



# GLOBAL STRATEGY FOR THE CONSERVATION AND USE OF PEANUT GENETIC RESOURCES

With support from



Federal Ministry of Food and Agriculture

## COVER

Illustration of parts of *Arachis hypogaea* plant. Source: Franz Eugen Köhler, [Köhler's Medizinal-Pflanzen](#), Volume III, 1898

## DISCLAIMER

This document, developed with the input of a large number of experts, aims to provide a framework for the efficient conservation and effective use of globally important collections of peanut genetic resources. The Global Crop Diversity Trust (the Crop Trust) provided support for this initiative and considers this document to be an important context 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 January 2022, is expected to continue to evolve and be updated as circumstances change or new information becomes available. In case of any specific questions or comments, please direct them to the strategy coordinator, David E. Williams, [reddog.williams@gmail.com](mailto:red dog.williams@gmail.com).

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## EXECUTIVE SUMMARY

Peanut, also known as groundnut, is one of the most widely cultivated food legumes in the world. Native to South America, peanut is now grown in nearly every country with a tropical or sub-tropical climate. On the global market, peanut is valued as an industrial oilseed and a delicious, high-protein food commodity. It is also a nutritious subsistence crop, vital to the food security and culinary traditions of countless small-holder farmers and rural communities throughout the tropics. World peanut production continues to rise, currently approaching 50 million metric tons per year, with China and India being the largest producers.

The peanut's genepool is complex, consisting of the cultigen (*Arachis hypogaea* L.) with its many landraces and improved varieties, as well as the more than 83 wild species of the genus *Arachis* – including some newly discovered species soon to be described, and certainly other wild species yet to be discovered. Cultivated peanut is an allotetraploid ( $2n=4x=40$ ) derived from the natural hybridization of two wild diploid species, followed by the spontaneous polyploidization of the hybrid and its subsequent domestication by Neolithic proto-farmers 6–10,000 years ago. The combined effects of polyploidization and domestication are believed to have created an evolutionary bottleneck which severely restricted the genetic base of the cultigen. This genetic base has been reduced

even further in modern commercial varieties that have been bred from a rather limited suite of parental lines. The resulting narrowness of the peanut's genetic base poses a risk to global peanut production, which is already vulnerable to a long list of pests and diseases, as well as climate change. Consequently, the much broader genetic diversity existing, not only in the peanut's less-common botanical varieties and landraces, but also in the many wild species of the genus *Arachis*, is of great value and importance for peanut improvement.

Cultivated peanut is classified into two subspecies, subsp. *fastigiata* and subsp. *hypogaea*, based on the presence or absence of flowers on the main stem and other distinguishing traits. The two subspecies are further divided into six botanical varieties (subspecies *hypogaea* comprised of var. *hypogaea* and var. *hirsuta*; and subspecies *fastigiata* comprised of var. *fastigiata*, var. *vulgaris*, var. *peruviana*, and var. *aequatoriana*) based on a range of morphological and physiological characteristics. Each botanical variety, in turn, is comprised of an abundance of local landraces, representing a rich source of agro-morphological variation within the crop's primary genepool.

Today, the number of wild and cultivated *Arachis* accessions conserved *ex situ* in germplasm collec-

tions total nearly 90,000 samples worldwide, which includes extensive redundant duplication of accessions across collections. The six largest collections of *Arachis* germplasm are currently maintained by (1) the International Crop Research Institute for the Semi-Arid Tropics (ICRISAT) in India; (2) the Indian Council of Agricultural Research (ICAR) in India; (3) the US Department of Agriculture (USDA) in the United States; (4) the Oil Crops Research Institute of the Chinese Academy of Agricultural Sciences (OCRI-CAAS) in China; (5) the Texas AgriLife Research Center of Texas A&M University (TAMU) in the United States; and (6) the Empresa Brasileira de Pesquisa Agropecuária (EMBRAPA) in Brazil. Additional *Arachis* collections containing unique materials are also maintained by several national, regional and international organizations around the world.

The current global system for conserving peanut genetic resources is quite large in terms of the numbers of institutions and germplasm accessions held, but as a system it is not entirely secure, efficient or rational. Most *Arachis* collection holders report a variety of persistent challenges, gaps and vulnerabilities that threaten the germplasm's conservation, hamper its study, and limit its use. Much of the genetic diversity existing within the peanut's botanical varieties and traditional landraces remains unstudied and uncollected, while it undergoes relentless genetic erosion and loss in smallholders' fields around the world. Similarly, the wild *Arachis* species, many of whose natural populations in South America are imminently threatened with extinction, are poorly represented in most genebanks, if at all. Safeguarding the full spectrum of peanut genetic diversity will require a concerted international effort, involving a combination of both *ex situ* and *in situ* conservation approaches, within the context of an integrated global strategy.

The *Global Strategy for the Conservation and Use of Peanut Genetic Resources* was developed "virtually" during the second half of 2020 and early 2021, at the height of the global COVID-19 coronavirus pandemic. The Strategy's structure and development process followed the Standard Model Outline for Global Crop Strategies, provided by the Crop Trust. An International Advisory Group (IAG) of eight peanut experts was formed to help guide the Strategy's development and validate its content. This document is based upon an analysis of information retrieved from global

genetic resources databases, the responses to an online survey of genebank managers, and a review of current scientific literature. The online survey consisted of a detailed questionnaire that was distributed to the managers and/or curators of more than 80 genebanks worldwide that are known, or reported in WIEWS, to maintain *Arachis* collections. Responses to the online survey were received from 27 genebanks, including most of the largest and strategic, or "key," germplasm collections. Together, these collections maintain over 72,000 accessions, or about 80% of the estimated total of *Arachis* germplasm samples conserved *ex situ* worldwide. The up-to-date information provided by the participating genebanks served as the foundation for the conclusions and recommendations presented in this Strategy.

The germplasm holdings, conservation methods, distribution policies, and challenges faced by these key germplasm collections are briefly described in the context of their potential role in the implementation of a Global Peanut Conservation Strategy. This document explores options and opportunities for the many institutions holding peanut germplasm collections around the world, as well as the countries where wild *Arachis* populations occur, to engage in more effective partnerships through their eventual integration into a rational global system for *Arachis* genetic resources conservation and use.

Salient issues and recommendations for priority strategic actions include:

1. Regeneration and characterization of unidentified materials currently conserved *ex situ*;
2. Filling outstanding taxonomic, genetic, and ecogeographic gaps in the collections;
3. Adopting updated documentation standards and a common data-sharing platform;
4. Security duplication of germplasm collections;
5. Addressing outstanding training and staffing needs;
6. Integration of complementary *in situ* and *ex situ* conservation approaches;
7. Promoting greater inter-institutional collaboration through partnerships and networking;
8. Initiating policy dialogues on issues impeding peanut germplasm exchange and use; and
9. Mobilization of a coordinating committee to guide the implementation of the Strategy.

# 1 INTRODUCTION

The Global Crop Diversity Trust (Crop Trust) is an international organization working to safeguard crop diversity through long-term *ex situ* conservation in genebanks. Since 2006, the Crop Trust has hired crop specialists to work with crop conservation communities to develop global *ex situ* conservation strategies for key global food crops and their wild relatives, including internationally important commodities such as coffee and tea. Global conservation strategies facilitate a transition from a complex, fragmented and independent national or local crop conservation system to a more integrated, collaborative and cooperative global conservation system.

*Arachis hypogaea* L., also known as groundnut, but hereafter peanut, is one of the most commercially important and widespread food legumes in the world. Cultivated throughout the tropics and subtropics as an industrial oilseed and a high-protein food for direct consumption, peanut makes a significant contribution to global nutrition and food security. Breeding efforts of past decades achieved noteworthy improvements in peanut yields, oil content and nutritional quality, as well as resistance or tolerance to numerous biotic and abiotic stresses. However, progress in peanut breeding has plateaued in recent years due to the peanut's relative lack of genetic variability (compared to other crops), and the reproductive barriers that complicate the incorporation of desirable traits from related wild *Arachis* species. Since 1994, huge strides have been made in the fields of peanut taxonomy, genetics, and genomics which have greatly improved our understanding of the crop's evolution, domestication, and the genetic affinities with and among its wild relatives. This knowledge, enabled by significant recent advances in biotechnology and genomics, is opening up an exciting new chapter of peanut improvement opportunities that are beginning to make the broad range of valuable genetic diversity present in the crop's secondary genepool available to breeders.

## 1.1 Rationale

A large amount of the peanut's genepool is already being conserved in different genebanks around the world, with each collection having its particular objectives, strengths, and challenges. While a great deal of duplication of accessions exists amongst genebanks, most collections contain some unique materials. However, not even the largest collections encompass the full range of *Arachis* diversity, neither of the domesticated peanut, nor of its related wild species. A significant proportion of the peanut genepool still remains

uncollected, undiscovered and/or unprotected, either in remote wilderness areas of South America, or in the cultivated plots of traditional smallholder farmers in rural areas of Latin America, Africa and Asia. Moreover, the implementation (or non-implementation) of various national and international policy regimes governing the access and exchange of *Arachis* germplasm currently presents a confusing, often lopsided and sometimes conflicting legal scenario that severely hampers international collaboration and restricts the exchange of materials, information, and expertise. This document provides an update on the current status of *Arachis* germplasm conservation and use worldwide, identifies outstanding gaps and research priorities, and proposes an action plan to guide and facilitate greater collaboration and efficiency through participation in a more effective global system for the conservation and sustainable use of peanut genetic resources.

