked about the number of seeds tested for health and viability, the quantity of seeds stored, as well as the number of accessions that have been regenerated, multiplied, and characterized for minimal traits. Overall, about 80% of accessions were under long-term conservation and 63% under medium-term conservation. Across all the genebanks, 62% of accessions have been tested for baseline seed viability, 10% have had a baseline seed health test, 67% have been quantified (seed number), 57% have been regenerated, 28% have been multiplied to increase the seed number, and 77% have been characterized for a minimum set of traits.

The survey also asked about the status of routine operations separately for the different types of accession: landraces or farmers' varieties, research materials (old cultivars, released varieties and research lines, populations or genetic stocks) and wild relatives. The proportion of accessions in each of these categories that has been subjected to each operation is shown in Figure 4.5. For all operations except multiplication, accessions in the research category accounted for the highest proportion. This could be an indication of the greater distribution and use of this germplasm type. About 70% of the landraces were under long- and

medium-term conservation, but only 40%–50% of them had been regenerated, multiplied or had seed viability tested. A high proportion of wild relative accessions were under long-term storage, and just over 40% of them had been subjected to baseline seed viability testing. Less than 20% of wild accessions had been regenerated or multiplied because of the difficulties in growing these materials in the field or greenhouse.

The genebanks were asked about the written procedures and protocols used in their routine operations. Only five of the respondents indicated they had no written protocol. Seventeen of the institutes indicated they use the procedures given in Rao et al. (2006), while 10 genebanks used the earlier manual by Hanson (1985). About one-quarter of the respondents had their own genebank operations manual and/or written standard operating procedures for key processes. Five of the institutes used a quality management system (QMS) or referred to the FAO (2014) international genebank standards.

Finally, the survey asked if the genebanks were undertaking research on conservation or if they had the expertise to undertake conservation research in the future. The question identified four possible areas for conservation research: improvements to protocols; increasing the efficiency of operations; increasing the security of conservation; and addressing crop-specific constraints for conservation such as seed dormancy, seed health and seed longevity. The results are shown in Figure 4.6. Eleven institutions were not engaged in research, or considered research as a future activity. Only eight to 10 institutions were undertaking research in at least one of the areas identified. However, there were more institutions that considered these areas of research as important in the future, especially to address specific constraints in their collection such as seed dormancy.

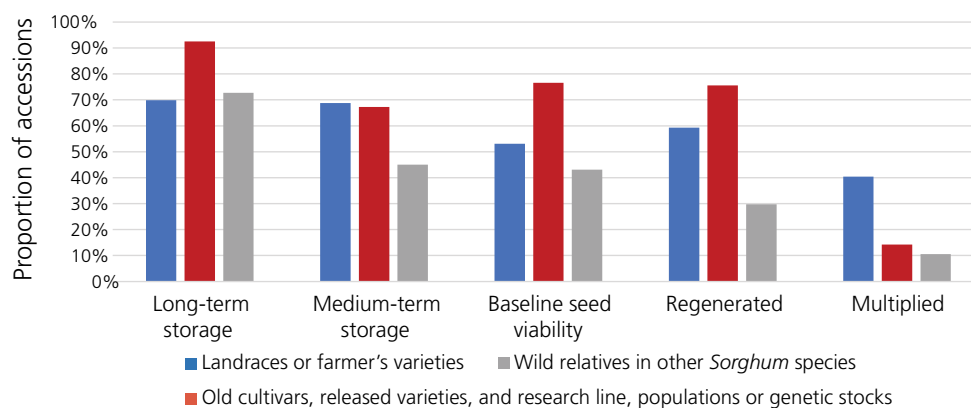


Figure 4.5 Proportions (%) of different germplasm types under long-term and medium-term conservation, tested for seed viability, regenerated and multiplied.

4.3 Safety duplication

The international standards for safety duplication (FAO 2014) specify that accessions that are original in a collection should be safety-duplicated at a site that is geographically distant under conditions that are equal to, or better than, those at the original genebank. Geographically distant is usually understood to mean another country. The safety duplication should be done in a way that maintains the integrity of the original sample. When possible, this is best done through a black-box arrangement where the accessions are only conserved by the host institution and the monitoring and replacement of low-viability seeds is done by the original institution. It is generally not seen as secure practice to have the accessions regenerated and managed actively by the host institution unless the risk to genetic integrity is managed and monitored. The survey asked the genebanks to indicate the proportion of their accessions that were safety duplicated at distant sites. The options were: The Svalbard Global Seed Vault; an institution outside the country in a black-box arrangement; an institution outside the country but with dynamic management by the host institution; in the same country at another institution, and/or in the same country but at another site within the same institution. The respondents could indicate more than one option if they had multiple safety duplicate sites. Only four of the genebanks did not have their collection duplicated at any other site. Of the 10 institutes with their collection's safety duplicated at only one site, six were conserved outside the country. About one-third of the respondents had some portion of their collec-

tion duplicated outside the country or at Svalbard. For each of the safety duplicate sites, fewer institutions had more than 50% of their collections duplicated at that site, except for the site within the institute or within the country (Table 4.2). So while respondents did utilize safety duplication sites outside the country or Svalbard, only three had a significant portion of their accessions conserved there.

Secure safety duplication also requires formal agreements that clearly state the terms and conditions for monitoring, conservation and use. The survey identified several conditions that could be considered for safety duplication in a black-box arrangement or in more active conservation. The survey recipients were asked to report on the conditions for their duplications and to indicate whether it was a formal or informal arrangement. Nearly all the respondents had formal arrangements in place for long-term conservation of their duplicates (Figure 4.7). Less than half had other arrangements to monitor viability and replace samples if necessary. Most of these were specified in formal agreements. In total, only 15 genebanks had safety duplicates that could be actively used by the host institution, and these were mainly based on formal agreements. For two institutions with informal arrangements, their duplicates were conserved at another research site in the same country.

In 2007, eight of the 19 institutes had safety backups. However, the proportion of accessions backed-up, the number of sites used, and the terms and conditions for these safety back-ups were not specified. In this

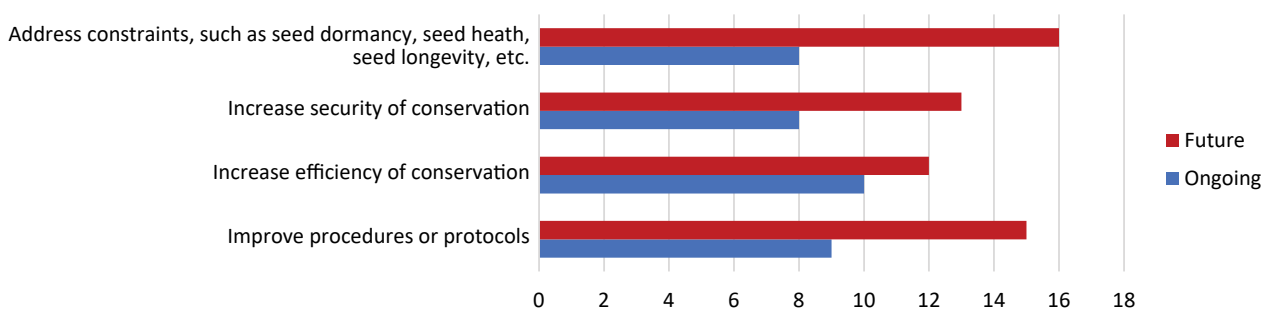


Figure 4.6 Number of genebanks undertaking or planning to undertake research in different areas of conservation.

Table 4.2 Number of genebanks with less than 50% or more than 50% of the accessions safety duplicated at other sites.

	Conserved at another research site in the country	Conserved in another collection in the country	Conserved at one site outside country	Conserved at least two sites outside the country	Conserved in Svalbard
Number of institutes with less than 50% of accessions conserved	4	4	11	5	12
Number of institutes with more than 50% of accessions conserved	7	4	5	2	1

update, there is an increased awareness of the need for safety duplication, but significant constraints remain. Twelve of the institutions said they had no constraints to safety duplication, but the others listed various constraints related to national policies, phytosanitary requirements, the costs of permits, packing and shipping, and seed multiplication and processing. This lack of adequate safety duplication for many of the accessions conserved around the world is a key vulnerability that still needs to be addressed.

4.4 Human and financial resources

Most of the genebanks reported that staff numbers and expertise were adequate for routine operations and meeting distribution requests. About one-third of the respondents reported inadequate staff training for information management. Several institutes indicated they had an inadequate number of skilled staff due to a lack of resources for positions, retirements and poor retention of staff. They planned to address gaps with training and recruitment. Retention of trained staff was an issue for only a few of the institutions, mainly due to poor remuneration, the remote location of the genebank, and/or the lack of opportunities for new staff.

Most of the institutions reported that they received funds from governments or international donors. One institute reported that its genebank was supported by breeding programs. Figure 4.8 shows the source of funds for each routine operation and for upgrades of facilities/equipment. About half of the institutions reported that annual budgets were the main source of funds for routine conservation activities, regeneration, multiplication and characterization. Six institutions reported that they had annual and project funds for collections and for the upgrade of facilities and equipment. Twelve institutions reported that no funds were allocated to conservation research, and eight reported that no funds were allocated to evaluation.

The dependence of genebanks on project funds for routine activities such as multiplication, characterization, evaluation, collection and upgrades is clearly problematic. One approach to address this situation is advocacy for higher annual budgets, and safety duplication to ensure the security of the collection. A global competitive fund to address urgent shortfalls in funds for routine operations and upgrades for collection holders of unique accessions could be considered.

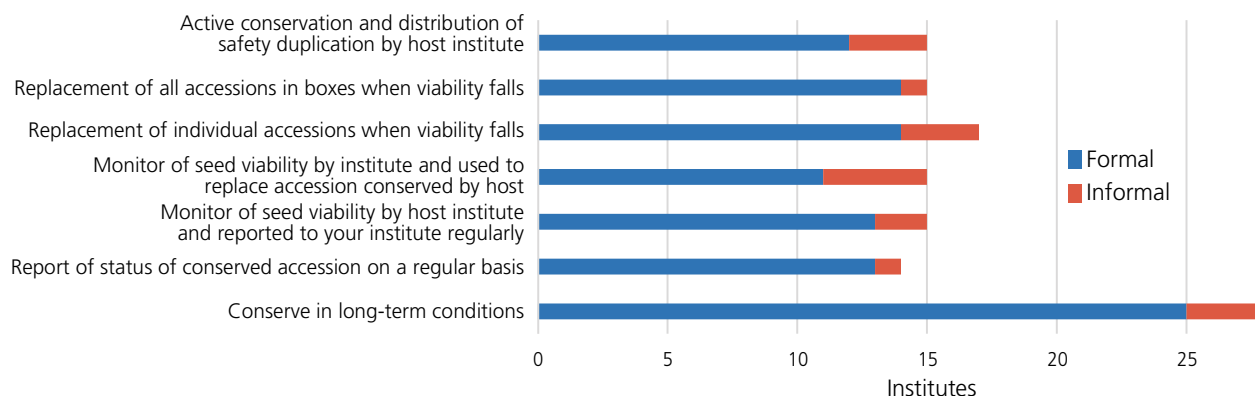


Figure 4.7 Number of institutions with formal or informal arrangements for safety duplication.

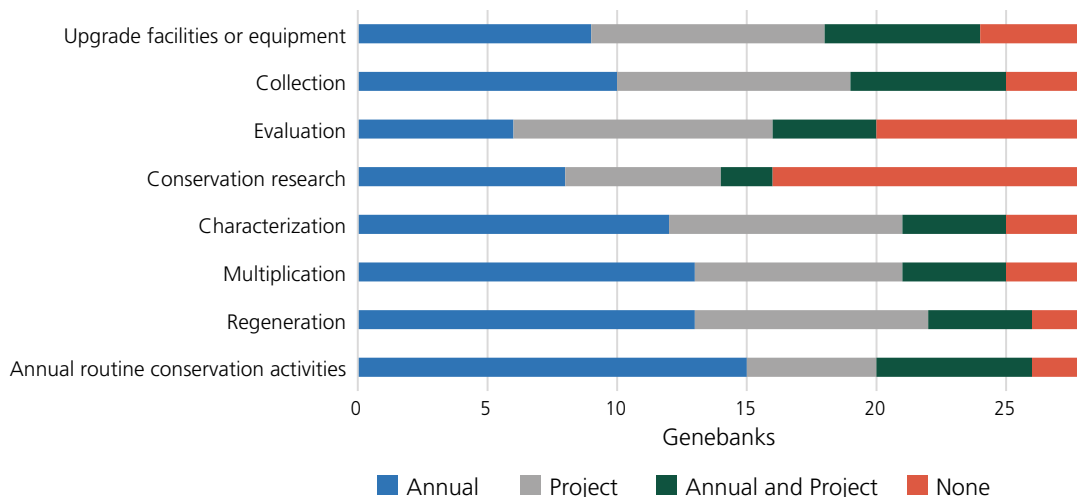


Figure 4.8 Number of genebanks that had annual budget allocations, project funds, both annual and project funds, or no funds for various activities.

4.5 Risk assessment

The identification of the risks faced by the collections, as well as developing a plan for mitigation that can be regularly monitored, is a key aspect of a quality management system and a recommendation of the FAO (2014) international genebank standards. Nine institutions have conducted a risk assessment. The primary risks described by the respondents were as follows:

- Fire, drought, storms, theft, vandalism, and natural calamities.
- Security threats to genebanks, fields, and staff.
- Construction of new roads and buildings in the area.
- Uncertain and irregular supply of electricity for low-temperature storage and no investment in alternatives such as solar power.
- Lack of secure and regular funding for long-term conservation and collection management activities.
- Uncertain and inadequate funds for staff and their training, equipment purchases, infrastructure construction, repairs and maintenance.
- Inadequate and insufficient infrastructure to support routine operations and seed storage.
- Inadequate representation of national diversity of landraces
- Mistakes and mix-up of seeds with handwritten labels
- Large regeneration backlogs and insufficient resources for regeneration/multiplication.
- Difficulty in regenerating photoperiod-sensitive accessions.
- High grain moisture content at harvest with loss of seed viability that require frequent regeneration.
- Disease and insect pests in the field during regeneration/multiplication and pests that damage seeds during storage
- A lack of pathologists and entomologists to identify and control pathogens and insect pests in the field and in stored seeds, and those transmitted by seeds
- Lack of seeds for distribution, inadequate facilities to store enough seeds for distribution, and inadequate packaging for storage and distribution.
- Unavailability of accessions to users
- Inadequate safety duplication.
- No back-up of genebank data
- No plans for staff succession

Some of these risks were also evident when the genebanks were asked to identify specific constraints to the conservation of their collections. Some of the key constraints identified were:

- Unknown redundancy with other collections.
- Insufficient funds, expertise, facilities, equipment and consumables for conservation, regeneration, characterization, distribution and documentation.
- Backlogs in regeneration and viability testing.
- Insufficient staffing.

- Accession identifiers not unique and changed over time.
- Lack of safety duplication, no seed health monitoring.
- No capacity for genotyping.

All of these issues are sources of vulnerability for the long-term conservation and use of sorghum genetic resources and need to be addressed, including through global collaboration.

4.6 Summary of the status of conservation

In 2007, nine of the 19 institutions were conserving materials long term, so storage was seen as a significant issue. Most respondents identified significant regeneration backlogs and recommended this be addressed urgently through global action. In fact, a project managed by the Crop Trust undertook to regenerate and safety back-up the most critical collections (Halewood et al. 2020). This effort resulted in securing some key collections and could account for the reduction in the backlogs in the current assessment. However, regeneration is still an issue for many of the collections in 2021, because globally only about 50% of accessions have been regenerated. The problem is especially severe for wild relatives. The availability of regeneration guidelines for sorghum (Upadhyaya et al. 2008) is an important fulfillment of a recommendation from the 2007 strategy as well. In the latest survey, 18 of the genebanks reported using these guidelines.

In general, there has been an improvement in the conservation status for many of the 38 institutions in the survey, which conserve 80% of sorghum accessions. The global collections have smaller backlogs in routine operations than the national collections, some of which have inadequate facilities and equipment. The current global system is not secure, efficient or rational, with many inadequacies and vulnerabilities in key routine operations and facilities for some collection holders. These inadequacies relate to knowledge of the viability and health of the conserved seed and a lack of effective information management. Globally, there is a backlog in the regeneration of accessions and in the multiplication of seed for distribution. Various collection holders in the survey had issues with their facilities and equipment. There are also inadequacies in ensuring the use of the best and most efficient procedures and protocols through standard operating procedures, quality management systems and conservation research. There is a need to consider the role of the global system to address these backlogs and upgrade facilities and equipment at national collections that conserve unique local diversity.



5 STATUS OF *EX SITU* COLLECTIONS – DOCUMENTATION

The 2007 strategy reported that passport and characterization data were recorded and stored electronically at a reasonable but variable rate. However, it did not include any of the specific information from the survey to demonstrate the issues. To address this issue, the 2021 survey asked the genebanks to indicate the number of sorghum accessions with passport and characterization data in a searchable database. The FAO (2014) international genebank standards for documentation suggest that “passport data of 100% of the accessions should be documented using FAO/Bioversity multi-crop passport descriptors.” However, the 2007 questionnaire did not address the issue of the use of FAO/Bioversity passport descriptors. The 2007 strategy concluded that genebanks should use a standard taxonomy and nomenclature and consider the utility of characterization data. It also concluded that the availability of data online and its sharing needed to be addressed. The strategy suggested key actions for the future related to a global sorghum information system. The actions included the identification of duplicates and gaps in collections using passport information, using a minimum set of descriptors, and a strengthened global database. Some of these issues have been addressed through global actions, such as improved taxonomy and nomenclature (Dahlberg, 2000) and the identification of minimum descriptors for characterization derived from IBPGR and ICRISAT (1993) (Alercia, 2011). The survey respondents were asked about their use of these publications as guide-

lines for their documentation. More than 80% used the IBPGR and ICRISAT (1993) descriptors but only 25% used the minimum descriptors reported in Alercia (2011). Only four institutions used Dahlberg (2000) as guidance for improved race classification.

As in 2007, the 2021 survey asked about the types of data held for accessions and how it was made available to users. More than 85% of the genebanks surveyed reported that passport and characterization data were available for accessions. One-quarter of the respondents noted that images of accessions were available. Seven of the respondents noted that accession-level information from evaluation or genotyping was available to users. Across the institutions, 95% of accessions had passport data and 85% were in a searchable database. Over all respondents, 77% of accessions had been characterized for minimal traits, and 69% of accessions had characterization data in a searchable database. While the documentation of passport and characterization data has improved, most of the institutes made data available internally (82%), mainly in a catalog or through the curator (75%), but did not make the data available externally. Less than 40% of the genebanks shared data online within the institute or more widely. While this is probably an improvement over 2007, it is still an issue when compared with global platforms such as Genesys that share accession-level information, and genebank information systems such GRIN-Global that facilitate

information management and sharing online.

Overall, a high proportion of accessions are listed in a searchable database with their passport and characterization data, but further improvements are required. Only three institutions had passport data for less than 75% of their accessions. Fourteen institutions reported that less than 25% of their accessions had passport data available in a searchable database (Figure 5.1). Fourteen institutions had characterization data for a minimum set of traits for less than 25% of their accessions, and eight of them had no documentation of characterization data. Twenty-five institutions had entered characterization data into a searchable database for less than 25% of their accessions, and 21 of them had no characterization database. In the ICRISAT and USDA-ARS collections, more than 97% of their accessions have documentation for passport and characterization data that can be shared online through Genesys. This should be the target for all other sorghum collections around the world.

The survey also requested information on the status of evaluation of accessions in the collection. Seventeen institutions responded that accessions had been at least partially evaluated phenotypically or genotypically. Nine to 10 of the genebanks had evaluated at least some accessions (Figure 5.2). Only two institutions had evaluated most accessions for tolerance to biotic and abiotic stresses. Only one collection had been (nearly) fully genotyped. Core collections and trait-specific subsets had been designated and evaluated at less than 25% of the institutions that

responded to the question. The lack of evaluation of collections and data sharing were identified as constraints for use in the 2007 strategy. At that time, there was a recommendation to make more use of cores and trait-specific subsets. The current situation seems to be an improvement, especially for genotyping, but less than 50% of the institutions answered this question in the 2021 survey. Some institutions have evaluated accessions for their resistance to biotic stresses (downy mildew, grain mold, anthracnose, leaf blight, rust, elongated smut, gray spot and oval spot, stem borer, shoot fly, aphids, fall armyworm, head bug, midge, striga) and abiotic stresses (water shortage and low phosphorus). Some of the respondents have shared characterization data with users. One institution indicated they did not store evaluation data generated by others, but instead linked to the source when it was available. The 2007 strategy identified the development of a collaborative evaluation program as a global priority, but this has not been implemented. Thus, there is still room for improvement for sorghum evaluation, and for the sharing of data with users.

Hay and Sershen (2021) illustrated the critical data collection points in the flow of routine activities in a genebank that ensure secure, efficient operations. They concluded that a robust information system is needed to capture all the data and track accessions in the process. Unfortunately, investment into data management is not seen as a key priority by many genebanks when resources are limited. Weise et al. (2020) reviewed all the important information needs

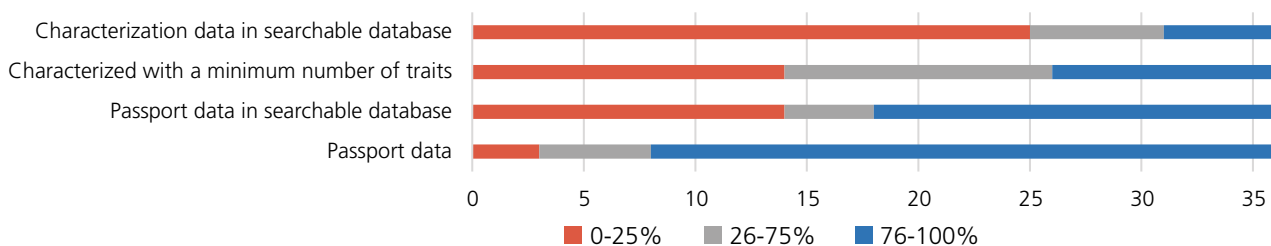


Figure 5.1 Number of institutions that have passport data and characterization data for accessions available (or not available) in a searchable database.

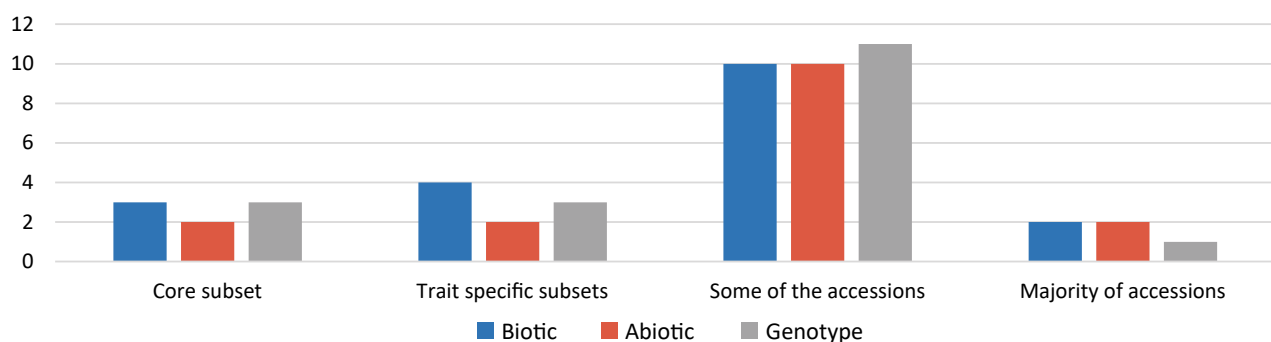


Figure 5.2 Number of institutions that have genotyped and evaluated core collections, trait-specific subsets, some of the accessions and the majority of accessions.

for a genebank. This included an assessment of the current options for an electronic information system, such as GRIN-Global, Genebank Information System (GBIS), MS Excel, and paper documentation. They concluded that the biggest challenges for the future will revolve around the collection, storage, and sharing of phenomics and genomics data. Both Hay and Sershen (2021) and Weise et al. (2020) also concluded that the adoption of currently available genebank information systems should facilitate capturing data, sharing it with users and increasing access to germplasm.

The FAO (2014) also recommended that “all data and information generated in the genebank relating to all aspects of conservation and use of the material should be recorded in a suitably designed database.” Six of the respondents had adopted or planned to adopt GRIN-Global, while one institute was using ŞEŞTO; six were using the SADC Plant Genetic Resources Center Documentation & Information System (SPGRC-SDIS); and three were using systems they developed themselves. There has been increasing adoption and use of dedicated genebank information management systems, as many institutes felt that their current system was inadequate for their information needs.

The survey asked how data are collected and stored in a genebank information management system (GBMS). For some routine operations, such as inventory, seed viability test results, characterization and 100-/1000-seed weight as an indicator of seed number, less than 20% of the respondents still used only paper documentation (Figure 5.3). For some operations, like seed health assessments, packet weight and multiplication history, about 40% of genebanks used only paper documentation. For nearly all operations, a significant proportion of the institutions initially recorded data on paper and then entered them into the database. This approach can result in a delay in data availability, and can also introduce errors when transcribing a handwritten entry into the database. This is an issue for many genebanks.

Adopting a dedicated genebank information system is a very important step towards increasing the security and efficiency of conservation through better monitoring and reporting. To optimize such a system, the processes and procedures used in the genebank must be carefully considered. A barcoding system will reduce the risk of mislabeling and better protect the genetic integrity of accessions. The use of electronic tablets for data capture directly into a database will facilitate some key tasks. In the survey, 16 institutes indicated that they used both barcoding and electronic tablets.

This effort to adopt a dedicated information system by sorghum genebanks needs to continue and be supported, because it will lead to more opportunities to share accession-level information, both through global platforms such as Genesys and on each institute’s own website. National genebanks and other institutions seeking to upgrade their information systems can refer to those used at the global collections for guidance. As suggested by Weise et al. (2020), Sorghum genebanks should also adopt a unique identifier, such as a digital object identifier, to allow duplicates to be identified and to track use and impact. It is also important to document the origin of accessions to support access and benefit-sharing policy implementation, as reviewed by Brink and van Hintum (2020).

The adoption of a fully integrated GBMS that links to global sharing platforms such as Genesys should also increase the security of these databases. The survey did not ask about the security of genebank databases, but this is an important issue that needs to be considered. Genebank databases should be backed-up frequently. One option for passport and characterization data is to upload them to Genesys under a data-sharing agreement. Such practices need to be considered more widely to allow for greater user access to accession-level information. Globally, users still need better access to key sorghum accession information to increase the use of materials.

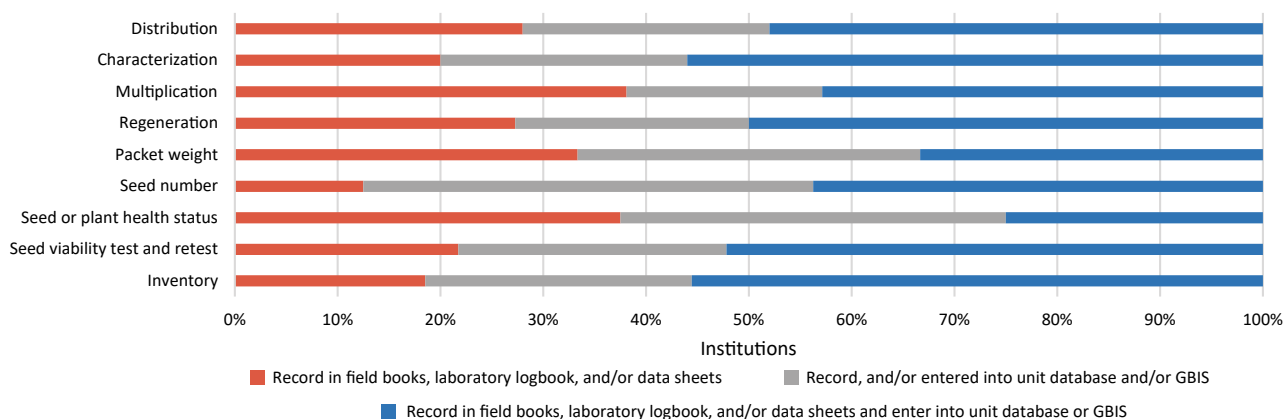


Figure 5.3 Proportions of institutions recording data generated from operations in different ways.

6 STATUS OF *EX SITU* COLLECTIONS – USE

The survey asked about the distribution of accessions to various end users. All but two of the respondents distributed to users within their institute and nationally. About 60% of the respondents distributed materials internationally under a standard materials transfer agreement (SMTA) or a government- or institutionally-mandated materials transfer agreement (MTA) (Figure 6.1). The largest proportion of institutions distributed landraces collected from the same country nationally and within the institute. The results of the survey suggested that there are still difficulties in distributing accessions to users outside the country. Sorghum is listed in Annex I of the ITPGRFA, so the use of a SMTA is common across institutions that distribute the crop internationally.

The distribution of accessions requires an adequate procedure to be in place and to be followed. The genebanks were asked if they had adequate procedures and supplies to distribute materials following both technical and policy guidelines. Of the 28 respondents, 25 reported that they had adequate processes in place to manage the SMTA and/or MTA. The main issue for two of the institutes was the lack of national legislation to facilitate this process. Eighteen of the

respondents indicated they had adequate processes to obtain phytosanitary certificates. For those that could not obtain such certificates, the main obstacles were cost and administrative challenges. The packaging and shipping of seed was an issue for 10 of the respondents, mainly because of the difficulty and cost of obtaining appropriate packaging material locally. These are major constraints for international distribution.

The survey gathered information on the frequency of distribution to seven user types in the last 5 years. The most frequent distribution was to users within the country, such as academic researchers and students, farmers and farmers' organizations, and plant breeders in the public sector (Figure 6.2). Many respondents had not distributed any sorghum materials to users outside the country or to the private sector within the country. There is likely low investment in sorghum breeding in these countries, and this might account for the lack of requests. However, it could also be indicative of restricted distribution to the private sector for commercial use. The lack of accession-level information could also account for the low frequency of users outside the country. For

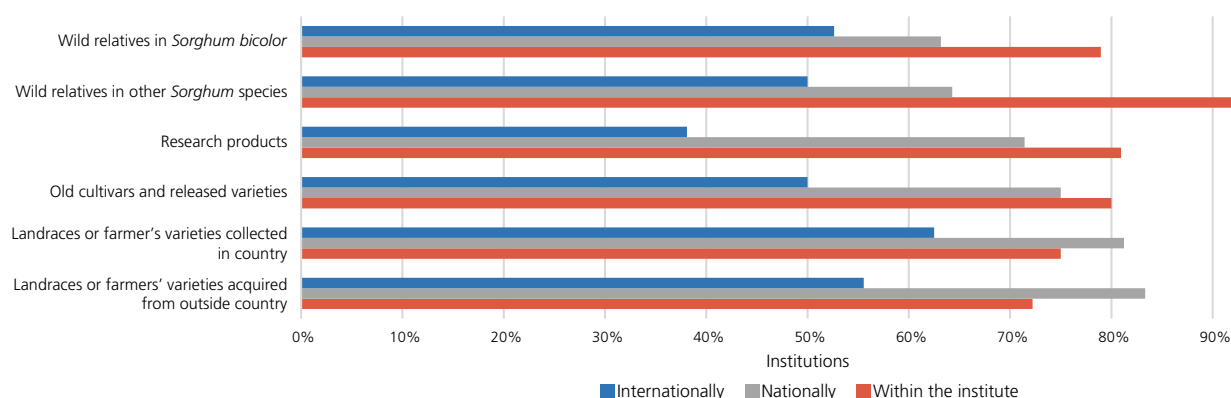


Figure 6.1 Number of institutions that distribute various types of accessions internationally, nationally or within the institute.

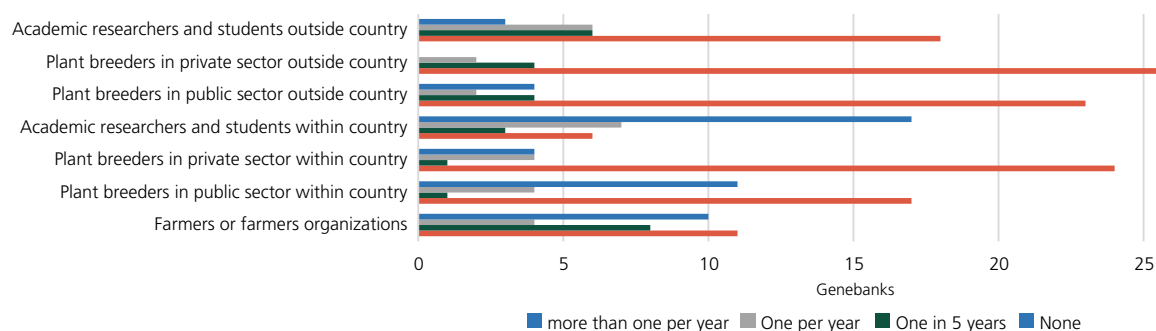


Figure 6.2 Frequency of distribution of sorghum materials to different users in the last 5 years.

many of the respondents, the distribution of accessions at least once per year within the country is an improvement over the 2007 survey. The fact that many institutions are distributing accessions directly to farmers or farmers' groups may be indicative of an increasing need for sorghum diversity to adapt to climate change.