## 1.2 Objectives

1. An assessment of the peanut germplasm collections of greatest national, regional and global importance in terms of their size, the extent and nature of their genetic diversity and geographic coverage, their standards of conservation and documentation, and the current availability and use of their accessions.
2. A global assessment of outstanding gaps in the germplasm collections, predominant impediments to both *ex situ* and *in situ* conservation, current research priorities, prevailing policy constraints, and opportunities to achieve greater efficiency and impact through partnerships.
3. An outline of a practical, evidence-based global strategy for improving the conservation and use of peanut genetic resources, with recommendations for priority actions and key partnerships.

## 1.3 Process of developing the Global Peanut Conservation Strategy

The development of this strategy was facilitated by the Global Crop Diversity Trust (Crop Trust) within the context of the ongoing project, *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 project is supported by the German Government (BMEL-BLE) in partnership with the Secretariat of the International Plant Treaty (ITPGRFA) in an effort to revise and update some of the 26 global crop conservation strategies produced between 2006 and 2019, as well

as to develop a number of strategies for a new set of crops or crop groups. Following the outcome of the project's initiation meeting in October 2019 in which crop experts from around the world participated, peanut was one of the crops/crop groups chosen for the development of a new global conservation strategy. An independent consultant, David E. Williams ([reddog.williams@gmail.com](mailto:reddog.williams@gmail.com)), was contracted in June 2020 to coordinate the development of a Global Strategy for the Conservation of Peanut Diversity (*Arachis* spp.).

Due to travel restrictions imposed by the global COVID-19 pandemic, it was not possible to convene an international meeting of peanut experts to engage in a strategy development workshop, as was typically done in the preparation of earlier global crop strategies. In light of the prevailing circumstances, the following steps were undertaken in the development of the present draft *Global Strategy for the Conservation of Peanut Diversity*:

1. A *Standard Model Outline for Crop Strategies*, developed for the Crop Trust in 2019, was used to guide the structure, content and format of the Global Peanut Conservation Strategy.
2. National and international collections of peanut germplasm were identified through online searches of public databases, including those managed by FAO (WIEWS), Crop Trust (Genesys), and USDA (GRIN-Global). For information on the status of peanut conservation and use at the global level, the Second Report of the State of the World's Plant Genetic Resources for Food and Agriculture (FAO 2010) was consulted. For additional information regarding peanut conservation and use at the regional level, eight Regional Conservation Strategies for plant genetic resources were also consulted: The Americas; West and Central Africa; Eastern Africa; Southern Africa; West Asia and North Africa; Central Asia and the Caucasus; and South, Southeast and East Asia.
3. An International Advisory Group (IAG), consisting of eight prominent international peanut collection curators, geneticists, breeders and plant explorers, was formed to provide expert guidance and contribute to the development of this strategy. A list of the IAG members with their affiliations and contact information is provided as Annex 1.
4. A literature review was conducted to capture foundation references as well as recent research developments in the prehistory, evolution, taxonomy, genetics and genomics, utilization, and conservation of peanut genetic resources worldwide.
5. A survey questionnaire was developed to send to peanut germplasm collections around the globe for the purpose of gathering basic, up-to-date information on the numbers and types of accessions held, the conditions under which they are stored, their accessibility, and the uniqueness, perceived gaps, and research priorities associated with the collection. The survey questionnaire is presented as Annex 2. The questionnaire was uploaded to the SurveyMonkey online survey platform. Invitations to participate and the link to the online survey were sent on 15 August 2020 to the curators of 84 peanut germplasm collections reported in WIEWS as having at least 100 accessions of *Arachis*. By the cutoff date of 30 October 2020, a total of 27 responses to the online survey were received, of which 24 were complete. The organizations that contributed to the strategy development process by completing the online survey questionnaire are listed in Annex 3. The survey results were compiled and analyzed and formed the primary basis for Section 3 (Current Status of *Ex Situ* Conservation), and informed the conclusions and recommendations presented in this document.
6. Based on the information recovered from the literature review and the survey analysis, together with the consultant's personal experience and specific inputs from IAG members, draft texts for Section 1 (Introduction), Section 2 (Crop Overview), Section 3 (Current Status of *Ex Situ* Conservation), and Section 5 (Global Strategy) were prepared. A draft text of Section 4 (Current Status of *In Situ* Conservation) was prepared by Ehsan Dulloo under a separate agreement with the Crop Trust, and incorporated information and orientation provided by D. Williams. Section 5 (Global Peanut Conservation Strategy) was formulated to identify and describe (a) the most pressing research and development challenges, (b) priority actions that address those challenges, and (c) key partnerships that can implement an action plan that will facilitate more efficient and effective conservation and use of peanut genetic resources within the context of a global system.
7. Early drafts of the document were shared with managers at the Crop Trust in November and December 2020 for their observations and recommendations. After incorporating the recommendations received from the Crop Trust, a consolidated first draft of the Global Peanut Conservation Strategy document was sent to the eight members of the IAG for their comments, corrections, recommendations and additions.
8. Expert inputs from the IAG members were received in February, March, and November 2021 and were incorporated into the document. A final draft of the Global Peanut Conservation Strategy was reviewed by the Crop Trust in September 2021, and a revised final manuscript was prepared and submitted to the Crop Trust in January 2022 for final approval, layout and publication.



## 2 CROP OVERVIEW

The peanut (*Arachis hypogaea* L.), also known as groundnut, is a grain legume native to South America. The peanut is believed to have originated in the area of southern Bolivia and northwestern Argentina, as a result of a fortuitous hybridization of two wild diploid species, that then underwent spontaneous polyploidization, producing the allotetraploid species *A. hypogaea* ( $2n=4x=40$ ). The novel allotetraploid species subsequently became domesticated sometime between 6,000 and 10,000 years ago (YBP) through its interactions with incipient agriculturalists living around the present-day frontier between southeastern Bolivia and northern Argentina (Bertioli et al. 2016, 2021; Fávero et al. 2006; Grabile et al. 2012; Seijo et al. 2007). From this center of origin, the crop eventually spread throughout the Neotropics, where it evolved and diversified in response to not only the different ecogeographic conditions it encountered, but also the anthropocentric selection pressures it received over time from the multitude of human cultures and civilizations that adopted and modified it along the way. As a result of the peanut's extensive prehistoric dispersion throughout South and Central America and the Caribbean, an astonishing amount of phenotypic diversity arose in the form of two distinct subspecies, six botanical varieties, and many hundreds of local landraces.

### 2.1 Prehistoric evidence

Archeological evidence provides important information for establishing the peanut's early dispersal, and longstanding importance for different pre-Hispanic

cultures and civilizations. The arid conditions of northern Peru's coastal region are conducive to the long-term preservation of human and plant remains, and numerous examples of early peanut cultivation and use have been discovered there. Excavations of preceramic sites in the Ñanchoc Valley of northern Peru produced evidence of apparent peanut cultivation with radiocarbon dates from around 8,000 YBP (Dillehay et al. 2007), although the peanut fragments recovered there appear more like wild *Arachis*. The peanut species encountered in this excavation was probably introduced from the eastern side of the Andes mountains, and may represent an introduced wild species in an early stage of domestication.

The earliest unequivocal evidence of domesticated peanut (*A. hypogaea*) comes from Peru, where remains of cultivated peanuts were recovered from Los Gavilanes, a coastal site dating from ~3,500–4,500 YBP, and from the Huarmey Valley dating from around 5,000 YBP (Bonavia 1982, Pearsall 1992, Hammons et al. 2016). Much later, during the Early Intermediate Period of the Moche civilization (2,200 – 1,140 YBP), peanuts had attained special status as an elite food consumed by high-ranking individuals at ceremonial feasts. Peanuts were a recurrent theme in the finely executed polychrome ceramic dishes, jars and other artistic objects for which the Moche are well known (Figure 2.1). Peanuts also played an important role in Moche funerary practices for high status individuals, where offerings of actual peanuts were included as



Figure 2.1 Stirrup Spout Bottle with Peanut Figure, 5th–7th century, Moche culture, Peru. Photo: The Metropolitan Museum of Art

ritual food for the deceased's journey to the after-world. These burials were frequently accompanied by a variety of artistic peanut representations such as peanut-themed funerary vases, ceramic peanut pendants molded from peanut pods, and peanut jewelry skillfully crafted from precious metals. The most notable of these is the gold and silver peanut necklace that formed part of the lavish personal adornments recovered from the tomb of the Moche Lord of Sipán (Alva and Donnan 1993, Masur et al. 2020).

Funerary practices involving peanuts were also discovered further south, on the Argentina-Chile border, where well-preserved peanut pods and seeds were discovered among the mummified remains of three children who had been ritually sacrificed on a mountain peak at 6,715 m elevation, dating from the last days of the Inca empire, sometime between 1471 and 1532 AD (Krapovickas and Vanni 2009). In North America, remains of fully domesticated peanuts, dating from as early as 2,200 YBP, were recovered from archeobotanical excavations of dry caves in the Tehuacan Valley of central Mexico (Smith 1967), reflecting the broad extent of the cultigen's dissemination in early prehistoric times.

By the time of the arrival of the first Europeans in the New World, the peanut was widely known and cultivated throughout the tropical and sub-tropical regions of the Americas.