Finally, the survey collated feedback provided to genebanks by users about the accessions they received. All institutions asked for feedback from recipients, but only nine used a formal process. The most frequent feedback requested was on the quality of the samples dispatched, the usefulness of the accession received, sharing of reports or publications, and sharing of characterization or evaluation data sets (Table 6.1). A few of the respondents solicited feedback on the quality of the packaging used. Those that used a formal process mainly used a survey sent after distribution. One institution reported that:

“Feedback was used to improve the quality of seed, information on accessions, and efficiency of operations as well as to track use of accessions sent. It allowed for the opportunity to incorporate additional characterization or evaluation data that was shared. It was used to be able to report or communicate on use of the accessions distributed or the value of collections. The collation of research publications was used to enhance future research by sharing research results derived from the germplasm distributed.”

This general view was shared by a number of other institutions.

Generally, the distribution of sorghum genetic resources was focused within the institution or nationally. International distribution was a challenge because of constraints imposed by policies, costs and complex administrative procedures. The main users of sorghum collections were nationally based researchers and breeders, as well as farmers. The lack of private-sector breeding programs has limited the commercial use of these collections. Soliciting feed-

back from recipients should be formalized to improve quality of seed and services, to better understand user interest, and to communicate the value of the collections.

6.1 Links between *ex situ* collections and users

Strong links among *ex situ* collection holders and to their various end users are critical to secure long-term conservation and ensure effective use. The survey explored the degree and diversity of these interactions by considering the types of activities and the types of partnerships the collection holders have established for conservation and use. As summarized in Table 6.2, the most frequent partnership was with other national collection holders (20 out of 24 responses) and regional/international collection holders (15 out of 24 responses). The least frequent partnership was with protected sites for wild species (four institutes). The main collaborative activities were research and training; but there were specific activities and partners, such as seed multiplication with regional/international collection holders, where all 14 respondents had experience. More than half of the institutions had col-

Table 6.1 Number of respondents that solicited feedback on different aspects of their service to users.

Specific areas for feedback from users	Number of respondents
Timeliness of the distribution	10
Helpfulness of information or advice from genebank staff in selection of accessions	10
Quality of samples sent	11
Quality of packaging used	6
Quality and the usefulness of the accession-level information received	9
Usefulness of the accession received	17
Sharing of report or publication on any specific research result from the evaluation or use of the accession received	19
Sharing of evaluation or characterization data sets	15
Variety releases, adoption studies or case studies from the use of an accession received	9

Table 6.2 Number of institutions collaborating with various other stakeholders internationally, nationally or locally for different activities.

	Collecting	Repatriation	Research	Training	Seed multiplication	Total number of institutions
Regional or international <i>ex situ</i> collection holders	7	7	8	12	14	15
National <i>ex situ</i> collection holders	7	4	8	8	5	20
Community seed banks	5	2	4	7	3	7
<i>In situ</i> conservation sites	2	2	1	4	3	7
On-farm conservation sites	5	2	3	5	3	10
Protected sites for wild relatives			2	2	1	4

lected materials in collaboration with other national collection holders, community seed banks and on-farm conservation sites. Two institutions had conducted safety duplication for national collection holders.

Ten of the respondents indicated that they had received additional support to participate in these collaborative activities given in Table 6.2. When asked if these activities were increasing or decreasing, 16 respondents indicated they were increasing for some or all the various types of partners. These results indicate that there is a significant degree of interaction among stakeholders in the current global system, with a focus on national- or local-level partnerships to collect, conserve and enhance the use of sorghum genetic resources. For the future, the level of interaction with more locally focused stakeholders needs to be strengthened, as sorghum landraces are still mainly conserved on-farm by local farmers in many areas of Africa and Asia. Few genebanks have links with *in situ* protected sites and this is a missed opportunity and a risk for wild relatives under threat.

The survey also explored the links and level of activities between collection holders and various types of users. Twenty-eight institutions reported on their partnerships with various users (Table 6.3). The most frequent partnership was with local users (23/28) and national researchers and breeders (24/28). Local users included farmers, farmers' organizations, NGOs, and extension services. The least frequent partnership was with the private sector. Again, that could be an indication of the low level of investment into the private seed sector for sorghum. Regarding local users, the most frequent joint activities were demonstration and training. For research users such as national and international researcher/breeders, academic researchers and private sector breeders, the most frequent joint activity was research. Several genebanks reported joint activities involving field testing, promotion and training with various partners. The survey results

demonstrated a significant level of engagement with users at all levels in the current global system. These partnerships and experiences can be built upon for the future.

Overall, direct engagement of the collection holders with local users is very encouraging for sorghum conservation. Sorghum landraces are still mainly grown by local farmers for their own or local consumption. Thus, a collection holder's engagement with local farmers, directly or indirectly, increases opportunities to share the conserved accessions as well as to collect and conserve more of the germplasm held by these farmers. This secures genetic resources that are under threat from genetic erosion or loss in the field, and also contributes to adaptation to climate change, rural development and food security.

While there is active engagement among *ex situ* collection holders, the research community, and local farmers or communities, there are few networks or collaborative initiatives that engage the respondents globally. ICRISAT, as a CGIAR center with an international collection, has taken the lead in actively engaging with partners for the crops they conserve and the Institut de Recherche pour le Développement (IRD, France) continues to engage with mainly West African countries. The SPGRC involves all sorghum national collections in SADC countries. For European collection holders, there is the European Cooperative Programme for Plant Genetic Resources (ECPGR). Unfortunately, there are few international platforms for collaborations on sorghum genetic resources, except for a few specific sequencing and genotyping efforts that have involved global coalitions. This was recognized as a constraint in the 2007 strategy. The suggested action included enhanced global sharing of accession-level information and strengthening the links between genebanks and researchers/breeders for evaluation and pre-breeding. However, there has been limited progress for this action.

Table 6.3 Number of genebanks engaging with different types of users for various activities.

	Local users	National researchers and breeders	International researchers and breeders	University faculty and students	Private seed companies
Repatriation	4	5	4		
Seed multiplication	9	14	4	3	2
Participatory evaluation	8	12	4	2	4
Demonstrations	13	13	3	4	5
Field days	8	11	4	5	4
Research	6	22	9	18	6
Training	11	11	5	8	1
Seed fairs	1	1			1
Collection		3	1	2	
Total number of genebanks	23	24	12	19	8



Sorghum fructu rubro.

Sorgo fructu albo.



7 STATUS OF *EX SITU* COLLECTIONS – CONSTRAINTS AND VULNERABILITIES

The institutes were also asked to identify the key constraints for the use of their collections. There were 36 responses to these questions, and most of them had been suggested as areas for improvement in the 2007 strategy. Collectively, the constraints they described were as follows:

- Sorghum is not a national priority so there is a lack of resources for research and development that limited the use of the collections.
- Sorghum is not a priority for commercialization through new uses so low investment in the crop and in seed production limit use by the private sector.
- Lack of a clear strategy for conservation and use of the collection.
- Lack of human resources in terms of quantity and quality at national genebank levels.
- Lack of awareness of users of the genebank and the conserved accessions.
- Weak links among breeding programs nationally, regionally, and internationally limit information sharing on genetic resources.
- Insufficient accession-level information that could be useful to users and no sharing of information.
- Lack of sufficient and sustainable investment into integrating phenotyping and genomics to link traits and alleles to use, especially for the whole collection.
- Lack of funds for evaluation that need to be systematically assessed in the whole collection, including nutritional profiling.
- No funds for promotion of germplasm with multi-location demonstration plots and other activities.
- Lack of appropriate sites for regeneration of accession, especially those with photoperiod sensitivity and wild relatives.
- Insufficient quantity and quality of seed for distribution as well as the cost and administrative burden for distribution.
- Unclear, complex process for accessing germplasm.

Finally, the survey requested feedback from the genebanks on the overall status of their collection in relation to key issues for future conservation and

use. About 40% of the genebanks considered their status as deteriorating (Figure 7.1). For key issues for conservation (such as resources for long-term conservation, collection expansion, timely regeneration, safety duplication, accession-level information sharing and use), the conditions were at least stable. Encouragingly, many genebanks considered they had stable or improving engagement with users, and a collection that had adequate genetic diversity and accession-level information to meet the needs of users. There was an increased or stable level of requests for accessions and feedback from users. All these responses are very positive in terms of future conservation and use, but the deteriorating conservation status is still a concern and highlights the need for greater collaboration to secure these collections.

The genebanks were also asked to describe some specific contributions that their collections could make to the global system. Many of these related to the security of their conservation, the availability and accessibility of the accessions to users, the high level of local diversity conserved, the importance of their collection to local farmers and researchers, and the specific traits of accessions in their collections. Here are some of the verbatim responses:

- National collections with rich unexplored and highly underutilized germplasm offer an opportunity for exploration for key traits for drought, pest resistance and other desirable attributes. Some of that diversity is still being actively managed on-farm by farmers and the key traits have been observed from among the local landraces.
- Accessions have been used to restore lost varieties to farmers and breeding programs.
- Protection of landraces which have disappeared among local farmers (for example long-duration accessions).
- Accessions have been exchanged within the East African countries in one of the projects called the open-source seed system in which farmers were able to select preferred varieties for adoption into their farming systems.

- Nationally, ensure diversity of land races from different agro-ecological zones are conserved for the future that could be utilized by farmers or for crop improvement programs.
- The collection conserves a great variability of sorghum morphologically and physiologically, and certainly genetically that will enrich the global collection and its accessibility will be easier for various improvement programs around the world.
- Crop wild relatives collected and available via a SMTA.
- Regional collection from different SADC Member States with a breadth variety of diversity is securely conserved.
- Unique accessions of Australian indigenous crop wild relatives in the tertiary genepool. Many of these species are not represented in any other global collection. Active collecting program to collect and conserve gaps in Australian indigenous crop wild relative species.
- Many accessions from the country are accessible through other genebanks where they are also conserved, distributed, and often used in research.
- Secure conservation of diverse germplasm that is accessible for research purposes.
- Ease of use so accessions are available, core subsets identified, evaluated and used for breeding new varieties.
- Unique local landraces with traits such as scented sorghum, high-protein lines, drought-tolerant lines, shoot fly-resistant lines, resistant to leafy disease, early flowering and early maturing, high grain yielding, high biomass lines, high brix lines, striga- and midge-resistant lines, stay green, and salinity tolerant.
- Agro-morphological characterization activities have been implemented and data available for use of relevant accessions for further activities mainly by breeding programs.
- Facilitates the opportunity for safety duplication of sorghum accessions at Svalbard Vault and at other genebanks, like ICRISAT.

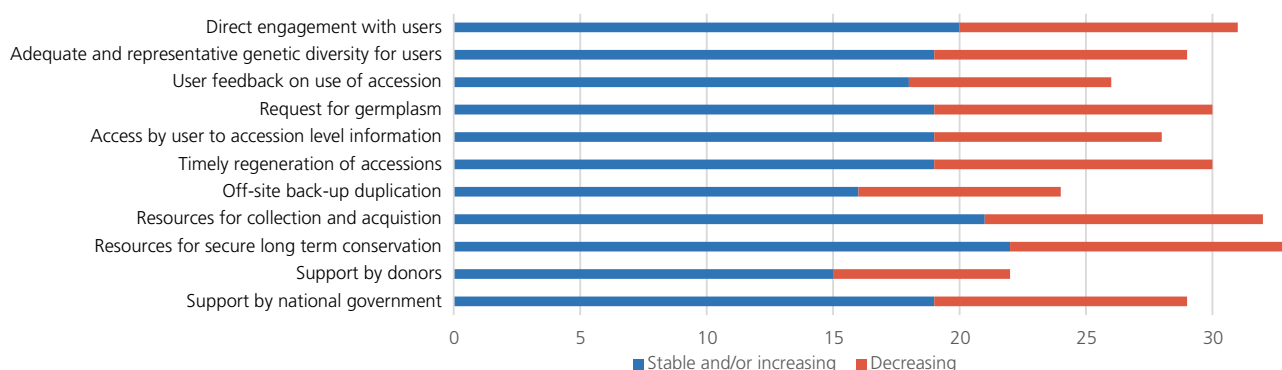


Figure 7.1 Number of intuitions that have a stable and/or improving status or a deteriorating status for various aspects of conservation and use (n=36 respondents).

Each institute was also asked to identify some key advantages of participating in a global conservation system. They described several benefits from global collaboration related to access to funds for upgrades of facilities, equipment, capacity, and routine operations. The respondents also highlighted the opportunities for safety duplication with other genebanks, greater sharing of accession-level information and increased access to diversity. In summary, some of the specific advantages identified by the respondents were:

- Information about the global status of sorghum collection, diversity, conservation strategy and recommendations will strengthen collection and use globally.
- Opportunities to identify and fill gaps in collections for landraces, wild relative, and improved varieties, and research material.
- Secure the conservation and enhance use of national collection of locally adapted landraces.
- Greater opportunities for collaborations and access to resources, training, and equipment to upgrade routine operations to ensure long term viability with reduced risk of genetic erosion for unique accessions.
- Opportunity for sharing services, facilities, and collective capacity building in collection management.
- Secure the conservation of the collection to reduce regenerations that risk loss of diversity.
- Providing sharing and management of information on sorghum collection through GRIN-Global and Genesys.
- Safety duplication in back-up sites with other genebanks and in Svalbard.

- Enhanced availability to the interested users both nationally and internationally with clear term and conditions for accessibility.
- Facilitate evaluation programs across sorghum growing countries to identify trait specific germplasm and make available.
- Exchange of genetic material and scientific techniques in breeding and phenotyping to enhance gain from breeding.
- Make use of collections to safeguard global food security and contribute to national and global crop breeding objectives.

One of the national genebanks noted the following advantage of a global system:

“Participating in a global conservation system will enable me to realize critical gaps and areas of improvement in long-term conservation of sorghum accessions for the benefit of current and future generations. It will shed more light on possible funding agencies to enhance genetic diversity of the sorghum collections. This will also increase global recognition, as it is currently not widely known, resulting in more requests of the conserved sorghum accessions, and subsequently more benefits to be realized.”

In summary, there was a broad consensus amongst the survey respondents that global collective actions would benefit their collection, and that their collection would make specific significant contributions to this global effort.



Sorghum breeding at KALRO Kibos, Kenya.
Photo: Michael Major/Crop Trust



Staff at the National Plant Genetic Resources Centre of the Zambia Agriculture Research Institute check sorghum growing in the field genebank. Photo: Neil Palmer for the Crop Trust

8 SORGHUM USER COMMUNITY CONSULTATION

Over the past 15 years, significant national and global investment has been made in generating genomic resources to advance sorghum breeding and conservation activities. In 2004, members of the worldwide sorghum community, including private sector and international scientists as well as community representatives from closely related crops (sugarcane and maize), met to coordinate and plan future advances in sorghum genomics and the sequencing of the sorghum genome (Kresovich et al. 2005). Key developments that made this workshop timely are discussed in Kresovich et al. (2005).

In 2009, the first assembled and annotated sorghum genome was completed (Paterson et al. 2009) and this major effort provided the foundation for an explosion in the development of valuable resources for sorghum genetics and breeding. For recent updates on the status of available sorghum genomic resources, see Boyles et al. (2019), Mace et al. (2019), and Hao et al. (2021). In addition to providing valuable insights, tools, technologies and methods for sorghum improvement, these resources have also proven useful to advance sorghum conservation and to link conservation and use. Recognizing this promising position

of sorghum genomics globally, in formulating the current sorghum conservation strategy, we also sought to obtain the views of other stakeholders (rather than just genebanks) as to how genomic resources are and could be used to improve conservation efforts and enhance the use of genebank collections.

An expert consultation on “Securing the Long-Term Conservation and Use of Sorghum Genetic Resources Globally” was held on 23 September 2021. The goal of the session was to bring together global experts (with insights in genomics, bioinformatics, conservation, gene and trait discovery, phenomics, breeding informatics and statistics and pre-breeding) to provide recommendations regarding conservation activities from a user perspective. This information was additional, and complementary, to that obtained from the curators of global sorghum collections. The half-day session was attended by about 25 researchers from around the world. The agenda of the meeting and attendees are listed in Annex IV of this report.