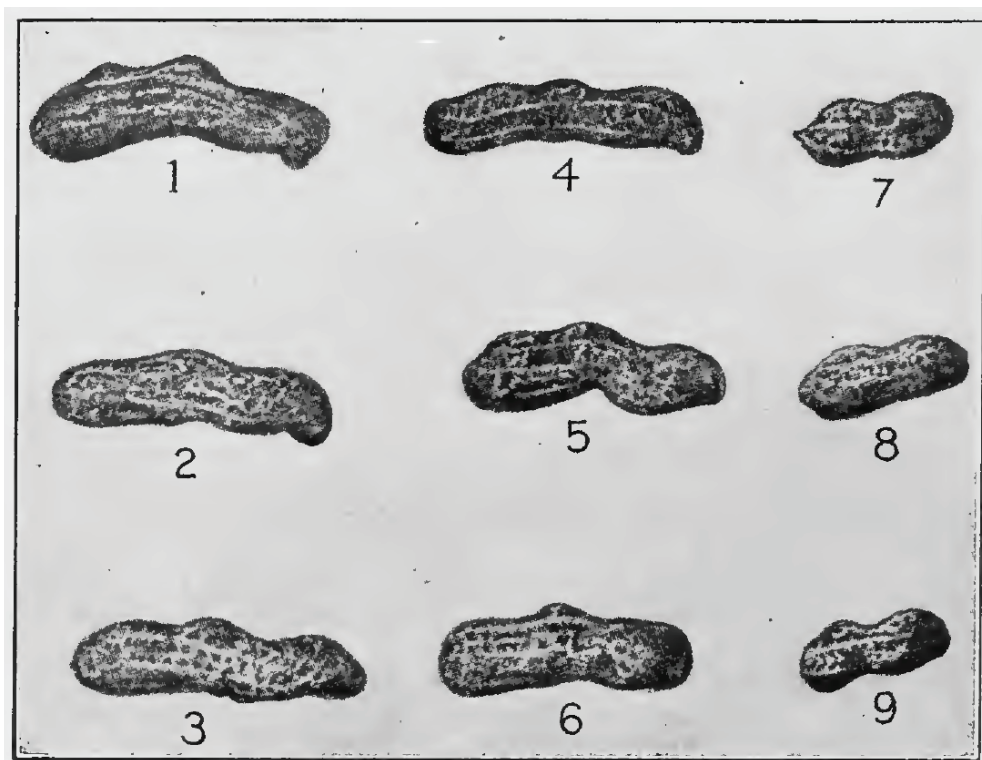
## 2.2 Colonial history and dissemination

Christopher Columbus, during his initial voyage to the New World in 1492, became the first European

to encounter the peanut when he visited the north-west coast of Hispaniola, in what is now Haiti (Fuson 1987). Soon thereafter, early Spanish and Portuguese explorers reported peanuts being cultivated by native peoples on several of the islands of the West Indies, in Mexico, on the northeast and east coasts of Brazil, in the warm lands of the Rio de la Plata basin, and extensively in Peru. From these regions, the peanut was disseminated by early Spanish and Portuguese traders to Europe, and along the coasts of Africa, Asia, and the Pacific Islands (Hammons et al. 2016).

Peanut was introduced to West Africa from Brazil by Portuguese traders in the 16<sup>th</sup> century (Hammons et al. 2016). The acceptance of the peanut by African farmers was undoubtedly facilitated by the existence there of the Bambara groundnut (*Vigna subterranea*), an analogue of the peanut already cultivated widely in Africa at the time. The pre-existence of a native, geocarpic leguminous cultigen clearly favored the peanut's rapid expansion across the continent, where it may well have displaced traditional Bambara groundnut cultivation in many areas (Williams 2004). In the centuries following its introduction, the peanut became fully integrated into subsistence farming systems and various ethnic African cuisines, causing the crop to diversify into dozens of distinct African landraces.

In Asia, the peanut was first introduced into south-eastern China (Fujian) early in the 16<sup>th</sup> century, evidently by Portuguese traders, after which the crop spread rapidly throughout the warmer, southern regions of the country where it became widely



**Figure 2.2** Types of peanuts taken at random from: (1) tombs at Ancon, Peru, (2) Java, (3) Tonkin, (4) Madagascar, (5) Madagascar, (6) Spain, (7) Dahomey, (8) Senegal, and (9) Spain. Based entirely upon the illustrated pod morphology and the geographic origins provided, examples (1) through (5) almost certainly represent var. *hirsuta* types; example (6) represents a "Valencia" market type; example (7) is most likely a "Runner" market type; example (8) appears to be a "Virginia" market type; and example (9) shows a typical "Spanish" market type. Illustration from R.A. Waldron, 1918, p. 308, Figure 3 (after Dubard 1905)

adopted and cultivated (Ho 1955). The activity of the “Manila Galleons,” a transpacific trade route with regularly scheduled voyages sustained by the Spanish crown from 1565 to 1815, enabled a constant flow of materials and culture between the New World ports of Lima, Peru, and Acapulco, Mexico, and Manila, the Philippines, a gateway to the Orient. Throughout this 250-year period, the Manila Galleons were instrumental in introducing numerous American crops and crop varieties to southeast Asia. Among these were peanut landraces of the botanical variety *hirsuta*, which became known as “dragon-type” peanuts in China. These distinctive “dragon” peanuts were also introduced to Indonesia, from where they were evidently carried to Madagascar by the Indonesian settlers of that East African island (Krapovickas 1998).

There has been some debate regarding the peanut’s introduction to India, but the most credible accounts suggest that the crop was introduced, via the Philippines, to the South Arcot district of Madras State (now Tamil Nadu) sometime during the 18<sup>th</sup> century, either directly by Portuguese traders or as a result of the Manila Galleons (Talawar 2003). Badami (1936) found a close resemblance between the indigenous [*sic*] peanut he found growing in Mysore and herbarium specimens he examined at the Royal Botanic Gardens, Kew, from South America, the Philippines, China and Java, which could all have corresponded to the distinctive, easily recognizable pod and leaf morphology of the botanical variety *hirsuta* (see Figure 2.2).

The first successful introductions of peanut to the United States most likely came directly from West Africa on ships carrying enslaved people to the colonial southeastern seaboard, sometime during the late 17<sup>th</sup> or 18<sup>th</sup> century, although the exact time and place of its introduction there was not documented (Hammons et al. 2016).

## 2.3 Modern cultivation and use

Today, peanut is the most widespread grain legume in the world, cultivated as an oilseed and food crop in 111 countries throughout the tropics and sub-tropics, with a total commercial production approaching 49 million metric tons in 2019 (FAOSTAT 2021). The world’s 10 largest producers of in-shell peanuts are shown in Table 2.1. Khoury et al. (2021) compiled a series of indicators and metrics for a number of economically important crops, including peanut, a summary of which are presented in Annex 4 of this document. In the latter part of the 20<sup>th</sup> century, a few wild *Arachis* species, particularly *A. pinto* and *A. glabrata*, have been cultivated as groundcover and forage species, and improved varieties have been developed and distributed commercially around the world.

## 2.4 Genetic diversity and genetic resources

### 2.4.1 Biology

The genus *Arachis* belongs to the Fabaceae (pea) family, and currently consists of 83 described species, all of which are endemic to southern South America, where the ranges of its wild species are limited to five countries: Argentina, Bolivia, Brazil, Paraguay, and Uruguay (Table 2.2). Wild *Arachis* species may be annual or perennial, and are typically diploid ( $2n=2x=20$ ), although a few aneuploid ( $2n=2x=18$ ) and tetraploid ( $2n=4x=40$ ) species are known. The wild species are variously adapted to diverse and harsh conditions that range from wetlands or seasonally inundated areas with heavy soils, to dry environments with deep sand or rocky soils (Simpson et al. 2001, Bertioli et al. 2011). They are widely distributed across their natural range in South America, a vast area stretching from the foothills of the Bolivian and Argentine Andes in the west, to NE Brazil and along the Atlantic coast from SE Brazil to southern Uruguay (Valls et al. 1985, Krapovickas & Gregory 1994, 2007).

All *Arachis* species are characterized by geocarpy, that is, the underground development of their fruits and seeds. While having aerial flowers typical of papilionaceous legumes, the most defining morphological features of the genus are the subterranean plant parts – root systems, hypocotyls, rhizomatous structures, and fruits – organs that are not often included in herbarium specimens or noted by collectors (Krapovickas

**Table 2.1** Ten largest peanut producing countries in 2019 (source: FAOSTAT 2021)

Rank	Country	Production 2019 (metric tons)	Percentage of world total
1	Peoples Republic of China	17,519,600	35.9
2	India	6,727,180	13.8
3	Nigeria	4,450,050	9.1
4	Sudan	2,828,000	5.8
5	USA	2,492,980	5.1
6	Myanmar	1,615,715	3.3
7	Senegal	1,421,288	3.0
8	Argentina	1,337,229	2.7
9	Guinea	957,662	2.0
10	Chad	939,252	1.9
<b>Subtotal of top 10 producers</b>		<b>40,288,956</b>	<b>82.6</b>
<b>World total</b>		<b>48,756,790</b>	<b>100%</b>

**Table 2.2** *Arachis* species, by taxonomic section and country of occurrence. (Contributed by J.F.M. Valls, 10 July 2020, updated 10 December 2021)

	ARG	BOL	BRA	PRY	URY
<b>Sect. <i>Arachis</i></b>					
<i>Arachis batizocoi</i> Krapov. & W.C.Greg.		X		X	
<i>Arachis benensis</i> Krapov., W.C.Greg. & C.E.Simpson		E			
<i>Arachis cardenasii</i> Krapov. & W.C.Greg.		X		X	
<i>Arachis correntina</i> (Burkart) Krapov. & W.C.Greg.	X			X	
<i>Arachis cruziana</i> Krapov., W.C.Greg. & C.E.Simpson		E			
<i>Arachis decora</i> Krapov., W.C.Greg. & Valls			E		
<i>Arachis diogeni</i> Hoehne	[RC]	X	X	X	
<i>Arachis duranensis</i> Krapov. & W.C.Greg.	X	X		X	
<i>Arachis glandulifera</i> Stalker		X	X		
<i>Arachis gregoryi</i> C.E.Simpson, Krapov. & Valls		[X]	X		
<i>Arachis helodes</i> Mart. ex Krapov. & Rigoni				E	
<i>Arachis herzogii</i> Krapov., W.C.Greg. & C.E.Simpson		E			
<i>Arachis hoehnei</i> Krapov. & W.C.Greg.			E		
<i>Arachis hypogaea</i> L.	[TC]	[TC]	[TC]	[TC]	[TC]
<i>Arachis inflata</i> Seijo, Atahuachi, C.E.Simpson & Krapov.		E			
<i>Arachis ipaënsis</i> Krapov. & W.C.Greg.		E			
<i>Arachis kempff-mercadoi</i> Krapov., W.C.Greg. & C.E.Simpson		E	[RC]		
<i>Arachis krapovickasii</i> C.E.Simpson, D.E.Williams, Valls & I.G.Vargas		E			
<i>Arachis kuhlmannii</i> Krapov. & W.C.Greg.			E		
<i>Arachis linearifolia</i> Valls, Krapov. & C.E.Simpson			E		
<i>Arachis magna</i> Krapov., W.C.Greg. & C.E.Simpson		X	X		
<i>Arachis microsperma</i> Krapov., W.C.Greg. & Valls			X	X	
<i>Arachis monticola</i> Krapov. & Rigoni	E				
<i>Arachis palustris</i> Krapov., W.C.Greg. & Valls			E		
<i>Arachis porphyrocalyx</i> Valls & C.E.Simpson			E		
<i>Arachis praecox</i> Krapov., W.C.Greg. & Valls			E		
<i>Arachis schininii</i> Krapov., Valls & C.E.Simpson				E	
<i>Arachis simpsonii</i> Krapov. & W.C.Greg.		X	X		
<i>Arachis stenosperma</i> Krapov. & W.C.Greg.			E		
<i>Arachis trinitensis</i> Krapov. & W.C.Greg.		E			
<i>Arachis valida</i> Krapov. & W.C.Greg.			E		
<i>Arachis vallsii</i> Krapov. & W.C.Greg.			E		
<i>Arachis villosa</i> Benth.	X		X		X
<i>Arachis williamsii</i> Krapov. & W.C.Greg.		E			
<b>Sect. <i>Caulorrhizae</i> Krapov. &amp; W.C.Greg.</b>					
<i>Arachis pintoii</i> Krapov. & W.C.Greg.	[RC]	[RC]	E	[RC]	
<i>Arachis repens</i> Handro		[RC]	E		
<b>Sect. <i>Erectoides</i> Krapov. &amp; W.C.Greg.</b>					
<i>Arachis archeri</i> Krapov. & W.C.Greg.			E		
<i>Arachis benthamii</i> Handro			E		
<i>Arachis brevipetiolata</i> Krapov. & W.C.Greg.			E		
<i>Arachis cryptopotamica</i> Krapov. & W.C.Greg.			E		
<i>Arachis douradiana</i> Krapov. & W.C.Greg.			E		
<i>Arachis gracilis</i> Krapov. & W.C.Greg.			E		
<i>Arachis hatschbachii</i> Krapov. & W.C.Greg.			E		
<i>Arachis hermannii</i> Krapov. & W.C.Greg.			E		
<i>Arachis major</i> Krapov. & W.C.Greg.			X	X	

	ARG	BOL	BRA	PRY	URY
<i>Arachis martii</i> Handro			E		
<i>Arachis oteroi</i> Krapov. & W.C.Greg.			E		
<i>Arachis paraguayensis</i> Chodat & Hassl.			X	X	
<i>Arachis stenophylla</i> Krapov. & W.C.Greg.			E		
<b>Sect. Extranervosae Krapov. &amp; W.C.Greg.</b>					
<i>Arachis burchellii</i> Krapov. & W.C.Greg.			E		
<i>Arachis lutescens</i> Krapov. & Rigoni			E		
<i>Arachis macedoi</i> Krapov. & W.C.Greg.			E		
<i>Arachis marginata</i> Gardner			E		
<i>Arachis pietrarellii</i> Krapov. & W.C.Greg.			E		
<i>Arachis prostrata</i> Benth.			E		
<i>Arachis retusa</i> Krapov., W.C.Greg. & Valls			E		
<i>Arachis setinervosa</i> Krapov. & W.C.Greg.			E		
<i>Arachis submarginata</i> Valls, Krapov. & C.E.Simpson			E		
<i>Arachis villosulicarpa</i> Hoehne			E		
<b>Sect. Heteranthae Krapov. &amp; W.C.Greg.</b>					
<i>Arachis dardani</i> Krapov. & W.C.Greg.			E		
<i>Arachis giacomettii</i> Krapov., W.C.Greg., Valls & C.E.Simpson			E		
<i>Arachis interrupta</i> Valls & C.E.Simpson			E		
<i>Arachis pusilla</i> Benth.			E		
<i>Arachis seridoënsis</i> Valls, C.E.Simpson, Krapov. & R.Veiga			E		
<i>Arachis veigae</i> S.H. Santana & Valls			E		
<b>Sect. Procumbentes Krapov. &amp; W.C.Greg.</b>					
<i>Arachis appressipila</i> Krapov. & W.C.Greg.			E		
<i>Arachis chiquitana</i> Krapov., W.C.Greg. & C.E.Simpson		E			
<i>Arachis hassleri</i> Krapov., Valls & C.E.Simpson				E	
<i>Arachis jacobinensis</i> Valls & Simpson			E		
<i>Arachis kretschmeri</i> Krapov. & W.C.Greg.			E		
<i>Arachis lignosa</i> (Chodat & Hassl.) Krapov. & W.C.Greg.			X	X	
<i>Arachis matiensis</i> Krapov., W.C.Greg. & C.E.Simpson		X	X		
<i>Arachis pflugeae</i> C.E.Simpson, Krapov. & Valls			X	X	
<i>Arachis rigonii</i> Krapov. & W.C.Greg.		E			
<i>Arachis subcoriacea</i> Krapov. & W.C.Greg.			E		
<b>Sect. Rhizomatosae Krapov. &amp; W.C.Greg.</b>					
<i>Arachis burkartii</i> Handro	X		X		X
<i>Arachis glabrata</i> Benth.	X	[X]	X	X	
<i>Arachis nitida</i> Valls, Krapov. & C.E.Simpson			X	X	
<i>Arachis pseudovillosa</i> (Chodat & Hassl.) Krapov. & W.C.Greg.			X	X	
<b>Sect. Trierectoides Krapov. &amp; W.C.Greg.</b>					
<i>Arachis guaranitica</i> Chodat & Hassl.			X	X	
<i>Arachis tuberosa</i> Bong. ex Benth.			X	[X]	
<b>Sect. Triseminatae Krapov. &amp; W.C.Greg.</b>					
<i>Arachis triseminata</i> Krapov. & W.C.Greg.			E		
<b>Taxonomic section yet to be defined</b>					
<i>Arachis sesquijuga</i> Valls, Costa & Custodio			E		
<b>Species naturally or traditionally occurring per country</b>	<b>7</b>	<b>22</b>	<b>65</b>	<b>19</b>	<b>3</b>
<b>Endemic species per country</b>	<b>1</b>	<b>11</b>	<b>46</b>	<b>2</b>	<b>-</b>

X = Country of natural occurrence, eventually including cultivated populations

[X] = Natural occurrence confirmed by collection, though not yet reported in literature

E = Country of endemic natural occurrence

TC = Occurrence under cultivation only, traditional (many centuries)

RC = Occurrence under cultivation only, recent (few decades)

& Gregory 1994, 2007). This particular combination of distinguishing aerial and subterranean features presents special challenges for collecting, characterizing and describing wild *Arachis* species as well as cultivated landraces.

For example, in the process of classifying the peanut landraces of Bolivia, Peru, and Ecuador, researchers confronted the fact that when analyzing the plants at their peak of growth and flowering, the fruits had not yet fully developed; and when the time came to harvest and study the mature fruits, the plants were on their last legs. To overcome this problem, it became necessary to carefully record the distinguishing agro-morphological characteristics of the plants and the fruits in their respective seasons of optimum development, repeat these observations over successive cycles, make representative herbarium and fruit specimens for each accession, and later integrate the information in a systematic way to achieve a practical classification based on the combination of said characteristics (Krapovickas et al. 2009, 2013, 2021).

The cultivated peanut, *Arachis hypogaea* L., is a self-pollinated allotetraploid ( $2n=4x=40$ ) that originated from a single hybridization event between diploid progenitors followed by spontaneous chromosome duplication (polyploidization) estimated between 3,500 and 9,400 years ago (Bonavia 1982, Simpson et al 2001, Bertioli et al. 2016, 2019). Cytological and molecular studies suggest that *A. duranensis* (AA) and *A. ipaënsis* (BB) are the most probable diploid progenitors of cultivated peanut (Fernandez & Krapovickas 1994, Seijo et al. 2004, Nascimento et al. 2020). Neolithic hunter-gatherers or proto-agriculturalists, who had already been interacting with and exploiting other wild *Arachis* populations as nutritious food sources, readily detected and exploited the new polyploid species, *A. hypogaea*, leading to its eventual domestication (Hammons et al. 2016).