From a stakeholder’s viewpoint, the indicators of a “good” collection are as follows: (1) The holdings represent key genetic and phenotypic diversity of the

species and its wild and weedy relatives; (2) there is good characterization and evaluation of the materials; (3) information is available from the collection; and (4) high-quality seed and/or other propagules are easily available. With these standards in mind, the following are the key observations and recommendations that arose from the consultation.

- There is an explosion of genomic and phenotypic data, and data curation is a concern. Genebank curators need to be aware of such scientific advances and need access to the data. However, there was consensus among participants that information curation would be best done by those generating the data.
- Genebank curators need to establish close ties with appropriate global genotyping and phenotyping networks. When feasible, genebanks should integrate key, proven technologies to improve characterization and evaluation of holdings.
- While molecular techniques may play a useful role in characterizing diversity, many technologies lack the ability to identify novel variation among accessions. However, future advances in DNA sequencing will improve discovery capabilities.
- There needs to be improvement in interoperability among databases that store genetic and phenotypic data and genebank information systems. Some efforts are underway to link publications (*via* their DOI) with the germplasm resources they refer to.
- While there is clearly some need to address redundancies among collections, the long-term cost of maintaining those holdings is low compared with the cost of addressing the problem.
- Gap analysis and more coordinated strategies for assessing diversity across all genebanks are necessary to enhance the conservation and use of diversity.
- Additional funding will be critical to link genebanks and their users for advances in breeding and genetics. For example, a “win-win” opportunity could be created by providing support to genebanks for pre-breeding activities that integrate useful genetic and phenotypic variation into more agronomically relevant backgrounds for ready use by stakeholders.
- Major genebanks should proactively engage with public breeding programs at universities and the National Agricultural Research System (NARS) to ensure that key breeding lines and varieties are conserved securely in national and/or international genebanks. This would support better understanding of germplasm and traits by facilitating collaborations that bridge landrace diversity and breeding materials.
- Crop-specific curators, with improved training in genetics and breeding, will be required as collections develop in size and complexity. For example, many collections now accept genetic stocks and extensive genetic resources (e.g., nested association mapping populations) in addition to classical landrace accessions. Therefore, effective, tailored genetic management of holdings is essential.
- New tools, such as gene editing, might enhance and expedite the use of germplasm diversity if genebank collections are more aggressively used for allele mining.



Photo: Kansas State University Research and Extension

9 A GLOBAL STRATEGY FOR THE *EX SITU* CONSERVATION OF SORGHUM CROP GENETIC RESOURCES

Sorghum is an important cereal crop for trade internationally. It is also important for food security in many areas in the tropics where traditional production is in marginal environments. In such areas, the crop is dependent upon increasingly erratic rainfall, the land is subject to degradation, and temperatures are increasing due to climate change. In more temperate regions, declining sorghum production is related to reduced traditional use and limited commercialization, because there are more profitable alternative cereal grains and fodder species. These changes pose significant risks to genetic resources. A decline in importance may lead to less investment in research and development, including in *ex situ* collections. The challenges of climate change in traditional production areas may lead to losses of crop diversity from farmers' fields and of wild relatives from natural habitats. It is also a challenge for farmers to use sorghum to adapt to climate change, given the poor productivity of the crop in Africa and the lack of investment into sorghum research and development in these regions. Thus, the production of sorghum globally is vulnerable, and it is facing many constraints that will depend on the use of the genetic diversity that is itself under threat.

The current global system for the conservation and use of sorghum genetic resources consists of:

- Natural areas where most of the diversity of the wild relatives are still conserved
- Local farmers and households who conserve and manage most of the cultivated diversity
- National collections in the center of diversity that conserve a high proportion of local diversity and have significant opportunities for local engagement with users for conservation and use
- National collections located outside the center of diversity that conserve accessions that are likely duplicates of those held by others or local materials with unique traits. These collections may face an uncertain future as national priorities change.
- Three international, one regional and 11 national genebanks that conserve mainly accessions from other geographical origins

Many of these collection holders are not meeting international standards for conservation. In addition, the system is generally insecure, with inefficient and poorly resourced operations for many national institutions, limited availability of seed, limited sharing of accession-level information, and limited engagement with users locally, nationally, and globally. This is not the sustainable, rational, secure and cost-effective system that is needed for long-term conservation and use of sorghum genetic resources to meet the challenges of the future.

Some of the main disadvantages of the current system are the lack of committed annual support for conser-

vation of sorghum in many genebanks, the general lack of knowledge of how much diversity is conserved and the low level of support for research on sorghum. In addition, much of the diversity is vulnerable to loss, both from *ex situ* collections in genebanks and from farmers' fields and natural areas.

The current global conservation system does have some positive features that can be built upon. For example, skilled genebank staff can provide expertise and guidance to other conservers who are striving to meet international standards. Genebanks can also serve as conveners and facilitators in any global effort to increase security of conservation, adopt new technologies and methods, enhance staff capacity and expertise to collectively address some of the major constraints hampering the shift to a more efficient, sustainable global system. Genebanks could also take on a leadership role in advocacy and communication on the importance of conservation and the use of sorghum diversity. Another strength of the current system is participatory nature of the national and local conservation with the interest and involvement of local farmers and consumers.

The 2007 strategy highlighted the need for global collaboration as a priority and included the input of experts who committed to take the necessary actions to secure conservation and enhance use. In 2021, the need for action globally is just as urgent, but there has been progress at some of the individual genebanks in the establishment of a global information system to share accession-level information. Unfortunately, this has not increased use of sorghum resources, even with the increased availability of core and trait-specific subsets from some key collections.

Consultation with stakeholders has highlighted the importance of *ex situ* collections to users. However, it is interesting that their definition for a 'good' collection differs from that of curators, with much greater focus on availability and facilitated access to accessions and accession-level information that relates to potential use. The key action areas for global collaboration identified by the users will challenge the genebanks to reconsider the information shared, the type of germplasm conserved, the application of genomics, phenomics, and informatics to facilitate the discovery and use of allelic diversity, and the need to take on a greater role as a bridge to users through pre-breeding.

Many future needs could be addressed by individual actions or even limited collaboration between genebanks and users, as has been done so far. However, this approach is probably insufficient to address the vulnerability of the genetic diversity of sorghum

and its wild relatives. Although the value of a global system is well recognized, its implementation will require commitment by individual genebanks and scientists to long-term collective actions. The issue is not *what* needs to be done, that was clear in 2007 and is clear now, but *how* do we take the necessary actions and sustain the gains made for long-term secure conservation given the vulnerability of current conservation and the likely future demand for genetic diversity in sorghum.

The specific objective of this updated strategy is to recommend priority actions to shift from the current system to a more coordinated global conservation and use system that is more secure, rational, cost-effective, and engaged with users. These recommended actions may be used to identify the key investments needed to secure conservation and use for the long-term, both nationally and internationally. To reiterate, three strategic initiatives have been identified from the survey and the consultations, along with the key actions required:

1. Secure conservation of sorghum genetic resources for the long term by:
 - a. Increasing the security of *ex situ* conservation by improving routine operations, facilities, and safety duplication in key national genebanks
 - b. Identifying duplicates across genebanks and gaps in the conservation of unique diversity in *ex situ* collections and in farmers' fields and natural areas
 - c. Conserving research materials
 - d. Enhancing global engagement among conservers and between conservers and users
 - e. Advocating for the importance of sorghum and its conservation to the public, local governments and communities, policy makers and other research communities to increase awareness and financial support.
2. Increase the availability and exchange of sorghum germplasm by:
 - a. Increasing the quantity, quality, and viability of seed available for distribution from genebanks
 - b. Identifying key administrative, technical and policy bottlenecks to distribution in different genebanks, and then find solutions.
3. Increase the use of conserved genetic diversity by:
 - a. improving access to accession-level information that meets the needs of users, preferably online
 - b. Increasing evaluation (via phenomics) and genotyping with input from users to facilitate use
 - c. Continuing to establish and make available core collections and other subsets to facilitate the discovery and use of valuable traits
 - d. Enhancing engagement between genebanks and a wide range of users, including researchers and farmers.

Implementing the key actions in these three strategic areas will help move towards a sustainable, longer-term and rational global system of conservation and use. The primary recommendations for collaboration in 2007 aimed to increase the availability of accession-level information to identify redundancies and to better meet the needs of the users. Little action has been taken globally since 2007, however. Thus, taking lessons from the previous strategy, two priority actions have been identified for the initial implementation of the current strategy.

Priority Action 1: Global initiative to fill global gaps in conservation

As in 2007, elite materials and landraces are still the main types of accessions conserved, and there are significant gaps in the conservation of wild relatives. There is evidence of significant redundancies across collections that need to be assessed, as recommended in 2007. As discussed in the consultation with users, there would be some benefits from global action to explore this duplication but the cost for addressing the redundancies is too high to merit any concerted effort. There are also significant gaps in the conservation of diversity. Thus, the top priority action for global collaboration is an initiative to identify and fill global gaps in the conservation of sorghum genetic resources. The global initiative includes four important activities.

The 2007 strategy suggested that the top priority for global collaboration was the development of a global information system for sorghum genetic resources as the first step to strengthen the global system. Genesys is a global platform for sharing accession-level information across crops. The publication of data from USDA-ARS, ICRISAT, AGG in Australia, and the European collections on Genesys has increased the availability of accession-level information. Most of the genebanks that responded to the survey reported very limited availability of accession-level information through online, searchable platforms. Much accession-level information is still not digitized or only in internal databases. There is a need for wider adoption of genebank information systems such as GRIN-Global. This will not only facilitate monitoring of genebank metrics and increase the efficiency of genebank management, but also allow for easy online sharing of accession-level information according to formal data sharing agreements. **Thus, the first key activity of this initiative is to upgrade the information systems in national collections with key sorghum collections and ensure that complete passport data for sorghum accessions are added to Genesys.**

Global collaboration is needed both to assess duplication and to identify the priority gaps in traits and accessions that need to be secured through collecting, on-farm conservation or *in situ* conservation in protected areas. Greater sharing of complete passport information on accessions through Genesys will allow for a global assessment of conservation gaps, so that unique gene and genotypic diversity that is at risk of loss can be conserved. The gap assessment needs to consider cultural and social influences on the distribution of diversity and the use of genomic tools to incorporate allelic diversity measures of uniqueness and potential value. Numerous approaches have been used to identify gaps in the past. This assessment of gaps would serve to expand links among, and activities of, *ex situ* collections with on-farm conservation sites, community seedbanks and protected areas to secure the global diversity of sorghum and its wild relatives. **Thus, the second key activity in the global initiative is to convene a broad range of sorghum diversity conservers and users. This group will decide on the goals and approach for a comprehensive global gap analysis. The results of the gap analysis will guide investment in collecting for *ex situ* conservation and a global conservation planning exercise to determine key priority sites for on-farm and *in situ* conservation activities.**

Greater application of genomic tools will provide allelic-level measures of gene and genotypic diversity. This information can be used to identify and quantify duplication and gaps in collections. **Therefore, the third key activity is to establish a working group to provide expert guidance for investments into a global sorghum genotyping (and eventually also phenotyping) initiative.**

It is concerning that collection holders in Europe, China, Japan and other areas where sorghum production is in decline did not reply to the survey. Many of the collection curators that did not respond represent small but diverse or specialist collections. They are likely to maintain some unique germplasm that could be at risk of loss if priorities for research and development in the country and institute change. This gap needs to be addressed and these collections engaged more fully in the global system through this global initiative. The global system needs to be able to respond to the risk of loss of diversity in *ex situ* collections. Through this global initiative, the ability to monitor the status of conservation of unique accessions in individual collections will be enhanced with greater sharing of accession-level information and stronger partnerships. It will also facilitate the establishment of an early warning monitoring system to track the loss of sorghum genetic diversity from farmers' fields and in the wild.

Priority Action 2: Global initiative to secure the conservation and use of collections for future users

Generally, national genebanks in the center of sorghum diversity face significant limitations related to inadequate facilities, equipment, staffing, regeneration sites and funding. This has led to dangerous backlogs in viability testing, regeneration and multiplication that are a risk for long-term conservation and have limited the quantity and quality of seed available for distribution. There are also constraints to routine operations to ensure the use of the most efficient and secure procedures. Genebanks are aware of the need for safety duplication and many have committed to securing their collections with a back-up, but there are significant constraints, and this is not a clear priority for action currently. This is a significant vulnerability for the global system that needs to be corrected.

Priority needs have been identified in terms of improvements to routine operations, facilities, equipment, and procedures. These problems have arisen because genebanks tend to rely on short-term project funds that are not predictable and seem to be declining. Financial support for long-term conservation and availability is not a priority for many donors. The relatively lower priority that is given internationally and nationally to sorghum has resulted in few opportunities to acquire funds to address these gaps. The lack of global action to address these collection-specific constraints is a risk for the conservation of a high proportion of unique diversity. A global initiative is therefore needed to address the insecurity of conservation and the constraints to distribution.

The first activity will be the development of a competitive grants program for sorghum collection holders. Institutions can then apply for funds to address much-needed upgrades. Competitive grants could be set up to require matching funds from governments or NGOs for specific projects and a commitment to an increased annual allocation to secure long-term conservation of diversity with significant national value. The coordinated, collective action of most of the major collection holders would provide opportunities to share resources, experiences, and capacity globally. A global working group of conservation and use experts, including representatives of the major collection holders, will have the important role of setting priorities for projects, ensuring global collaboration, recommend projects to fund, monitoring projects and communicating results.

For the future sustainability of the improvements made through investment in the above priority actions, one option is to establish a platform that will enable the conservers of sorghum genetic resources to collaborate more easily with each other and with users. The platform could serve as the convener for the global collaborative activities to assess duplications and identify global gaps described above. It could be operated mainly virtually, with in-person meetings when funds are available. Global collections, such as ICRISAT, USDA-ARS, NBPGR, AGG, EMBRAPA and some key national collections could serve as the foundational group. It would not necessarily be a crop network with a formal structure or leadership, but would need to have a commitment for facilitation. It could serve as the focus not just for implementing the strategy, but also revising it as necessary.

ACRONYMS AND ABBREVIATIONS

ABS	Access and benefit sharing	ILRI	International Livestock Research Institute
AGG	Australian Grains Genebank	INIA	El Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria
BMEL	Government of Germany	IRD	Institut de Recherche pour le Développement
CAAS	Chinese Academy for Agricultural Sciences	IPGRI	International Plant Genetic Resources Institute
CGIAR	Consultative Group on International Agricultural Research	ITPGRFA	International Treaty for Plant Genetic Resources for Food and Agriculture
CIAT	The International Center for Tropical Agriculture	MSSRF	M.S. Swaminathan Research Foundation
DRC	Democratic Republic of Congo	MTA	Material transfer agreement
EBI	Ethiopian Biodiversity Institute	NARO	National Agricultural Research Organization
ECPGR	European Cooperative Programme for Plant Genetic Resources	NARS	National Agricultural Research System
EMBRAPA	Brazilian Agricultural Research Corporation	NBPGR	National Bureau of Plant Genetic Resources
FAO	Food and Agriculture Organization	NGO	Non-Governmental Organization
FAO-WIEWS	FAO-World Information and Early Warning System	NORAD	Norwegian Agency for Development Cooperation
FAS/USDA	Foreign Agricultural Service/United States Department of Agriculture	QMS	Quality management system
GBIS	Genebank Information System	SMTA	Standard material transfer agreement
GRIN-Global	Germplasm Resources Information Network-Global	SOP	Standard operating procedures
HTP	High-throughput phenotyping	SPGRC	SADC Plant Genetic Resources Center
ICBA	International Center for Biosaline Agriculture	SPGRC-SDIS	SPGRC Documentation and Information System
ICRISAT	International Centre for Research in the Semi-Arid Tropics	USDA-ARS	United States Department of Agriculture-Agricultural Research Service
IIMR	Indian Institute of Millets Research	USDA-NPGS	USDA-National Plant Germplasm System
IITA	International Institute for Tropical Agriculture	VIR	N. I. Vavilov Institute of Plant Genetic Resources