Ethnographic, ethnohistoric, and biological evidence reveal that *A. villosulicarpa* and *A. stenosperma* were also domesticated at some point by indigenous groups in Brazil, who cultivated them on a limited scale (Simpson et al. 2001). But today, only *A. hypogaea* is economically important as an oilseed and food crop (Stalker et al. 2016).

A few wild *Arachis* species – particularly *A. pintoi* (section *Caulorrhizae*) and *A. glabrata* (section *Rhizomatosae*) – are valued as forage crops, and commercial varieties of these are now used as cultivated pastures in numerous countries around the world. Others – such as *A. repens* (section *Caulorrhizae*) and *A. kempff-mercadoi* (section *Arachis*) – are used locally as ornamental groundcovers, for erosion control and soil restoration, and as green fertilizer crops.

Wild *Arachis* species are important to peanut improvement due to their wide range of diverse traits (Barkley et al. 2016), and their use in peanut breeding can increase the genetic diversity in the cultivated peanut. For example, there is evidence of high levels of disease and pest resistance in many of the wild *Arachis* species (Stalker et al. 2013; 2017). The selection and introgression of genes from wild *Arachis* species for resistance to important pests and diseases such as root-knot nematode (*Meloidogyne arenaria*), early and late leaf spot, rust (*Thecaphora frezii*), and *Sclerotinia* blight, have been successfully used to produce improved peanut cultivars (Simpson & Star 2001, Simpson et al. 2003, Holbrook et al. 2008, Isleib et al. 2011, de Blas et al. 2019).

Introgression of traits from wild species into the cultivated peanut by conventional hybridization is very challenging because interspecific hybrids between diploid wild species and tetraploid cultivated peanut are triploid and sterile. However, recent advances in genomic studies, chromosome mapping, and other biotechnological tools, including the development of artificial amphidiploids, show great potential for achieving targeted gene introgression.

#### 2.4.2 Taxonomy

The cultivated peanut had been known by various names to 16<sup>th</sup> and 17<sup>th</sup> century European botanists, but the species was not formally identified as *Arachis hypogaea* until it was described by Carl Linnaeus, the “father of modern taxonomy,” in his landmark botanical treatise, *Species Plantarum*, published in 1753. At that time, it was the only species known to represent the genus *Arachis*. It wasn’t until nearly 90 years later that Bentham (1841) published the first descriptions of five wild *Arachis* species; he later expanded his treatment to include seven species, including *A. hypogaea* (Bentham 1859). Over the next century, various other botanists grappled with the identification, description and classification of *Arachis* species, a task complicated by the distinctive, often cryptic, morphological features of the species, noted above. These efforts resulted in a confusing plethora of species names and synonyms. The ensuing taxonomic muddle was compounded by the fact that many of the names for *Arachis* species and varieties used until nearly the end of the 20<sup>th</sup> century did not conform to the International Code of Botanical Nomenclature. These informal taxa were considered *nomina nuda* (“naked names”) and were therefore invalid taxonomically, which hampered further research.

Then, in 1994, the genus *Arachis* was once again (and for the first time since Linnaeus) placed on firm taxonomic ground with the publication (in Spanish) of a comprehensive treatise in which 69 species were described (Krapovickas & Gregory 1994). An autho-

rized English translation of the monograph was published later (Krapovickas & Gregory 2007), making it accessible to a wider audience. The monograph provided peanut researchers with a solid systematic foundation, which has since been built upon by the authors' former students and colleagues (Stalker 1991; Valls & Simpson 2005; Krapovickas & Gregory 2007; Seijo et al. 2007, 2021; Krapovickas et al. 2009, 2013, 2021; Valls et al. 2013, 2017; Santana & Valls 2015) with a current total of 83 species described, and abundant germplasm samples obtained and widely distributed for further study and *ex situ* conservation. The taxonomic work is ongoing, as several new *Arachis* species have been discovered in recent years and these are currently being described and their germplasm conserved *ex situ* for future research and development (J.G. Seijo, pers. comm.; J.F.M. Valls, pers. comm.).

### Sections of the genus *Arachis*

In their monograph, Krapovickas & Gregory (1994, 2007) subdivided the genus into nine sections (*Arachis*, *Caulorrhizae*, *Erectoides*, *Extranervosae*, *Heteranthae*, *Procumbentes*, *Rhizomatosae*, *Trierectoides*, and *Triseminatae*) based on species' morphological traits, chromosomal characteristics, geographic distribution, and crossability studies.

Subsequent genetic studies have, on the whole, tended to confirm and substantiate the sectional and genomic classifications proposed by Krapovickas & Gregory in 1994 (Barkley et al. 2007, Bechara et al. 2010). The systematic relationships among *Arachis* species have also been inferred using cytology (Fernandez & Krapovickas 1994; Lavia 2001; Lavia et al. 2001, 2009; Silvestri et al. 2017), seed storage proteins (Grosso et al. 1994), isozymes, various molecular markers such as RAPDs, RFLPs (Burow et al. 2009), microsatellites (Moretzsohn et al. 2004), AFLPs (Milla et al. 2005), cytogenetic and molecular data from AFLP and the *trnT-F* plastid region (Tallury et al. 2005), FISH and GISH (Seijo et al. 2004, 2007), and ITS and 5.8S rDNA (Bechara et al. 2010). Most of these studies have focused on species belonging to section *Arachis* due to their affinity to the cultigen, although some concentrate on *Arachis* species with forage potential (Angelici et al. 2008, Azêvedo et al. 2016, Ortiz et al. 2013).

### Genomes within the section *Arachis*

Section *Arachis* is the largest, most diverse, and presumably the most recently evolved section of the genus (Simpson et al. 2001). Section *Arachis* is comprised of the cultigen, *A. hypogaea*, its tetraploid wild sister, *A. monticola*, plus 32 diploid wild species (Table 2.2).

Initially all species within the section *Arachis* were believed to possess either an A or a B genome. The use of increasingly sophisticated molecular and genomic tools has permitted the identification of additional

genomes in the section *Arachis*. *Arachis glandulifera* was classified as having a D genome when the species was first described by Stalker (1991). Some section *Arachis* species that were formerly assigned to the B genome have been reassigned to K and F genomes (Seijo et al. 2004, Robledo & Seijo 2010), and the aneuploid species with  $2n=18$  were assigned to the G genome (Silvestri et al. 2015).

Several diploid species of the section *Arachis* have been considered as potential ancestors of the cultivated peanut. These include the A genome species *A. correntina*, *A. duranensis*, and *A. cardenasii*; the K genome species *A. batizocoi*; and the B genome species *A. ipaënsis* (Gregory & Gregory 1976; Singh & Smartt 1998; Stalker et al. 1991). Based on current scientific evidence, *A. duranensis* (AA) and *A. ipaënsis* (BB) are considered the most closely related to the component A and B subgenomes of cultivated peanut (Kochert et al. 1996; Moretzsohn et al. 2013; Robledo & Seijo 2010; Seijo et al. 2004, 2007; Grabiele et al. 2011; Bertoli et al. 2016, 2019). Nonetheless, the other diploid species within the section *Arachis* with either A or B genomes also represent candidate gene donors to the cultivated peanut and thereby constitute the crop's secondary gene pool.

*Arachis hypogaea* is an allotetraploid species ( $2n = 4x = 40$ ) with an AABB-type genome (Husted 1936; Smartt et al. 1978). The tetraploid genomic make-up of *A. hypogaea* is derived from its two diploid parental species – one with an AA genome and the other with a BB genome – which spontaneously hybridized (AB), followed by a polyploidization event yielding the tetraploid (AABB). The only other tetraploid species in the section *Arachis* is *A. monticola*, a wild-living taxon that shares the same allopolyploid genome (AABB) as *A. hypogaea*. While the precise evolutionary relationship between the two taxa remains unclear, it is generally accepted that both were somehow derived from the same hybridization event that led to the domestication of *A. hypogaea*. Because the two taxa are interfertile and essentially conspecific, *A. monticola* joins *A. hypogaea* to constitute the crop's primary gene pool.

It is now generally accepted that *A. hypogaea* is a monophyletic allopolyploid, meaning that it resulted from a single, spontaneous hybridization/polyploidization event, followed by domestication. This suggests that the crop experienced a severe genetic bottleneck as a result of its domestication, leaving it reproductively isolated from its closest diploid relatives. This helps explain the peanut's apparent dearth of genetic diversity, as reported by numerous investigators (Kochert et al. 1991, Moretzsohn et al. 2004, Burow et al. 2009). In order to broaden the cultivated peanut's genetic base, breeders have long been keen



to introgress valuable genes from closely related wild species. In an effort to identify the crop's progenitor species, Gregory and Gregory (1979) conducted an extensive crossing program that enabled them to divide the wild species in section *Arachis* into potential A and B genome donors based on their genetic affinities. This knowledge has served to guide further studies and experimentation, including some early success in using wild species in peanut breeding programs (Singh & Moss 1982; Simpson & Starr 2001, Simpson et al. 2003, Burow et al. 2001, 2008, 2009).

Most wild species of *Arachis* are diploid and produce infertile triploid offspring when crossed directly with cultivated peanut. To overcome this hurdle, recent efforts to use wild *Arachis* species in peanut breeding have focused on the development of artificial allotetraploids, also referred to as amphidiploids (Simpson et al. 1993; Mallikarjuna et al. 2010; Stalker 2017; Leal-Bertioli et al. 2015, 2017; Levinson et al. 2021). These artificial, or synthetic, allotetraploid plants are typically produced by crossing a combination of two (or more) wild species representing both AA and BB genomes, and the subsequent treatment of the sterile diploid F<sub>1</sub> hybrids with colchicine (to induce chromosome doubling), resulting in an AABB genome similar to – and compatible with – the cultigen. The incorporation of a growing number of wild diploid species in the creation of new artificial allotetraploids, or neotetraploids, is proving to be a major breakthrough in the understanding of the genetics and genome structure of the peanut crop (Bertioli et al. 2016, 2021) and shows great promise for contributing significantly to peanut improvement through the incorporation of agronomically valuable traits present in wild *Arachis* species.