LITERATURE CITED

- Adugna, A. 2014. Analysis of in situ diversity and population structure in Ethiopian cultivated *Sorghum bicolor* (L.) landraces using phenotypic traits and SSR markers. *Springerplus* 3: 212. doi:10.1186/2193-1801-3-212
- Alercia A. 2011. Key Characterization and Evaluation Descriptors: Methodologies for the Assessment of 22 Crops. Bioersivity International, Rome, Italy.
- Amelework, B., Shimelis, H., Tongoona, P., Laing, M., Mengistu, F. 2015. Genetic variation in lowland sorghum (*Sorghum bicolor* (L.) Moench) landraces assessed by simple sequence repeats. *Plant Genetic Resources* 13(2): 131–141. doi:10.1017/S1479262114000744
- Ananda, G.K.S., Myrans, H., Norton, S.L., Gleadow, R., Furtado, A., Henry, R.J. 2020. Wild sorghum as a promising resource for crop improvement. *Frontiers in Plant Science* 11:1108. doi:10.3389/fpls.2020.01108
- Barnaud, A., Deu, M., Garine, E., Chantereau, J., Bolteu, J., Koïda, E.O., McKey, D., Joly, H.I. 2009. A weed–crop complex in sorghum: the dynamics of genetic diversity in a traditional farming system. *American Journal of Botany* 96(10): 1869–1879. doi:10.3732/ajb.0800284
- Barro-Kondombo, C., Sagnard, F., Chantereau, J., Deu, M., Vom Brocke, K., Durand, P., Gozé, E., Zongo, J.D. 2010. Genetic structure among sorghum landraces as revealed by morphological variation and microsatellite markers in three agroclimatic regions of Burkina Faso. *Theoretical and Applied Genetics* 120(8): 1511–1523. doi:10.1007/s00122-010-1272-2
- Batey, I. (2017) The diversity of uses for cereal grains. In: Wrigley, C., Batey, I., Miskelly, D. (eds.) *Cereal grains*. Elsevier, Amsterdam, Netherlands, pp 41–53.
- Bezançon, G., Pham, J.L., Deu, M., Vigouroux, Y., Sagnard, F., Mariac, C., Kapran, I., Mamadou, A., Gérard, B., Ndjeunga, J., Chantereau, J. 2009. Changes in the diversity and geographic distribution of cultivated millet (*Pennisetum glaucum* (L.) R. Br.) and sorghum (*Sorghum bicolor* (L.) Moench) varieties in Niger between 1976 and 2003. *Genetic Resources and Crop Evolution* 56(2): 223–236. doi:10.1007/s10722-008-9357-3
- Bhagavatula, S., Parthasarathy Rao, P., Basavaraj, G., Nagaraj, N. 2013. Sorghum and Millet Economies in Asia – Facts, Trends and Outlook. *Patancheru* 502 324, Andhra Pradesh, India: International Crops Research Institute for the Semi-Arid Tropics. 80 pp. ISBN: 978-92-9066-557-1.
- Billot, C., Ramu, P., Bouchet, S., Chantereau, J., Deu, M., Gardes, L., Noyer, J.L., Rami, J.F., Rivallan, R., Li, Y., Lu, P. 2013. Massive sorghum collection genotyped with SSR markers to enhance use of global genetic resources. *PloS One*, 8(4):e59714. doi:10.1371/journal.pone.0059714
- Boyles, R.E., Brenton, Z.W., Kresovich, S. 2019. Genetic and genomic resources of sorghum to connect genotype with phenotype in contrasting environments. *The Plant Journal* 97(1): 19–39. doi:10.1111/tbj.14113
- Brink, M., Van Hintum, T. 2020. Genebank operation in the arena of access and benefit-sharing policies. *Frontiers in Plant Science* 10:1712. doi:10.3389/fpls.2019.01712
- Bucheyekei, T.L., Gwanama, C., Mgonja, M., Chisi, M., Folkertsma, R., Mutegi, R. (2009) Genetic variability characterisation of Tanzania sorghum landraces based on simple sequence repeats (SSRs) molecular and morphological markers. *Journal of African Crop Science* 17: 71–86. doi:10.4314/acscj.v17i2.54201
- Burow, G., Franks, C.D., Xin, Z., Burke, J.J. 2012. Genetic diversity in a collection of Chinese sorghum landraces assessed by microsatellites. *American Journal of Plant Sciences* 3:1722–9. doi:10.4236/ajps.2012.312210
- Casa, A.M., Pressoir, G., Brown, P.J., Mitchell, S.E., Rooney, W.L., Tuinstra, M.R., Franks, C.D., Kresovich, S. 2008. Community resources and strategies for association mapping in sorghum. *Crop Science* 48(1): 30–40. doi:10.2135/cropsci2007.02.0080
- Cuevas, H.E., Prom, L.K. 2020. Evaluation of genetic diversity, agronomic traits, and anthracnose resistance in the NPGS Sudan sorghum core collection. *BMC Genomics* 21:88–102. doi:10.1186/s12864-020-6489-0
- Cuevas, H.E., Rosa-Valentin, G., Hayes, C.M., Rooney, W.L., Hoffmann, L. 2017. Genomic characterization of a core set of the USDANPGS Ethiopian sorghum germplasm collection: Implications for germplasm conservation, evaluation, and utilization in crop improvement. *BMC Genomics* 18: 108–124 doi:10.1186/s12864-016-3475-7
- Dahlberg, J.A. 2000. Classification and Characterization of Sorghum. In: Smith, C.W., Frederiksen, R.A. (eds.), *Sorghum: Origin, History, Technology, and Production*, John Wiley & Sons, New York, pp. 99–130.
- Dahlberg, J., Rosenow, D.T. 2018. Classifying the genetic diversity of sorghum: a revised classification of sorghum. In: Rooney, W. (ed.), *Achieving sustain-*

- able cultivation of sorghum Volume 1: Genetics, breeding and production techniques, Burleigh Dodds Science Publishing, Cambridge, UK.
- Danquah, A., Galyuon, I.K., Otwe, E.P., Asante, D.K. 2019. Genetic diversity in some Ghanaian and Malian sorghum [*Sorghum bicolor* (L) Moench] accessions using SSR markers. *African Journal of Biotechnology* 18(27): 591–602. doi:10.5897/AJB2019.16767
- de Wet, J.M.J. 1978. Systematics and evolution of Sorghum sect. Sorghum (Gramineae). *American Journal of Botany* 65: 477–484. doi:10.1002/j.1537-2197.1978.tb06096.x
- de Wet, J.M.J. and Harlan, J.R., 1971. The origin and domestication of *Sorghum bicolor*. *Economic Botany* 25(2): 128–135. <https://www.jstor.org/stable/4253238>
- Deu, M., Rattunde, F., Chantereau, J. 2006. A global view of genetic diversity in cultivated sorghums using a core collection. *Genome* 49(2): 168–180. doi:10.1139/g05-092
- Deu, M., Sagnard, F., Chantereau, J., Calatayud, C., Herault, D., Mariac, C., Pham, J.L., Vigoroux, Y., Kapran, I., Traore, P.S., Mamadou, A., Gerard, B., Ndjeunga, J. Bezançon, G. 2008. Niger-wide assessment of in situ sorghum genetic diversity with microsatellite markers. *Theoretical and Applied Genetics*, 116(7): 903–913.
- Deu, M., Sagnard, F., Chantereau, J., Calatayud, C., Vigouroux, Y., Pham, J.L., Mariac, C., Kapran, I., Mamadou, A., Gérard, B., Ndjeunga, J. 2010. Spatio-temporal dynamics of genetic diversity in *Sorghum bicolor* in Niger. *Theoretical and Applied Genetics* 120: 1301–1313. doi:10.1007/s00122-009-1257-1
- Djè, Y., Heuertz, M., Ater, M., Lefèbvre, C., Veke-mans, X. 2004. In situ estimation of outcrossing rate in sorghum landraces using microsatellite markers. *Euphytica* 138(3): 205–212. doi:10.1023/B:EUPH.0000047082.10626.cb
- Doggett, H. 1988. Sorghum. Longman Scientific and Technical, New York.
- Dossou-Aminon, I., Loko, L.Y., Adjatin, A., Ewédjè, E.E.B., Dansi, A., Rakshit, S., Cissé, N., Patil, J.V., Agbangla, C., Sanni, A., Akoègninou, A. 2015. Genetic divergence in northern Benin sorghum (*Sorghum bicolor* L. Moench) landraces as revealed by agromorphological traits and selection of candidate genotypes. *The Scientific World Journal*. Volume 2015:916476. doi:10.1155/2015/916476
- Duncan, R.R., Bramel-Cox, P.J., Miller, F.R., 1991. Contributions of introduced sorghum germplasm to hybrid development in the USA. In: Shands, H.L., Wiesner L.E. (eds.) Use of plant introductions in cultivar development Part 1, Vol. 17, CSSA Special Publication Madison, WI: Crop Science Society of America. pp. 69–102. doi:10.2135/cssaspecpub17.c5
- Elangovan, M., Tonapi, V. A., Reddy, D. 2009. Collection and characterization of Indian sorghum landraces. *Indian Journal of Plant Genetic Resources*, 22(3): 173–181.
- Engels, J.M.M., Ebert, A.W. 2021a. A critical review of the current global ex situ conservation system for plant agrobiodiversity. I. History of the development of the global system in the context of the political/legal framework and its major conservation components. *Plants* 10: 1557. doi:10.3390/plants10081557
- Engels, J.M.M., Ebert, A.W. 2021b. A critical review of the current global ex situ conservation system for plant agrobiodiversity. II. Strengths and weaknesses of the current system and recommendations for its improvement. *Plants* 10: 1904. doi:10.3390/plants10091904
- FAO. 2014. Genebank Standards for Plant Genetic Resources for Food and Agriculture. Rev. ed. Rome.
- FAO (UN Food and Agriculture Organization). 2021. FAOSTAT Available at www.fao.org/faostat/en/#data/QC (accessed October 5, 2021).
- FAO-WIEWS. 2020. [WIEWS - World Information and Early Warning System on Plant Genetic Resources for Food and Agriculture](#). Ex situ Search. Assessed June 2020.
- Faye, J.M., Maina, F., Akata, E.A., Sine, B., Diatta, C., Mamadou, A., Marla, S., Bouchet, S., Teme, N., Rami, J.-F., Fonckea, D., Cisse, N., Morris, G.P. 2021. [A genomics resource for genetics, physiology, and breeding of West African sorghum](#). *The Plant Genome* 14: e20075.
- Faye, J.M., Maina, F., Hu, Z.B., Fonckea, D., Cisse, N., Morris, G.P. 2019. Genomic signatures of adaptation to Sahelian and Soudanian climates in sorghum landraces of Senegal. *Ecology and Evolution* 9:6038–6051. doi:10.1002/ece3.5187
- Fernandez, M.G.S., Okeno, J.A., Mutegi, E., Fessehaie, A., and Chalfant, S. 2014. Assessment of genetic diversity among sorghum landraces and their wild/weedy relatives in western Kenya using simple sequence repeat (SSR) markers. *Conservation Genetics* 15, 1269–1280. doi:10.1007/s10592-014-0616-x
- Figueiredo, D.L.F., Calatayud, C., Dupuits, C., Billot, C., Rami, J.F., Brunel, D., Perrier, X., Courtois, B., Deu, M., Glaszmann, J.C. 2008. Phylogeographic evidence of crop neodiversity in sorghum. *Genetics* 179(2): 997–1008. doi:10.1534/genetics.108.087312
- Foreign Agricultural Service/United States Department of Agriculture (FAS/USDA). 2021. Grain: World Markets and Trade. pp 38–40.
- Galluzzi, G., Seyoum, A., Halewood, M., López Noriega, I., Welch, E.W. 2020. The role of genetic resources in breeding for climate change: The case of public breeding programmes in eighteen developing countries. *Plants*, 9(9):1129. doi:10.3390/plants9091129

- Genesys 2020. <https://www.genesys-pgr.org/> (Accessed July 4, 2020).
- Ghebru, B., Schmidt, R.J. and Bennetzen, J.L. (2002) Genetic diversity of Eritrea sorghum landraces assessed with simple sequence repeats (SSR) markers. *Theoretical and Applied Genetics* 105: 229–236. doi:10.1007/s00122-002-0929-x
- Girma, G., Nida, H., Seyoum, A., Mekonen, M., Nega, A., Lule, D., Dessalegn, K., Bekele, A., Gebreyohannes, A., Adeyanju, A., Tirfessa, A. 2019. A large-scale genome-wide association analyses of Ethiopian sorghum landrace collection reveal loci associated with important traits. *Frontiers in Plant Science* 10:691–705. doi:10.3389/fpls.2019.00691
- Girma, G., Nida, H., Tirfessa, A., Lule, D., Bejiga, T., Seyoum, A., Mekonen, M., Nega, A., Dessalegn, K., Birhanu, C., Bekele, A. 2020. A comprehensive phenotypic and genomic characterization of Ethiopian sorghum germplasm defines core collection and reveals rich genetic potential in adaptive traits. *The Plant Genome* 13(3): e20055. doi:10.1002/tpg2.20055
- Gollin, D. 2020. Conserving genetic resources for agriculture: economic implications of emerging science. *Food Security* 12(5): 919–927. doi:10.1007/s12571-020-01035-w
- Gollin, D., Smale, M., Skovmand, B. 2000. Searching an ex situ collection of wheat genetic resources. *American Journal of Agricultural Economics* 82(4): 812–827.
- Grenier, C., Bramel, P. J., Dahlberg, J. A., El-Ahmadi, A., Mahmoud, M., Peterson, G. C., Rosenow, D.T., Ejeta, G. (2004). Sorghums of the Sudan: analysis of regional diversity and distribution. *Genetic Resources and Crop Evolution*, 51(5): 489–500.
- Halewood, M., Jamora, N., Noriega, I.L., Anglin, N.L., Wenzl, P., Payne, T., Ndjiondjop, M.-N., Guarino, L., Kumar, P.L., Yazbek, M., Muchugi, A., Azevedo, V., Tchamba, M., Jones, C.S., Venuprasad, R., Roux, N., Rojas, E., Lusty, C. 2020. Germplasm acquisition and distribution by CGIAR genebanks. *Plants* 9(10):1296. doi:10.3390/plants9101296
- Hao, H., Li, Z., Leng, C., Lu, C., Luo, H., Liu, Y., Wu, X., Liu, Z., Shang, L., Jing, H.C. 2021. Sorghum breeding in the genomic era: opportunities and challenges. *Theoretical and Applied Genetics* 134(7): 1899–1924.
- Hay, F.R.; Serphen, N. 2021. New Technologies to Improve the Ex situ Conservation of Plant Genetic Resources; Burleigh Dodds Series. In: *Agricultural Science*; Burleigh Dodds Science Publishing Limited: Cambridge, UK. pp. 1–32.
- Hyman, G., Barona, E., Biradar, C., Guevara, E., Dixon, J., Beebe, S., Castano, S.E., Alabi, T., Gumma, M.K., Sivasankar, S., Rivera, O. 2016. Priority regions for research on dryland cereals and legumes. *F1000Research* 5:885. doi:10.12688/f1000research.8657.2
- IBPGR and ICRISAT 1993. Descriptors for *sorghum bicolor* (L.) Moench. International Board for Plant Genetic Resources, Rome, Italy; International Crops Research Institute for the Semi-Arid Tropics, Patancheru, India.
- Jannink, J.-L. 2010. Dynamics of long-term genomic selection. *Genetics Selection Evolution* 42(1): 1–11. doi:10.1186/1297-9686-42-35.
- Klein, R.R., Mullet, J.E., Jordan, D.R., Miller, F.R., Rooney, W.L., Menz, M.A., Franks, C.D., Klein, P.E. 2008. The effect of tropical sorghum conversion and inbred development on genome diversity as revealed by high-resolution genotyping. *Crop Science* 48:5–12. doi:10.2135/cropsci2007.06.0319tpg
- Kresovich, S., Barbazuk, B., Bedell, J.A, Borrell, A., Buell, C.R., Burke, J., Clifton, S., Cordonnier-Pratt, M.M, Cox, S., Dahlberg, J, Erpelding, J, Fulton, T.M., Fulton, B., Fulton, L., Gingle, A.R., Hash, C.T., Huang, Y., Jordan, D., Klein, P.E., Klein, R.R., Magalhaes, J., McCombie, R., Moore, P., Mullet, J.E., Ozias-Akins, P., Paterson, A.H, Porter, K., Pratt, L., Roe, B., Rooney, W., Schnable, P.S., Stelly, D.M., Tuinstra, M, Ware, D., Warek, U. 2005. Toward sequencing the Sorghum genome: A US national foundation-sponsored workshop report. *Plant Physiology* 138: 1898–1902.
- Kuhlman, L.C., Burson, B.L., Stelly, D.M., Klein, P.E., Klein, R.R., Price, H.J., Rooney, W.L. 2010. Early-generation germplasm introgression from Sorghum macrospermum into sorghum (*S. bicolor*). *Genome* 53(6): 419–429. doi:10.1139/g10-027
- Labeyrie, V., Deu, M., Barnaud, A., Calatayud, C., Burion, M., Wanbugu, P., Manel, S., Glaszmann, N.-C., Leclerc, C. 2014. Influence of ethnolinguistic diversity on the sorghum genetic patterns in subsistence farming systems in eastern Kenya. *PLoS One* 9(3), e92178. doi:10.1371/journal.pone.0092178
- Lasky, J.R., Upadhyaya, H.D., Ramu, P., Deshpande, S., Hash, C.T., Bonnette, J., Juenger, T.E., Hyma, K., Acharya, C., Mitchell, S.E., Buckler, E.S. 2015. Genome-environment associations in sorghum landraces predict adaptive traits. *Science Advances* 1(6):e1400218. doi:10.1126/sciadv.1400218
- Leclerc, C., d’Eeckenbrugge, G.C. 2011. Social organization of crop genetic diversity. The G × E × S interaction model. *Diversity* 4(1): 1–32. doi:10.3390/d4010001
- Mace, E.S., Tai, S., Gilding, E.K., Li, Y., Prentis, P.J., Bian, L., Campbell, B.C., Hu, W., Innes, D.J., Han, X., Cruickshank, A., Dai, C.M., Frère, C., Zhang, H.K., Hunt, C.H., Wang, X.Y., Shatte, T., Wang, M.M., Su, Z., Li, J., Lin, X.Z., Godwin, I.D., Jordan, D.R., Wang, J. 2013. Whole-genome sequencing reveals untapped genetic potential in Africa’s indigenous cereal crop sorghum. *Nature Communications* 4(1): 1–9. doi:10.1038/ncomms3320
- Maina, F., Bouchet, S., Marla, S. R., Hu, Z., Wang, J., Mamadou, A., Abdou, M., Saidou, A.A, Morris, G. P. 2018. Population genomics of sorghum (*Sor-*

- ghum bicolor*) across diverse agroclimatic zones of Niger. *Genome*, 61(4): 223-232.
- Maunder, A.B. 2000. History of cultivar development in the United States: From memoirs of AB Maunder-sorghum breeder. In: Smith C.W., Frederiksen, R.A. (eds.) *Sorghum: Origin, history, technology and production*. John Wiley & Sons, New York, pp.191–223.
- Missihoun, A.A., Adoukonou-Sagbadja, H., Sedah, P., Agbangla, C., Ahanhanzo, C., Dagba, R.A. 2015. Genetic diversity of *Sorghum bicolor* (L.) Moench landraces from Northwestern Benin as revealed by microsatellite markers. *African Journal of Biotechnology* 14(16):1342–1353. Doi:[10.5897/AJB2014.14338](https://doi.org/10.5897/AJB2014.14338)
- Mofokeng, A., Shimelis, H., Tongoona, P., Laing, M. 2014. A genetic diversity analysis of South African sorghum genotypes using SSR markers. *South African Journal of Plant and Soil* 31(3): 145–152. doi:[10.1080/02571862.2014.923051](https://doi.org/10.1080/02571862.2014.923051)
- Morris, G. P., Ramu, P., Deshpande, S. P., Hash, C. T., Shah, T., Upadhyaya, H. D., Riera-Lizarazu, O., Brown, P.J. Acharya, C.B., Mitchell, S.E., Harriman, J., Glaubitz, J.C., Buckler, E.S., Kresovich, S. (2013). Population genomic and genome-wide association studies of agroclimatic traits in sorghum. *Proceedings of the National Academy of Sciences*, 110(2): 453-458.
- Mujaju, C., Chakauya, E. 2008. Morphological variation of sorghum landrace accessions on-farm in semi-arid areas of Zimbabwe. *International Journal of Botany* 4: 376–382. doi:[10.1080/10771220802376382](https://doi.org/10.1080/10771220802376382)
- Mundia, C.W., Secchi, S., Akamani, K., Wang, G. 2019. A regional comparison of factors affecting global sorghum production: The case of North America, Asia and Africa's Sahel. *Sustainability* 11(7):2135. doi:[10.3390/su11072135](https://doi.org/10.3390/su11072135)
- Mutegi, E., Sagnard, F., Muraya, M., Kanyenji, B., Rono, B., Mwangera, C., Marangu, C., Kamau, J., Parzies, H., de Villiers, S., Semagn, K. 2010. Eco-geographical distribution of wild, weedy and cultivated *Sorghum bicolor* (L.) Moench in Kenya: implications for conservation and crop-to-wild gene flow. *Genetic Resources and Crop Evolution* 57(2): 243–253. doi:[10.1007/s10722-009-9466-7](https://doi.org/10.1007/s10722-009-9466-7)
- Mutegi, E., Sagnard, F., Semagn, K., Deu, M., Muraya, M., Kanyenji, B., De Villiers, S., Kiambi, D., Herselman, L., Labuschagne, M. 2011. Genetic structure and relationships within and between cultivated and wild sorghum (*Sorghum bicolor* (L.) Moench) in Kenya as revealed by microsatellite markers. *Theoretical and Applied Genetics* 122(5): 989–1004. doi:[10.1007/s00122-010-1504-5](https://doi.org/10.1007/s00122-010-1504-5)
- Mutegi, E., Sagnard, F., Labuschagne, M., Herselman, L., Semagn, K., Deu, M., De Villiers, S., Kanyenji, B.M., Mwangera, C.N., Traore, P.C.S., Kiambi, D. 2012. Local scale patterns of gene flow and genetic diversity in a crop-wild-weedy complex of sorghum (*Sorghum bicolor* (L.) Moench) under traditional agricultural field conditions in Kenya. *Conservation Genetics* 13(4): 1059–1071. doi:[10.1007/s10592-012-0353-y](https://doi.org/10.1007/s10592-012-0353-y)
- Myrans, H., Diaz, M.V., Khoury, C.K., Carver, D., Henry, R.J., Gleadow, R. 2020. Modelled distributions and conservation priorities of wild sorghums (*Sorghum Moench*). *Diversity and Distributions* 26(12): 1727–1740. doi:[10.1111/ddi.13166](https://doi.org/10.1111/ddi.13166)
- Naoura, G., Sawadogo, N., Atchozou, E.A., Emen-dack, Y., Hassan, M.A., Reoungal, D., Amos, D.N., Djirabayé, N., Tabo, R., Laza, H. 2019. Assessment of agro-morphological variability of dry-season sorghum cultivars in Chad as novel sources of drought tolerance. *Scientific Reports* 9(1): 1–12. doi:[10.1038/s41598-019-56192-6](https://doi.org/10.1038/s41598-019-56192-6)
- Ng'uni, D., Geleta, M., Bryngelsson, T. 2011 Genetic diversity in sorghum (*Sorghum bicolor* (L.) Moench) accessions of Zambia as revealed by simple sequence repeats (SSR). *Hereditas* 148: 52–68. doi:[10.1111/j.1601-5223.2011.02208.x](https://doi.org/10.1111/j.1601-5223.2011.02208.x)
- Ngugi, K., Onyango, C. M. 2012. Analysis of the molecular diversity of Kenyan sorghum germplasm using microsatellites. *Journal of Crop Science and Biotechnology*, 15(3): 189-194.
- Nguyen, G.N., Norton, S.L. 2020. Genebank phenomics: A strategic approach to enhance value and utilization of crop germplasm. *Plants* 9(7): 817. doi:[10.3390/plants9070817](https://doi.org/10.3390/plants9070817)
- Nikiema, S.Z., Sanou, J., Ouedraogo, B., Gracen, V., Tongoona, B.P., Kwame, S.O. 2020. Genetic diversity of sorghum (*Sorghum bicolor* (L.) Moench) accessions from thirteen regions of Burkina Faso. *International Journal of Biological and Chemical Sciences* 14(5): 1547–1557. doi:[10.4314/ijbcs.v14i5.5](https://doi.org/10.4314/ijbcs.v14i5.5)
- OECD. 2016. Consensus Document on the Biology of Sorghum (*Sorghum bicolor* L. Moench). OECD Environment, Health and Safety Publications, Series on Harmonisation of Regulatory Oversight in Biotechnology, No. 62, Organization for Economic Co-operation and Development: Paris, France.
- Ohadi, S., Hodnett, G., Rooney, W., Bagavathiannan, M. (2017). Gene flow and its consequences in Sorghum spp. *Critical Reviews in Plant Science* 36: 367–385. doi:[10.1080/07352689.2018.1446813](https://doi.org/10.1080/07352689.2018.1446813)
- Okeno, J.A., Mutegi, E., De Villiers, S., Wolt, J.D., Misra, M.K. (2012). Morphological variation in the wild-weedy complex of *Sorghum bicolor* in situ in Western Kenya: Preliminary evidence of crop-to-wild gene flow? *International Journal of Plant Science* 173: 507–515. doi:[10.1086/665266](https://doi.org/10.1086/665266)
- Olatoye, M.O., Hu, Z., Maina, F., Morris, G.P. 2018. Genomic signatures of adaptation to a precipitation gradient in Nigerian sorghum. *G3: Genes, Genomes, Genetics* 8, 3269–3281. doi:[10.1534/g3.118.200551](https://doi.org/10.1534/g3.118.200551)
- Orr, A.C., Schipmann-Schwarze, A. Gierend, S. Nedumarman. C. Mwema, E. Muange, E. Manyasa, Ojulong, H. 2020. Why invest in Research & Develop-

- ment for sorghum and millets? The business case for East and Southern Africa. *Global Food Security* 26: 100458 doi:10.1016/j.gfs.2020.100458
- Paterson, A. H., Bowers, J. E., Bruggmann, R., Dubchak, I., Grimwood, J., Gundlach, H., Haberer, G., Hellsten, U., Mitros, T., Poliakov, A., Schmutz, J., Spannag, M., Tang, H., Wang, X., Wicker, T., Bharti, A.K., Chapman, J., Feltus, F.A., Gowik, U., Grigoriev, I.V., Lyons, E., Maher, C.A., Martis, M., Narechania, A., Ollilar, R.P., Penning, B.W., Salamov, A.A., Wang, Y., Zhang, L., Carpita, N.C., Freeling, M., Gingle, A.R., Hash, C.T., Keller, B., Klein, P., Kresovich, S., M.C. McCann, Ming, R., Peterson, D. G., Mehboob-ur-Rahman, Ware, D., Westhoff, P., Mayer, K. F. X., Messing, J., Rokhsar, D. S. (2009). The *Sorghum bicolor* genome and the diversification of grasses. *Nature*, 457(7229), 551-556.
- Prasad, V.R., Govindaraj, M., Djanaguiraman, M., Djalovic, I., Shailani, A., Rawat, N., Singla-Pareek, S.L., Pareek, A., Prasad, P.V. 2021. Drought and high temperature stress in sorghum: Physiological, genetic, and molecular insights and breeding approaches. *International Journal of Molecular Sciences* 22(18): 9826. doi:10.3390/ijms22189826
- Qingshan, L., Dahlberg, J.A. 2001. Chinese Sorghum Genetic Resources. *Economic Botany* 55: 401–425. doi:10.1007/BF02866563
- Rabbi, I.Y., Geiger, H.H., Haussmann, B.I., Kiambi, D., Folkertsma, R., Parzies, H.K. 2010. Impact of farmers' practices and seed systems on the genetic structure of common sorghum varieties in Kenya and Sudan. *Plant Genetic Resources* 8(2): 116–126. doi:10.1017/S147926211000002X
- Reddy, B.V., Kumar, A.A., Reddy, P.S. and Elangovan, M. 2008. Sorghum germplasm: diversity and utilization. In: *Sorghum genetic enhancement: research process, dissemination and impacts*. International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Andhra Pradesh, India, pp. 153–169. ISBN 978-92-9066-512-0
- Rosenow, D.T., Dahlberg, J.A. 2000. Collection, conversion and utilization of sorghum. In: Smith C.W., Frederiksen, R.A. (eds.) *Sorghum: Origin, history, technology, and production*. John Wiley & Sons, New York. pp. 305–328.
- Sagnard, F., Deu, M., Dembélé, D., Leblois, R., Touré, L., Diakit, M., Calatayud, C., Vaksman, M., Bouchet, S., Malle, Y., Togola, S. 2011. Genetic diversity, structure, gene flow and evolutionary relationships within the *Sorghum bicolor* wild-weedy-crop complex in a western African region. *Theoretical and Applied Genetics* 123(7): 1231–1246. doi:10.1007/s00122-011-1662-0
- Sawadogo-Lingani, H., Owusu-Kwarteng, J., Glover, R., Diawara, B., Jakobsen, M., Jespersen, L. 2021. Sustainable production of African traditional beers with focus on dolo, a West African sorghum-based alcoholic beverage. *Frontiers in Sustainable Food Systems* 5: 672410. doi:10.3389/fsufs.2021.672410
- Shakoor, N., Ziegler, G., Dilkes, B. P., Brenton, Z., Boyles, R., Connolly, E. L., Kresovich, S., Baxter, I. 2016. Integration of experiments across diverse environments identifies the genetic determinants of variation in *Sorghum bicolor* seed element composition. *Plant Physiology*, 170(4): 1989-1998.
- Shakoor, N., Lee, S., Mockler, T. C. 2017. High throughput phenotyping to accelerate crop breeding and monitoring of diseases in the field. *Current opinion in plant biology*, 38:184-192.
- Stephens, J.C., Miller, F.R., Rosenow, D.T. 1967. Conversion of alien sorghum to early combine types. *Crop Science* 7:396. doi:10.2135/cropsci1967.0011183X000700040036x
- Tesso, T., Kapran, I., Grenier, C., Snow, A., Sweeney, P., Pedersen, J., Marx, D., Bothma, G., Ejeta, G. 2008. The potential for crop-to-wild gene flow in sorghum in Ethiopia and Niger: A geographic survey. *Crop Science* 48(4):1425–1431. doi:10.2135/cropsci2007.08.0441
- Tovignan, T.K., Luquet, D., Fonceka, D., Ndoye, I., Trouche, G., Cisse, N. 2016. Assessment of the variability of Senegalese landraces for phenology and sugar yield components to broaden the genetic pool of multi-purpose sorghum. *Plant Genetic Resources* 14(2): 121–131. doi:10.1017/S1479262115000155
- Upadhyaya H.D., Gopal Reddy V, Sastry D.V.S.S.R. 2008. Regeneration guidelines: sorghum. In: Dulloo M.E., Thormann I., Jorge M.A., Hanson J. (eds.) *Crop specific regeneration guidelines [CD-ROM]*. CGIAR System-wide Genetic Resource Programme, Rome, Italy. 8 pp.
- Upadhyaya, H.D., Reddy, K.N., Vetriventhan, M., Murali, K.G., Irshad, A.M., Manyasa, E., Reddy M.T., Singh, S.K. 2017a. Geographical distribution, diversity and gap analysis of East African sorghum collection conserved at the ICRISAT genebank. *Australian Journal of Crop Science* 11(4): 424–37. doi/10.3316/informit.886890609707739
- Upadhyaya, H.D., Reddy, K.N., Vetriventhan, M., Ahmed, M.I., Krishna, G.M., Reddy, M.T. Singh, S.K. 2017b. Sorghum germplasm from West and Central Africa maintained in the ICRISAT genebank: Status, gaps, and diversity. *The Crop Journal* 5(6): 518–532. doi:10.1016/j.cj.2017.07.002.
- Upadhyaya, H.D., Vetriventhan, M., Deshpande, S. 2016a. Sorghum germplasm resources characterization and trait mapping. In: Rakshit S., Wang, Y.-H. (eds.) *The Sorghum Genome, Compendium of Plant Genomes*, Springer, Cham. pp. 77–94. doi:10.1007/978-3-319-47789-3_4
- Upadhyaya, H.D., Reddy, K.N., Vetriventhan, M., Krishna, G.M., Ahmed, M.I., Reddy, M.T. Singh, S.K. 2016b. Status, genetic diversity and gaps in

- sorghum germplasm from South Asia conserved at ICRISAT genebank. *Plant Genetic Resources* 13 247–55. doi:10.1017/S147926211600023X
- Upadhyaya, H.D., Vetriventhan, M. 2018. Ensuring the genetic diversity of sorghum. In: Rooney, W. (ed.), *Achieving sustainable cultivation of sorghum Volume 1: Genetics, breeding and production techniques*, Burleigh Dodds Science Publishing, Cambridge, UK.
- USDA, Agricultural Research Service, National Plant Germplasm System. 2021. Germplasm Resources Information Network (GRIN Taxonomy). National Germplasm Resources Laboratory, Beltsville, Maryland. Accessed 13 October 2021.
- Wang, X., Singh, D., Marla, S., Morris, G., Poland, J. 2018. Field-based high-throughput phenotyping of plant height in sorghum using different sensing technologies. *Plant Methods*, 14(1): 1-16.
- Weise, S., Lohwasser, U. and Oppermann, M. 2020. Document or lose it—on the importance of information management for genetic resources conservation in genebanks. *Plants* 9(8): 1050. doi:10.3390/plants9081050
- Westengen, O.T., Okongo, M.A., Onek, L., Berg, T., Upadhyaya, H., Birkeland, S., Kaur Khalsa, S.D., Ring, K.H., Stenseth, N.C., Brysting, A.K. 2014. Ethnolinguistic structuring of sorghum genetic diversity in Africa and the role of local seed systems. *Proceedings of the National Academy of Sciences* 111(39): 14100–14105. doi:10.1073/pnas.1401646111
- Xin, Z., Wang, M., Cuevas, H.E., Chen, J., Harrison, M., Pugh, N., Morris, G. 2021. Sorghum genetic, genomic, and breeding resources. *Planta* 254(6): 1–24. doi:10.1007/s00425-021-03742-w
- Yu, X., Li, X., Guo, T., Zhu, C., Wu, Y., Mitchell, S.E., Roozeboom, K.L., Wang, D., Wang, M.L., Pederson, G.A., Tesso, T.T. 2016. Genomic prediction contributing to a promising global strategy to turbocharge gene banks. *Nature Plants* 2(10):1–7. doi:10.1038/NPLANTS.2016.150
- Zhang, L.M., Leng C.Y., Luo H., Wu X.Y., Liu, Z.Q., Zhang, Y.M., Zhang, H., Xia, Y., Shang, L., Liu, C.M., Hao, D.Y., Zhou, Y.H., Chu, C.C., Cai, H.W., Jing, H.C.. 2018. Sweet sorghum originated through selection of Dry, a plant-specific NAC transcription factor gene. *Plant Cell* 30:2286–2307
- Zereyesus, Y.A., Dalton, T.J. 2017 Rates of return to sorghum and millet research investments: A meta-analysis. *PLoS ONE* 12(7): e0180414. doi:10.1371/journal.pone.0180414

ANNEXES

Annex I. Respondents to the 2021 survey.