Fávero et al. (2006) created an artificially induced amphidiploid derived from *A. ipaënsis* and *A. duranensis*, the putative genome donors of the cultigen. This synthetic allotetraploid produced fertile hybrids when crossed with varieties of both subspecies of cultivated peanut, allowing for the construction of chromosome segment substitution lines in peanut (Fonckea et al. 2012). Recombinant inbred lines obtained from a hybrid of this synthetic allotetraploid and cultivated peanut are vigorous and fertile. These observations indicate that the artificially induced allotetraploid (*A. ipaënsis* × *A. duranensis*)<sup>4x</sup> and the spontaneous allotetraploid, *A. hypogaea*, have a similar genomic structure (Bertioli et al. 2016).

In the past decade, numerous artificially induced allotetraploids have been developed using wild *Arachis* species, in an effort to facilitate the introgression of pest and disease resistance and other desirable characteristics from those wild species into the cultigen through hybridization with and backcrossing to *A. hypogaea*. A team at ICRISAT led by Mallikarjuna et

al. (2010) developed a series of 17 synthetic tetraploid groundnuts using nine diploid *Arachis* species with A and B genomes. Kumari et al. (2014) used two synthetic amphidiploids generated from three wild *Arachis* species at ICRISAT to create backcross populations with five elite peanut varieties that resulted in several introgression lines possessing foliar disease resistance and other important traits that are now available to peanut breeders for future genetic enhancement of the crop. Michelotto et al. (2017) evaluated the resistance to thrips (*Enneothrips flavens*) of 10 wild *Arachis* species and nine artificially induced amphidiploids using 13 diploid *Arachis* species. They determined that accessions of *A. vallsii*, *A. kempff-mercadoi*, *A. batizocoi*, *A. williamsii*, *A. duranensis*, and *A. magna* are the most promising for obtaining resistant amphidiploids, and that the amphidiploids (*A. batizocoi* × *A. kempff-mercadoi*)<sup>4x</sup>, (*A. gregoryi* × *A. stenosperma*)<sup>4x</sup>, and (*A. magna* × *A. cardenasii*)<sup>4x</sup> presented high levels of resistance to *E. flavens* (Michelotto et al. 2017).

Fávero et al. (2015, 2020) used combinations of more than a dozen diploid wild species to produce various synthetic amphidiploids, and a series of complex hybrids between amphidiploids involving four wild species each, some of which were then hybridized with different cultivars of *A. hypogaea*. The progenies and parents of these crosses were then characterized using molecular, morphological, reproductive, phytopathological and entomological characterization techniques, demonstrating the feasibility of using complex crosses to introgress useful genes from non-closely related wild diploid species into the cultivated peanut (Fávero et al. 2020).

In an effort to develop pre-breeding materials for transferring to the cultivated peanut resistance to peanut smut (*T. frezii*) found in wild *Arachis* species, de Blas et al. (2019) developed an amphidiploid from three resistant diploid species [(*A. correntina* × *A. cardenasii*) × *A. batizocoi*]<sup>4x</sup>. A recombinant inbred line (RIL) population with high phenotypic variability for resistance to peanut smut was then obtained by crossing the synthetic amphidiploid with an experimental line of *A. hypogaea*. The synthetic amphidiploid itself and 22 of the RILs proved to be highly resistant to peanut smut, demonstrating that peanut smut resistance from wild diploid species can be effectively introgressed into the peanut crop using synthetic amphidiploids and recombinant inbred lines (de Blas et al. 2019).

Most recently, an artificially induced allotetraploid was derived from a cross between *A. valida* (BB) and *A. stenosperma* (AA) whose chromosomes were then doubled using colchicine to produce the allotetraploid, denominated ValSten (Gao et al. 2021). The synthetic ValSten plants were not only sexually

compatible with cultivated peanut, produced abundant seed and had well-developed fertile pollen, but they also demonstrated complete resistance to early and late leaf spot and rust diseases—as do their diploid parents. Levinson et al. (2021) developed four allotetraploid interspecific hybrids that are cross-compatible with *A. hypogaea*. These allotetraploids were artificially induced from various combinations of five diploid *Arachis* species, and were then characterized using morphological and reproductive parameters. It was found that at least one or more the artificial allotetraploids differed from the cultivated peanut control in nearly every parameter, making a much wider source of phenotypic diversity available to peanut breeders as part of the crop's primary genepool.

These recent results further manifest the potential of artificially induced allotetraploids, not only for facilitating the introgression of wild genes for peanut improvement, but also as another option for maintaining and distributing wild peanut genetic resources, particularly in locations where wild *Arachis* species are difficult or impossible to conserve or reproduce *ex situ* (Gao et al. 2021).

#### **Intraspecific taxa within the cultivated peanut (*A. hypogaea*)**

The genetic diversity contained within the different manifestations of the cultivated peanut and its conspecific wild form, *A. monticola*, constitutes the crop's primary genepool, and is the logical starting point for any peanut improvement program. In contrast to the frequent assertions of molecular biologists that *A. hypogaea* has a relatively low level of genetic diversity, the crop displays an astounding degree of phenotypic variation among its countless unimproved local varieties spread across its vast native range, a diversity of forms, habits, sizes, colors and shapes that is immediately apparent to the naked eye, but which few people (other than collection curators) have the opportunity to witness. Krapovickas and Gregory (1994) supported Waldron's (1919) recognition of two distinct subspecies within the cultigen, subsp. *hypogaea* and subsp. *fastigiata*, based on plant habit, leaf color, the presence or absence of flowers on the mainstem, and the flowering pattern on the lateral branches. Each subspecies was, in turn, subdivided into botanical varieties, numbering six in all. Subspecies *hypogaea* is composed of two botanical varieties: var. *hypogaea* and var. *hirsuta*. Subspecies *fastigiata* is composed of four botanical varieties: var. *fastigiata*, var. *vulgaris*, var. *peruviana*, and var. *aequatoriana*. The botanical varieties correspond generally to commercial market types, with the exceptions of var. *peruviana* and var. *aequatoriana* whose cultivation remains limited almost entirely to small-scale farmers in their respective areas of origin in South America (see Box 1)

Recent molecular and genomic studies of peanut botanical varieties have begun to shed new light on the phylogenetic relationships between the varieties, bringing into question the nature and placement of some of the botanical varieties within the current taxonomic scheme (He & Prakash 2001, Ferguson et al. 2004). Further molecular, genomic, morphological, ethnographic and archaeological research, based on a broader and more representative sampling of unimproved landraces corresponding to each of the six botanical varieties, will be required to fully ascertain the phylogenetic origins and identities of the botanical varieties and their taxonomic placement within *A. hypogaea*.

Modern commercial cultivars are frequently presumed to represent botanical varieties, when in reality they are of mixed origin. A typical example of this confusion is the registered cultivar 'Florigiant' which, due to its runner-type growth habit, seed size and pod type, is frequently regarded as pertaining to *Arachis hypogaea* subsp. *hypogaea* var. *hypogaea*. However, Florigiant's pedigree reveals that it is in fact the product of a series of deliberate crosses and backcrosses between parental lines corresponding to both subsp. *hypogaea* var. *hypogaea* and subsp. *fastigiata* var. *vulgaris* (Isleib et al. 2001). The advantages of using such inter-subspecific crosses in the development of commercial varieties is such that most of the current runner- and virginia-type cultivars grown in the United States trace their ancestry back to two inter-subspecific (subsp. *hypogaea* x subsp. *fastigiata*) and inter-varietal (var. *hypogaea* x var. *vulgaris*) crosses (Isleib et al. 2001). Such inter-subspecific and inter-varietal hybrids do not conform to the standard taxonomic classification system and cannot be unequivocally assigned to a particular subspecies or botanical variety. Therefore, to preclude unnecessary confusion, care should be taken to avoid including modern cultivars and complex hybrid varieties when conducting phylogenetic studies of the crop's primary genepool.

#### **Landraces**

The next level of diversity lies within each of the botanical varieties, that is, the locally developed farmer varieties, or landraces. A landrace is a less formal but nonetheless practical category for classifying and managing crop genetic diversity, and is a concept that is used and practiced widely by traditional farming communities throughout the peanut's native range as well as in its secondary centers of diversity in Africa and Asia. A landrace is genetically and morphologically heterogeneous by nature, but adheres to a certain set of defining characteristics that are best known to the traditional farmers who have been selecting, sowing and harvesting the landrace for generations. Many of the defining features of a landrace can be readily observed by an outsider, but

other important traits – such as agronomic characteristics, cooking qualities, ceremonial significance, or ethnic identity – may not be so obvious. In its original on-farm context, a landrace is a conceptual entity defined by traditional farmers, perhaps best understood as a population of related individual plants that grow well in a given environment and produce a harvest that exhibits a distinctive set of desired traits and qualities. In any case, a landrace represents the unit of management, that is, the object of the farmers' selection and propagation efforts to replenish and sustain their supply of a specific local variety.