FAO Code	Institute	Address	Contact
ARE003	International Center for Biosaline Agriculture (ICBA)	P.O. Box 14660, Al Ruwayyah 2, Academic City, Dubai, United Arab Emirates	Muhammad Shahid
ARG	Instituto Nacional de Tecnología Agropecuaria (INTA)	Manfredi 5988, Argentina	Diego Ortiz
AUS165	Australian Tropical Grains Germplasm Centre Crop and Food Science Agri-Science Agriculture Victoria	110 Natimuk Road, Horsham, 3400, Australia	Dr Sally Norton
BEN	Centre of Agricultural Research of the North West / National Institute of Agricultural Research of Benin (CRA-NO/INRAB)	Natitingou, BP 545, Benin	Guirguissou MABOUDOU ALIDOU
BFA	INERA Saria	BP 10, Koudougou, Burkina Faso	Clarisse Pulchérie Barro Kondombo
BRA003	EMBRAPA Recursos Genéticos e Biotecnologia (CENARGEN)	Peb A. W5 Norte (final), Brasília, 70770-901, Brazil	Juliano Gomes Pádua
BWA015	Botswana National Plant Genetic Resources Centre	Department of Agricultural Research, Private Bag 0033, Gaborone, Botswana	Dr Tiny Mpho Motlhaodi
ERI003	Ministry of Agriculture, National Agricultural Research Institute, Halhale	Asmara, 4627, Eritrea	Amanuel Mahdere Zerezghi
ESP004	Spain Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria. Centro Nacional de Recursos Fitogenéticos, INIA.	Autovía A-2, km. 36. Apdo 1045, Alcala de Henares 28805, Spain	Isaura Martin
ETH085	Ethiopian Biodiversity Institute	Addis Ababa, PO Box 30726, Ethiopia	Wubishet Teshome and Eyerusalem Arusi
FRA014	CIRAD, AGAP Institute	10 rue Arthur Young, Montpellier, 34090, France	Sylvie Vancoppenolle and Paule Teres
GBR004	Royal Botanic Gardens Kew/ Millennium Seed Bank, Wakehurst Place	Ardingly, West Sussex, United Kingdom	Janet Terry
GHA	CSIR-Savanna Agricultural Research Institute, Sorghum Improvement Section	P. O. Box TL 52, Tamale- Ghana.	Kenneth Opare-Obuobi
GHA091	CSIR-Plant Genetic Resources Research Institute	P.O.Box 7 Bunso, Ghana	Dr Lawrence Misa Aboagye and Dr Rashied Tetteh
HND005	Escuela Agrícola Panamericana, Zamorano University	Tegucigalpa Honduras	Dr. Juan Carlos Rosas
IND001	ICAR-National Bureau of Plant Genetic Resources	New Delhi, 110012, India	Dr Sushil Pandey
IND002	ICRISAT Niamey Regional Genebank	Niamey, BP 12404, Niger	Dr. Hamidou Falalou
IND002	ICRISAT	502324 Hyderabad, India	Kupldeep Singh, Mani Vetriventhan, Ovais Peerzada, Venkata Narayana
IND0182	ICAR-Indian Institute of Millets Research (IIMR)	Hyderabad 500030, Telangana, India	Dr. M. Elangoven
KEN212	Genetic Resources Research Institute, KALRO	P.O. Box 781 00902, Kikuyu, Kenya	Dr. Desterio Nyamongo and Joseph Ndungu Kimani
LKA036	Sri Lanka Plant Genetic Resources Centre, Gannoruwa	Peradeniya 20400, Sri Lanka	Mr. S. Wanigadeva and Dr. D.G.C. Jeewani

FAO Code	Institute	Address	Contact
LSO015	Lesotho National Plant Genetic Resources Center	Maseru, 100, Lesotho	Matsikoane Sefotho
MAR088	INRA Genebank - Centre Régional de la Recherche Agronomique de Settat	Route tertiaire 1406, A 5 Km de Settat Maroc, 26000	Dr, Hassan Ouabbou
MLI070	Unite des Ressources Genetique (UGR), Institute d'Economie Rurale	Bamako, BP 258, Mali	Amadou Sidibe
NAM006	Namibia National Plant Genetic Resources Center,	Hugel Street, Windhoek, 9000, Namibia	Heleni Heita and Rennie Hilukwa
NER001	Niger Institut national de la recherche agronomique du Niger (INRAN)	Corniche Yantala BP 429 Niamey Niger	Mahaman Mourtala Issa Zakari and Baina Danjimo
NGA010	National Centre for Genetic Resources and Biotechnology	Ibadan, PMB 5382, Nigeria	Dr. Sunday E. Aladele
NPL069	Nepal National Agriculture Genetic Resources Centre (NAGRC), Khumaltar	Katmandu, Nepal	Dr. Bal Krishna Joshi
SDN002	Sudan Agricultural Plant Genetic Resources Conservation and Research Centre, Agricultural Research Corporation (APGRC-ARC)	Wad Medani, 21111, Sudan	El Tahir Ibrahim Mohamed
SEN094	Institut Sénégalais de Recherches Agricoles (ISRA)	Bel Air, routes des hydrocarbures, Dakar, BP 3120, Senegal	Cyril Diatta
TCD	Institut Tchadien de Recherche Agricole pour le Développement (ITRAD)	BP : 5400 N'Djamena, Tchad	Dr Gapili Naoura
TGO	Togo Institut Togolais de Recherche Agronomique (ITRA)	Siège Cacaveli Lome Togo 1163	Akata Atchouzou Eyanawa and Dr Kombate Koffi
UGA132	Plant Genetic Resources Center	Entebbe, Uganda	Dr. J.W. Mulumba and Eva Zaake
USA016	PGRCU Southern Regional Plant Introduction Station USDA-ARS-SAA	1109 Experiment Street, Griffin, 30223, Georgia, USA	Melanie Harrison
ZAF062	South Africa National Plant Genetic Resources Centre	Directorate: Genetic Resources, Private Bag X973, Pretoria, 0001, South Africa	Ms. Mpolokeng Mokoena and Thabo Tjikana
ZMB030	SADC Plant Genetic Resources Centre (SPGRC)	Lusaka, Farm no. 6300, Zambia	Sthembiso A. Mbhele
ZMB048	Zambia National Plant Genetic Resources Centre, Zambia Agriculture Research Institute	Lusaka, Zambia	Graybill Munkombwe
ZWE049	Zimbabwe National Plant Genetic Resources Centre	Harare Research Center Fifth Street Extension Opposite Royal Harare Golf Club, Harare, Zimbabwe	Onismus Chipfunde

Annex II. Number of accessions reported in the 2007 strategy report, and in 2021 in the survey or in the consolidated global database.

Country	Institute	No. of accessions in 2007 strategy report	No. of accessions reported in 2021 survey	No. of accessions in consolidated global database
Institutions that responded to the 2021 survey				
USA	USDA-ARS-PGRCU	43104	47412	
India	ICRISAT	36774	42352	
India	ICRISAT Niamey Regional Genebank		3045	
India	NBPGR	18853	25507	
India	ICAR-IIMR	2767	2183	
Ethiopia	EBI	9772	11063	
Brazil	EMBRAPA CENARGEN	8017	4726	
Zimbabwe	NPGRC	7009	2032	
Australia	AGG	5403	7107	
Sudan	PGRU-ARC	4191	7212	
Mali	IER	2975	2658	
France	CIRAD AGAP Institute	2690	2263	
Kenya	KALRO GRRI	1320	6287	
Zambia	NPGRC	1005	960	
South Africa	NPGRC	428	559	
Nigeria	NCGRB	159	2276	
Argentina	INTA	3251	2976	
Uganda	Serere Ag. & Animal Prod Res. Inst	2635	950	
Burkina Faso	INERA-Saria		2800	
Ghana	CSIR-Plant Genetic Resources Research Institute	67	85	
Eritrea	National Agricultural Research Institute, Halhale		722	
Honduras	Escuela Agricola Panamericana El Zamorana	2000 ¹	19	
Morocco	INRA Genebank - Centre Régional de la Recherche Agronomique de Settat	1	237	
Zambia	SADC Plant Genetic Resources Centre (SPGRC)		4658	
Niger	Institut national de la recherche agronomique du Niger (INRAN)		3445	
Senegal	Institut Sénégalais de Recherches Agricoles (ISRA)		1221	
Botswana	National Plant Genetic Resources Centre	166	506	
Ghana	CSIR-SARI Ghana		471	
Lesotho	National Plant Genetic Resources Center		435	
UAE	ICBA	319	318	
UK	Royal Botanic Gardens Kew/ Millennium Seed Bank, Wakehurst Place	9	244	

¹Juan Carlos Rossa (email correspondence Nov 9, 2021) reported that the number of accessions in 2007 was an error since there were no accessions of sorghum being conserved by the institute at that time.

Country	Institute	No. of accessions in 2007 strategy report	No. of accessions reported in 2021 survey	No. of accessions in consolidated global database
Sri Lanka	Plant Genetic Resources Centre, Gannoruwa	52	217	
Togo	Institut Togolais de Recherche Agronomique (ITRA)		212	
Namibia	Namibia National Plant Genetic Resources Center,		192	
Chad	Institut Tchadien de Recherche Agricole pour le Développement (ITRAD)		139	
Benin	Centre of Agricultural Research of the North West / National Institute of Agricultural Research of Benin (CRA-NO/INRAB)		95	
Spain	Spain Instituto Nacional de Investigacion y Tecnologia Agraria y Alimentaria. Centro Nacional de Recursos Fitogeneticos, INIA.	42	79	
Nepal	Nepal National Agriculture Genetic Resources Centre (NAGRC), Khumaltar	20	60	
Institutions that only responded to 2007 survey				
Global	ILRI	52		61
China	CAAS	18250		
Russia	VIR	7335		
Malawi	NPGRC	401		433
Serbia	Inst. Field and Vegetable crops	152		
Institutions where additional information was needed in 2007 and no response for 2021				
Mexico	INIFAP	3990		68
Japan	NIAR	2583		5053
Philippines	IPB/UPLB	2285		6
Thailand	Dept. of Ag Univ. of Kasetsart	1500		10
Colombia	CORPOICA	1290		1104
Rwanda	ISAR	1144		
Hungary	Institute for Agrobotany	1013		873
Guatemala	ICTA	823		
Bulgaria	Institute for PGR "K.Malkov"	569		1046
Pakistan	Inst. of Ag. Biotech. and GR	492		933
El Salvadore	Centa	406		25
Nicaragua	REGEN Universida Nacional Agraria	30		21
Somalia	Central Agricultural Research Station	94		
Yemen	American Sorghum Project	4000		

Annex III. Number of accessions conserved at ICRISAT for each Sorghum race and intermediate races for each country, region, biome or altitude in the diversity tree.

Country or Region	Biome or altitude	No. of accessions
<i>S. bicolor</i> subsp. <i>bicolor</i> race Guinea		
Somalia		0
Kenya		7
Ethiopia		15
Uganda		21
Sudan		39
Tanzania		405
Lesotho		1
Botswana		13
Swaziland		14
Rep. South Africa		21
Mozambique		45
Zambia		120
Zimbabwe		256
Malawi		259
Guinea-Bissau		0
Ivory Coast		0
Liberia		0
Chad		22
Gambia		46
Niger		72
Sierra Leone		107
Ghana		158
Benin		184
Senegal		190
Cameroon		205
Burkina Faso		414
Mali	All	481
Mali	Inner Niger Delta flooded Savanna	4
Mali	Sahelian Acacia Savanna (part of biome 7)	12
Mali	West Sudanian Savanna (part of biome 7)	375
Mali	Others or unknown	90
Nigeria	All	640
Nigeria	Tropical & Subtropical moist broadleaf forest	24
Nigeria	Montane grasslands & shrublands	31
Nigeria	Others or unknown	63
Nigeria	Tropical & Subtropical Grasslands, Savannas & Shrublands	522
India		772
Others Asia		21
Other countries		47
subrace margaritifera (based on local name kende)		50

Country or Region	Biome or altitude	No. of accessions
<i>S. bicolor</i> subsp. <i>bicolor</i> race Bicolor		
Central Africa	Tropical & subtropical grasslands, savannas & shrublands	6
Central Africa	Tropical & subtropical moist broadleaf forests.	1
Central Africa	Other or unknown	15
East Africa	Lowland (<1200 m)	54
East Africa	Midlands (between 1200 and 1600 m)	33
East Africa	Highlands (> 1600 m)	49
East Africa	Unknown altitude	222
Southern Africa	Tropical & subtropical grasslands, savannas & shrublands	7
Southern Africa	Montane grasslands & shrublands	5
Southern Africa	Desert & Xeric shrublands	1
Southern Africa	other or unknown	23
West Africa	Tropical & subtropical grasslands, savannas & shrublands	36
West Africa	Tropical & subtropical moist broadleaf forests.	0
Asia		463
China		19
India		329
Others Asia		115
<i>S. bicolor</i> subsp. <i>bicolor</i> race Caudatum		
Cameroon		1331
Central African Republic		60
Nigeria		161
Tchad		46
Burundi		107
Eritrea		0
Ethiopia	Highlands (> 1600 m)	120
Ethiopia	Midlands (between 1200 and 1600 m)	36
Ethiopia	Lowland (<1200 m)	77
Ethiopia	Unknown altitude	170
Kenya	Highlands (> 1600 m)	1
Kenya	Midlands (between 1200 and 1600 m)	26
Kenya	Lowland (<1200 m)	187
Kenya	Unknown altitude	530
Rwanda	Highlands (> 1600 m)	38
Rwanda	Midlands (between 1200 and 1600 m)	13
Rwanda	Lowland (<1200 m)	0
Rwanda	Unknown altitude	168
Tanzania	Highlands (> 1600 m)	0

Country or Region	Biome or altitude	No. of accessions
Tanzania	Midlands (between 1200 and 1600 m)	53
Tanzania	Lowland (<1200 m)	21
Tanzania	Unknown altitude	32
Uganda	Highlands (> 1600 m)	100
Uganda	Midlands (between 1200 and 1600 m)	271
Uganda	Lowland (<1200 m)	379
Uganda	Unknown altitude	353
Malawi		18
Somalia		11
Sudan		1027
West Africa		140
India		109
China		204
Others		183
other regions		240
<i>S. bicolor</i> subsp. <i>bicolor</i> race <i>Durra</i>		
Burundi		4
Eritrea		0
Ethiopia		1935
Kenya		5
Malawi		5
Rwanda		44
Somalia		424
Sudan		221
Tanzania		51
Uganda		11
Burkina Faso		22
Cameroon		398
Chad		10
Mali		69
Mauritania		30
Niger		87
Nigeria		32
Senegal		10
Egypt		5
Morocco		0
India		3347
Others		80
Central America		36
Other countries in the Americas		59
Middle East	Turkey, Yemen, Saudi Arabia, Syria, Iraq, Iran	350

Country or Region	Biome or altitude	No. of accessions
<i>S. bicolor</i> subsp. <i>bicolor</i> race <i>Durra-Caudatum</i>		
Burundi		3
Eritrea		0
Ethiopia		476
Kenya		34
Malawi		8
Rwanda		19
Somalia		3
Sudan		471
Tanzania		25
Uganda		51
Other countries in Africa		1159
Asia		412
Middle East		1344
Others regions/countries		173
<i>S. bicolor</i> subsp. <i>bicolor</i> race <i>Guinea-Caudatum</i>		
Burundi		11
Eritrea		0
Ethiopia		199
Kenya		104
Malawi		57
Rwanda		2
Somalia		2
Sudan		505
Tanzania		103
Uganda		244
Other countries in Africa		1702
Other countries outside Africa		455
<i>S. bicolor</i> subsp. <i>bicolor</i> race <i>Guinea-Durra</i>		
Burundi		0
Chad		1
Eritrea		0
Ethiopia		10
Kenya		2
Malawi		12
Nigeria		8
Rwanda		1
Somalia		0
Sudan		36
Tanzania		5
Uganda		1
Other countries in Africa		74
India		38
Other countries in Asia		10
Other countries		14

Annex IV. Expert consultation

Expert consultation for securing the long-term conservation and use of sorghum genetic resources globally; 23 September 2021 at 9:00–13:00 Eastern Time Zone (U.S.).