Although local varieties are currently being displaced at a rapid rate around the world by improved commercial varieties, extant peanut landraces probably still number in the thousands, most of which have been scarcely collected and poorly documented beyond their local names. Three noteworthy exceptions to this trend are the monographic classifications of peanut landraces in Bolivia, Peru, and Ecuador (Krapovickas et al. 2009, 2013, 2021). These monographs are the product of extensive collecting campaigns in which hundreds of landrace materials were collected in each country and conserved *ex situ* at the INTA Experiment Station in Manfredi, Argentina. Over the course of several years, the accessions from each country were grown together in experimental plots during successive cycles of agro-morphological characterization, comparison, and botanical classifica-

tion. The resulting monographs identified, described, and categorized over 100 distinct and largely endemic peanut landraces: 62 for Bolivia, 47 for Peru, and 51 for Ecuador, representing the first systematic classifications of peanut diversity at the landrace level.

These and similar, ongoing studies reveal a large degree of endemism of peanut landraces among the Andean countries. For example, among the 51 landraces known from Ecuador and the 47 from Peru, only two are shared by both countries, despite their extensive shared border. Similarly, the peanut landraces from the State of Acre, Brazil, are entirely distinct from the landraces of Peru and Bolivia, despite the State of Acre sharing a border with both of those countries. The observed combination of great diversity with a high degree of endemism is a result of the intense selection practiced in different environments by diverse local cultures over the course of millennia (Krapovickas et al. 2009, 2013; Williams 1992). More basic work of this nature needs to be done in order to fully document, characterize, conserve, and utilize the rich spectrum of genetic diversity already present in the peanut's primary gene pool.

#### Improved varieties

Compared to many other crops, the cultivated peanut has a narrow genetic base, most likely the result of its inability to easily exchange alleles with its wild relatives. The genetic base is especially narrow in the

**Box 1** Intraspecific classification of *Arachis hypogaea* (after Stalker & Simpson 1995).

BOTANICAL VARIETY	MARKET TYPE	AREA OF PREHISTORIC DISTRIBUTION	TYPICAL CHARACTERISTICS
subspecies <i>hypogaea</i>			No flowers on mainstem Alternating pairs of floral axes on branches Prostrate habit    Long indeterminate cycle Pods 2-seeded    Seeds with long dormancy
var. <i>hypogaea</i>	Virginia	Bolivia Amazonia	Plants more upright, less hairy Pods large, reticulated, 2-seeded
	Runner	Bolivia Amazonia	Plants prostrate, less hairy, long branches Pods smaller, 2-seeded
var. <i>hirsuta</i>	Peruvian runner Dragon type	Peru, Ecuador, Colombia Guatemala, Mexico	Plants prostrate, much branched, very hairy Pods with beaks, humps, sharp reticulation 2-3-seeded    Purple or whitish seeds
subspecies <i>fastigiata</i>			Flowers on mainstem and lateral branches Sequential flowering Plants upright    Short determinate cycle Seeds with little or no dormancy
var. <i>fastigiata</i>	Valencia	Brazil, Paraguay, Uruguay, Peru	Plants erect, less branched Pods fairly smooth and straight, 3-4-seeded
var. <i>vulgaris</i>	Spanish	Brazil, Paraguay, Uruguay	Plants upright, compact, densely branched Short cycle. Pods small, with constriction 2-seeded, small seeds
var. <i>peruviana</i>	n/a	Peru, NW Bolivia, W Brazil	Plants erect, glabrous, sparsely branched Long, strong reproductive branches Pods deeply reticulated w/longitudinal ribs 3-4 seeded
var. <i>aequatoriana</i>	n/a	Ecuador	Plants erect, leaflets hairy Purple stems; more branched, purple flowers Pods deeply reticulated, 3-5 colorful seeds

case of commercial cultivars, many of which trace their ancestry back to just a few parent lines. Currently, the vast majority of peanuts entering the world market are produced by a few cultivars, which puts the crop at risk to new pests and diseases that may arise in the future (Barkley et al. 2016).

Major peanut pests and diseases, such as to *Sclerotinia* blight, Root-Knot Nematode, and Tomato Spotted Wilt Virus (TSWV) caused serious losses to commercial farmers until resistant varieties were developed using genetic resources conserved in genebanks. For example, a single peanut accession collected at a southern Brazilian market in 1952 – prior to the germplasm access restrictions now imposed – was found to have resistance to TSWV and was used to produce resistant runner cultivars (Barkley et al. 2016). Isleib et al. (2001) estimated that the economic impact to the US peanut industry of this single accession alone is about \$200 million annually.

An emerging new threat to global peanut production is the peanut smut disease (*Thecaphora frezii*). This disease has already spread throughout Argentina's peanut producing area, where current cultivars are highly susceptible, suffering up to 35–51% losses in yield (Rago et al. 2017, Wann et al. 2020). Resistance to peanut smut was detected in some old landraces from Bolivia and has been successfully transferred into elite varieties (Bresano et al. 2019). Fortunately, all of the wild diploid *Arachis* species tested so far are almost immune to the disease. Through the development of an artificial amphidiploid involving three wild species (*A. correntina*, *A. cardenasii* and *A. batizocoi*, their smut resistance can be transferred to elite varieties (de Blas et al. 2019). The first smut-resistant commercial cultivar was recently registered, and a few more are currently under development (G. Seijo pers. comm.).

### Genepools of *Arachis hypogaea*<sup>1</sup>

Adhering to the genepool concept as envisaged by Harlan & de Wet (1971), the concentric primary, secondary, and tertiary genepools of the cultivated peanut (*Arachis hypogaea*) can be delimited as shown in Box 2.

### The Peanut Diversity Tree

A diversity tree is a stratification of a genepool into groups and subgroups. The concept originated in a paper published by van Treuren et al. (2009) proposing a way to analyze and plan the composition of genebank collections. The Crop Trust has adapted this idea to visualize and understand the coverage of a crop genepool in *ex situ* conservation. By quantifying the accessions corresponding to each group in a Diversity Tree, one can evaluate a given crop collection for relative completeness, representativeness and uniqueness. The approach is also useful for identifying gaps in germplasm collections, and can facilitate the prioritization of those gaps in terms of their taxonomic identity, genetic affinity, or ecogeographic distribution. A Peanut Diversity Tree has been developed and provides an interactive graphic display of all the component taxa of the peanut genepool, the putative phylogenetic relationships between them, and their known regions of geographic occurrence. The [Peanut Diversity Tree](#) can be viewed on Genesys.

<sup>1</sup>This genepool structure corresponds to *A. hypogaea* (Sect. *Arachis*) as the focal crop. The composition of genepools would be entirely different were we to take, for example, the relict cultigen *A. villosulicarpa* (Sect. *Extranervosae*), or the commercially cultivated forage peanut *A. pintoii* (Sect. *Caulorrhizae*), as the focal crop for genepool definition. Because those species each pertain to different sections of the genus from one another and from *A. hypogaea*, their respective genepools are consequently composed of entirely different sets of *Arachis* species, reflecting in each case those most closely related to the focal crop in question.

## Box 2. Genepools of *Arachis hypogaea*

### Primary genepool (GP1)

- The cultigen, *Arachis hypogaea*, including all its subspecies, botanical varieties, landraces, obsolete and modern improved cultivars, and breeding lines.
- *Arachis monticola* Krapov. & Rigoni
- Artificially induced allotetraploids/amphidiploids that are cross-compatible with *A. hypogaea* (AABB genome)

### Secondary genepool (GP2)

- Wild diploid species in the section *Arachis* identified as either AA or BB genome that are cross-compatible with *A. hypogaea*:
  - AA genome: *Arachis duranensis*, *A. cardenasii*, *A. correntina*, *A. diogoi*, *A. helodes*, *A. herzogii*, *A. kempff-mercadoi*, *A. kuhlmannii*, *A. linearifolia*, *A. microsperma*, *A. schinonii*, *A. simpsonii*, *A. stenosperma*, *A. villosa*
  - BB genome: *Arachis ipaënsis*, *A. gregoryi*, *A. magna*, *A. valida*, *A. williamsii*, *A. trinitensis*

### Tertiary genepool (GP3)

- All other species in the genus *Arachis* (D, F, G, and K genomes)



Testing groundnut viability, ICRISAT genebank.  
Photo: Michael Major/Crop Trust

# 3 EX SITU CONSERVATION – CURRENT STATUS

## 3.1 Introduction

Peanut germplasm is conserved and maintained in a number of *ex situ* collections around the world. The Second Report on State of the World's Plant Genetic Resources (FAO 2010) related a global total of 128,435 *Arachis* germplasm accessions as reported by 145 nations in their individual Country Reports. More recent data gleaned from the WIEWS, Genesys, and GRIN-Global databases, together with responses to the online survey, indicate a current global aggregate of over 90,000 accessions of peanut germplasm presently conserved in genebanks (Tables 3.1 and 3.3). The aggregate numbers reported in Tables 3.1 and 3.3 reflect a high degree of duplication of accessions that currently exists across genebanks.

Historically, there has been much sharing, exchange, and duplication of peanut germplasm among genebanks. For example, the large global *Arachis* collection maintained by ICRISAT reflects their longstanding collaboration and participation in the historic collecting efforts of EMBRAPA, USDA, NCSU, TAMU, IBONE and INTA, and the sharing of collected materials. This resulted in the duplication of thousands of accessions across these institutions, much of which has been well documented (Stalker et al. 2002). On the other hand, extensive movement of other germplasm among these and other *Arachis* collections, combined with the prevalence of independent, inconsistent or incomplete record-keeping by different genebanks, makes it difficult, if not impossible, to precisely determine the degree of redundant (i.e., non-security) duplication of accessions – both within and among

genebanks. By the same token, it is equally difficult to determine with any precision the amount of truly unique accessions being conserved at the global level. This topic is taken up in greater detail in Section 5 of this report.