Background: The Crop Trust is updating the Global Sorghum Conservation Strategy, which was last done in 2007. In addition to the classical approach of surveying curators about their perspectives on collection quality, gaps, challenges, etc., we desire to bring together global leaders focused on the utilization of genetic resources and gain their perspectives on how to advance the value and usage of collections based on recent scientific progress in breeding, genetics, genomics, phenomics, data management and related disciplines.

The Consultation: We would like to address the following topics related to recent advances in the sciences of breeding, genetics and allied disciplines:

- A summary of cutting-edge science impacting how we think about populating, managing, enhancing and using collections in the 21st century.
- Feedback from users on *ex situ* collections in terms of accessibility, composition of collections accession-level information, etc.
- Input from users into the global needs for long-term conservation and use.
- Input from users on what should be improved to enhance conservation and distribution of research resources, tools, technologies and methods.
- Input on how to facilitate greater global collaboration and actions for scientific advancement and sharing of benefits from research and the use of germplasm.
- Highlight other critical issues for users in relation to strategic and effective and utilization of *ex situ* collections.

Agenda – 23 September

9:00–10:00: P Bramel

Highlights of the 2007 global conservation strategy

- Summary of the 2021 collections survey
- Composition of the current *ex situ* collections
- Security of conservation for sorghum genetic resources
- Constraints to use of conserved genetic resources
- Key points for our subsequent discussions
- Questions and discussion

Next sessions moderated by S Kresovich, with input from all consultation participants.

10:00–11:00: Current *ex situ* collection status for conservation and use: global perspectives

- What are the metrics of a “good” collection?
- What is working well in terms of composition of collections, accessibility of collections, accession-level information or the application of new tools?

List of Participants

Participant	Affiliation
Paula Bramel	Crop Trust
Stephen Kresovich	FtF Innovation Lab for Crop Improvement USA
Jura Magalhaes	EMBRAPA Brazil
Geoff Morris	Colorado State University USA
Sarah Hearne	CIMMYT Mexico
Mitch Tunstra	Purdue University USA
Diego Ortiz	EEA Manfredi Argentina
Clarisse Pulcherie	INERA/Saria Burkina Faso
Jean-Francois Rami	CIRAD France
Gilles Trouche	CIRAD France
Dr. Kuldeep Singh	ICRISAT India
Harish Gandhi	ICRISAT India
Santosh Deshpande	ICRISAT India
Mani Vetriventhan	ICRISAT India
Cyril Diatta	ISRA Senegal
M Elangovan	ICAR-IIMR India
El Tahir Ibrahim Mohamed	APGRC-ARC Sudan
Dr. Desterio Nyamongo	GERRI-KALRO Kenya
Gebisa Ejeta	Purdue University USA
Sally Norton	AGG Australia
Vania Azevedo	ICRISAT
Naoura Gapili	ITRAD Chad

- Where are the significant gaps or areas in need of improvement?
- How do we enhance progress and engagement of collections and researchers/breeders?

11:00–11:15: Break

11:15–12:00: Impacts of key scientific advancements on future sorghum conservation and use

- Opportunities?
- Challenges?
- What do curators need to know?
- How do we help curators be successful to secure conservation and increase use?

12:00w13:00: Identification of global actions needed for the scientific advancement and sharing of benefits from research and use of germplasm

Goals

- What are the roles and responsibilities?
- How do we maximize benefits for all?
- What are the next steps for global efforts to link and enhance sorghum conservation and use?

13:00: Final comments and adjournment

Annex V. Selected metrics for sorghum and maize (as comparison)

This summary was prepared by Felix Frey, International Consultant for the Crop Trust.

Khoury et al. (2021) compiled a comprehensive crop-based dataset as part of a project funded by the International Treaty on Plant Genetic Resources for Food and Agriculture and the Crop Trust, led by the International Center for Tropical Agriculture (CIAT). The aim was to develop five normalized, reproducible indicators that can provide an evidence base to prioritize actions with respect to the conservation and use of crop genetic resources for food and agriculture. The indicators incorporate metrics associated with the following domains:

1. USE of genetic diversity of a crop;
2. INTERDEPENDENCE between countries with respect to genetic resources of each crop;
3. DEMAND for genetic resources of the crop;
4. SUPPLY of genetic diversity; and
5. SECURITY of genetic resources conservation.

The results are publicly available on an interactive online website. To generate the five indicators, Khoury et al. (2021) collected comprehensive data from multiple sources. In the following, we do not present the indicators created by Khoury et al. (2021), but discuss the underlying raw data to shed light on the different aspects represented by the indicators.

To put the sorghum numbers in context, we compared the crop with maize (Table 1). These two crops are comparable with respect to type of growth, propagation and use (both are at least partly outcrossing cereals).

The metrics for “Global production”, “Food supply” and “Quantity exported globally” from the indicator domain USE are annual average values drawn from FAOSTAT data (FAOSTAT, 2019) between 2010 and 2014. The percentage of countries producing and consuming the crop is calculated as the number of countries where the crop is within the top 95% of most important crops, divided by the total number of countries reporting. The global production of sorghum is about 59 million tons annually, which is 6% of global maize production (about 918 M t). The average global consumption of sorghum is about 10 g/cap/day, about 20% that of maize (49 g/cap/day). Sorghum’s contribution to food supply is thus relatively high, compared with its production. Considering the low global production of sorghum compared with maize, the percentage of countries producing sorghum is relatively high, 50% of reporting countries. In comparison, maize is produced in 81% of the world’s countries. Maize is consumed in 99% of all the countries in the world, whereas sorghum is consumed in only 31% of all countries. Both maize and sorghum are interna-

tionally traded crops, about 11% (sorghum, 6 M t) and 13% (maize, 121 M t) of their total production being exported.

The crop USE metrics with respect to research were assessed by manual searches on Google Scholar, searching for the respective genus or species in the titles of publications, including patents and citations, between 2009 and 2019 (Khoury et al. 2021). Google Scholar search hits represent importance with respect to scientific interest in a crop. The *Sorghum* genus was found in 15,800 publication titles, almost as many as the publication titles including the maize genus *Zea*. However, we must take into account that the genus and common name of sorghum are both “sorghum” and thus the number of publication titles including “sorghum” represent both. In contrast, the common names of maize are “corn” and “maize”, whereas the scientific genus name is “*Zea*”. Thus, numbers for the two crops are not comparable. Publications with titles including the species names *S. bicolor* and *Z. mays* are more comparable. *Sorghum bicolor* appears in 4,550 publication titles, whereas *Zea mays* is included in 16,300 titles. In a research context, therefore, sorghum receives about 28% of the attention of maize. If related to production, sorghum research is overrepresented relative to maize research.

Khoury et al. (2021) defined INTERDEPENDENCE as a measure of the degree to which the crop is grown outside its center of diversity. Primary centers of diversity are represented by 23 agro-ecological zones (Khoury et al. 2016). Interdependence is high in crops that originated from a small area and are cultivated and used globally. For production, interdependence is calculated by dividing a crop’s production outside of its primary center of diversity by global production. If all production is outside the primary center of diversity, interdependence would be 100%. For food supply, interdependence is calculated by dividing the crop’s contribution to food supply by the world average. Food supply outside primary regions of diversity can be higher than that inside, and thus also be higher than the global mean. Therefore, interdependence with respect to food supply can exceed 100%. Primary centers of diversity of sorghum are located in Central, South, West and East Africa. As African countries like Nigeria, Ethiopia and Sudan are strong sorghum producers, interdependence of global production is 62%, which is relatively low compared with maize. The interdependence value for maize is 97%, since the primary centers of diversity are in Central America and Andean South America and the main producers are USA and China. The interdependence of food supply

Table 1. Selected metrics collected by Khoury et al. 2021 for sorghum and maize, subdivided by indicator domain.

Metric	Sorghum	Maize	Sorghum / Maize
Crop use			
Global production [tons]	58,927,804	917,517,036	6%
Food supply (Amount consumed) [g/capita/day]	10	49	20%
Percentage of countries producing crop *	50%	81%	62%
Percentage of countries consuming (being supplied with) crop *	31%	99%	32%
Quantity exported globally [t]	6,378,373	120,837,238	5%
Number of publications between 2009–2019, including patents and citations, searching title of publication (Google scholar search hits) for genus **	15,800	16,400	96%
Number of publications between 2009–2019, including patents and citations, searching title of publication (Google scholar search hits) for species ***	4,550	16,300	28%
Interdependence			
Interdependence of global production from germplasm from primary centers of diversity [0-1] ****	62%	97%	64%
Interdependence of global food supply from germplasm from primary centers of diversity [0-1] ****	41%	89%	46%
Demand			
Accessions distributed from genebanks (Annual average 2014–2017)	23,465	49,148	48%
Variety releases in 5 years (2014–2018)	4,683	126,232	4%
Supply			
Number of accessions in <i>ex situ</i> collections of genus **	169,377	213,337	79%
Number of accessions in <i>ex situ</i> collections of species ***	163,242	208,062	78%
Accessions of the genus ** available through Multilateral System (MLS) directly noted in databases [%]	0%	20%	
Accessions of the species *** available through Multilateral System (MLS) directly noted in databases [%]	0%	20%	
Accessions of the genus ** available through Multilateral System (MLS) indirectly by matching institute countries with party status [%]	95%	69%	
Accessions of the species *** available through Multilateral System (MLS) indirectly by matching institute countries with party status [%]	95%	69%	
Security			
Accessions of genus ** safety duplicated in Svalbard Global Seed Vault [%]	23%	15%	
Accessions of species *** safety duplicated in Svalbard Global Seed Vault [%]	24%	15%	
1-GINI index for equality of production across the world [0-1] *****	0.05	0.03	131%
1-GINI index for equality of food supply across the world [0-1] *****	0.05	0.15	31%

* Counting countries which list the crop as within top 95 % (FAOSTAT); Calculated as: Number of countries counting crop (top 95%) / Total number of countries (production 216, food supply 175)

** Sorghum: Sorghum; Maize: Zea

*** Sorghum: Sorghum bicolor; Maize: Zea mays

**** Global metric / Metric at primary center of diversity

***** Relative equality of crop use across world regions (same regions as used in interdependence domain), high equality give high indicator value

from sorghum per capita is, at 41%, much lower than interdependence with respect to production (62%, as stated above). This implies that most sorghum is consumed as a food source locally within Africa, whereas a greater share of sorghum produced outside Africa is used for non-food purposes.

The DEMAND for germplasm is defined by two metrics (Khoury et al. 2021). First, by the number of distributions of accessions by genebanks, as an annual average between 2014 and 2017. This information is drawn from the Plant Treaty's Global Information System. Second, by the number of varieties released during the 5 years between 2014 and 2018, obtained from the [International Union for the Protection of New Varieties of Plants \(UPOV\)](#). There is relatively strong use of sorghum germplasm, reflected by the 23,465 sorghum accessions per year distributed by genebanks (about half of yearly distributions of maize accessions, 49,148). However, this is in contrast to the relatively low development of sorghum cultivars. Only 4,683 varieties of sorghum were released during a 5-year period, which represents only 4% of the maize varieties released in the same time period (126,232 varieties).

Khoury et al. (2021) illustrated the SUPPLY of germplasm with the number of accessions available in *ex situ* collections around the world. Furthermore, Khoury et al. (2021) assessed the number of accessions available under the [Multilateral System \(MLS\) of the Plant Treaty](#). According to various databases, global *ex situ* collections harbor 169,377 accessions of the genus *Sorghum*, including 163,242 accessions of the species *S. bicolor*. These numbers are relatively high given that global maize collections harbor 213,337 *Zea* and 208,062 *Z. mays* accessions. Both sorghum and maize are in Annex I of the Plant Treaty.

The SECURITY of germplasm conservation is represented with two metrics: Safety duplication status at the Svalbard Global Seed Vault (SGSV); and the equality of global distribution with respect to several crop use metrics. To calculate the percentage of safety duplicated germplasm, the numbers of accessions safety duplicated with respect to genus and species listed at the [SGSV website](#) were divided by the total number of accessions stored in global *ex situ* collections (see above). To represent the equality of distribution across different agro-ecological regions of the world (Khoury et al. 2016), Khoury et al. (2021) used the reciprocal 1-Gini index with respect to the different crop use metrics. The Gini index (2008) is the most commonly used inequality index, and is best known for its use in quantifying global income inequality. The 1-Gini index, presented here, ranges

from 0 to 1, where 0 reflects a completely unequal distribution across world regions, and 1 represents a perfectly equal global distribution of the respective metric across the worlds' regions. This reflects the security of crop cultivation and use, where, for example, small levels of production and geographical restriction go hand in hand with a higher vulnerability of supply, such as in cases of natural disasters. A relatively high number of sorghum accessions are safety duplicated at the SGSV (about 23% of the total), compared to 15% of all *ex situ* maize accessions. The equality of distribution across the worlds' regions with respect to global production is 0.05 for sorghum, higher than that for maize (0.03). This is in contrast to the higher percentage of countries in the world producing more maize than sorghum. Thus, sorghum production is distributed more equally across regions, while maize production is concentrated in particular areas. For equality of the distribution of food supply, there is a contrasting situation. The value for sorghum (0.05) is lower than that for maize (0.15), indicating that the food supply from maize is more equally distributed throughout the world.

Literature cited

FAOSTAT 2019. Statistics for 2010-2014. www.fao.org. Accessed 2019.

Gini Index. 2008. In: [The Concise Encyclopedia of Statistics](#). Springer, New York, NY.

Khoury, C.K., Sotelo, S., Amariles, D., Guarino, L., Toledo A. 2021 A global indicator of the importance of cultivated plants, and interdependence with regard to their genetic resources worldwide. *Forthcoming*

Khoury, C., Sotelo, S., Amariles, D. 2019. The plants that feed the world: baseline information to underpin strategies for their conservation and use. *International Treaty on Plant Genetic Resources for Food and Agriculture (Rome) Project 2018 – 2019*.

Khoury, C.K., Achicanoy, H.A., Bjorkman, A.D., Navarro-Racines, C., Guarino, L., Flores-Palacios, X., Engels, J.M., Wiersema, J.H., Dempewolf, H., Sotelo, S., Ramírez-Villegas, J. 2016. Origins of food crops connect countries worldwide. *Proceedings of the Royal Society B: Biological Sciences*. 283(1832):20160792. doi:10.1098/rspb.2016.0792

Khoury, C.K., Achicanoy, H.A., Bjorkman, A.D., Navarro Racines, C., Guarino, L., Flores Palacios, X., Engels, J.M.M., Wiersema, J. H., Dempewolf, H., Ramírez-Villegas, J., Castañeda-Álvarez, N.P., Fowler, C., Jarvis, A., Rieseberg, L.H., Struik, P.C. 2015. Estimation of countries' interdependence in plant genetic resources provisioning national food supplies and production systems. *The International Treaty, Research Study 8*.



GENERAL CONTACT
+49 (0) 228 85427 122
info@croptrust.org

THE CROP TRUST
Platz Der Vereinten Nationen 7
53113 Bonn, Germany

MEDIA CONTACT
+49 (0) 228 85427 141
media@croptrust.org