The methods of choice for *ex situ* conservation of peanut genetic resources are storing germplasm accessions in the form of seeds in cold storage and/or as whole plants in greenhouses. These *ex situ* collections are maintained – at no small expense – to prevent the extinction of natural plant populations, and to have a collection of diverse materials on hand for breeding and other research purposes. Conservation of a crop's genetic diversity in genebanks provides a library of different traits that can be used in countless combinations to produce improved varieties. Genebanks play a number of vitally important roles beyond simply storing germplasm, ensuring its genetic integrity, and providing samples for breeding and research activities. Genebanks also compile and curate the invaluable passport, characterization, evaluation, and other relevant information specifically associated with each germplasm accession.

While the seed of the cultivated peanut is not as long-lived as the seeds of many other crops, it is still regarded as orthodox in terms of its capacity to remain viable for extended periods under cold and dry storage conditions. Under optimum conditions of temperature and humidity, a peanut seed accession can be expected to retain good viability (>85%) for 10–15 years or more.

In contrast to the cultivated peanut, the *ex situ* conservation of wild *Arachis* accessions is exceptionally labor- and resource-intensive, and can be operationally challenging for several reasons. Seeds obtained from collecting missions or from other genebanks are often received in limited quantities, and need to be substantially increased for storage, characterization and distribution purposes. Most wild *Arachis* species produce few seeds, which typically have a very high degree of dormancy that must somehow be overcome before they will germinate. And because wild *Arachis* species occur in many different, highly specialized habitats in their tropical countries of origin, it can be difficult to get the plants to germinate, grow, flower and set seed in a temperate latitude on a different continent. For these reasons, as well as conserving them as seed, many wild *Arachis* accessions also need to be permanently maintained in greenhouses as whole plants, and some need to be propagated vegetatively due to poor or nonexistent seed-set (Stalker and Simpson 1995). The various means of storage employed for wild *Arachis* accessions by the genebanks surveyed are shown in Table 3.1.

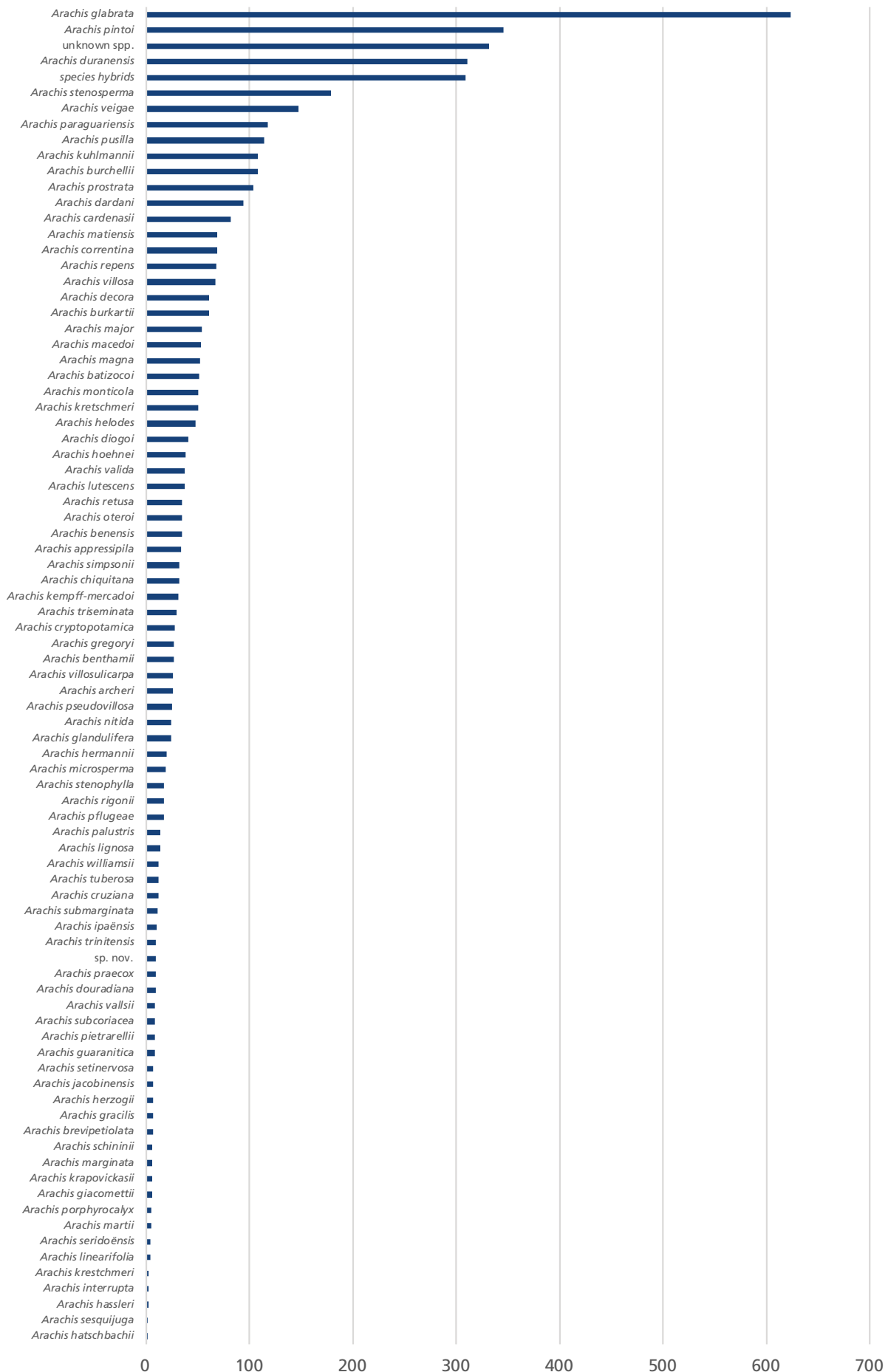
One of the biggest challenges of maintaining *ex situ* germplasm collections is having a steady source of adequate funding (labor, supplies, infrastructure, etc.) to support the routine operations required for the maintenance, monitoring and evaluation of

the germplasm collection. Ensuring the necessary financial and institutional resources to maintain a germplasm collection is a permanent commitment that represents a constant challenge for even the largest genebanks. Many institutions—and indeed nations—are unable to sustain a fully functioning genebank over the long term. Any sudden interruption of funding, staffing or electrical power can quickly result in the permanent loss of an entire collection and any unique genetic diversity contained therein—a tragic loss that, unfortunately, is an all-too-common occurrence around the world. To avoid such irreparable loss of investment and genetic resources, having back-up safety duplicates deposited in another genebank is imperative.

One of the limitations of conserving germplasm accessions *ex situ* is that the small sample size and infrequent reproductive cycles inhibit the plant's natural evolutionary processes such as gene flow, adaptation to pests, diseases and climate change, and the preservation of within-population genetic diversity. As a result, prolonged *ex situ* conservation can result in unwanted genetic drift of the conserved material over time. For these reasons, the integration of *ex situ* seed storage methods with some aspect of *in situ* or on-farm conservation activities is recommended where and when possible. The adoption of complementary *in situ/ex situ* conservation approaches helps ensure

**Table 3.1** Accessions of wild *Arachis* species conserved *ex situ* as reported by genebanks responding to the online survey, and the conservation methods used.

INSTCODE	Number of Wild <i>Arachis</i> Accessions	Number of Wild <i>Arachis</i> Species	Mean Accessions in Cold Storage (%)	Mean Accessions in Greenhouse (%)	Mean Accessions in Field Plots (%)
BRA002	1,559	84	69	31	0
USA520	954	76	75	71	0
USA317	600	59	97	8	0
USA016	559	65	100	12	0
IND002	480	47	–	–	–
ARG1133	260	57	77	78	2
CHN003	234	37	100	100	0
COL003	158	29	88	12	0
PRY027	109	12	35	100	0
ARG1211	106	29	97	0	100
IND025	97	43	100	0	0
IND001	81	16	100	0	0
AUS167	46	11	100	0	0
SEN002	16	9	100	0	0
TWN001	8	1	86	0	0
BOL316	1	1	100	0	0
URY003	3	1	–	–	–
<b>TOTAL</b>	<b>5,271 accessions of wild <i>Arachis</i> species held in surveyed collections</b>				



**Figure 3.1** Number of wild *Arachis* accessions conserved *ex situ*, sorted by species in decreasing order of abundance. Accession totals were obtained by summing the accessions reported by the 24 organizations responding to the survey.

the preservation of the highest possible amount of genetic variability (Section 4).

### 3.2 Core collections

When a germplasm collection grows large, it can become an overwhelming task to evaluate it in its entirety for traits of interest. The idea of developing a “core” collection, or subset of accessions that are representative of the overall scope of genetic diversity contained in the full collection, was proposed by Frankel (1984). Initially a source of much discussion and some dispute, the theory and methodologies for extracting a representative subset—typically around 10% of the total accessions—have advanced significantly since then, and the utility of using core collections to facilitate access to desirable traits in large collections has been amply demonstrated. Today, the development and use of core collections (also called core subsets) has become standard practice for large germplasm collections. Three of the world’s largest *Arachis* genebanks (ICRISAT, USDA, and OCRI-CAAS) have established and evaluated their own core collection, each using somewhat different approaches, described below.

A core collection of the USDA peanut collection was developed by stratifying the collection by country of origin, and these were then subdivided into groups using multivariate analysis of morphological traits. A random sample of 10% was then selected from each of these groups to form the core collection. An examination of the means and ranges of key morphological traits indicated that the resulting core collection is representative of the diversity present in the entire collection (Holbrook et al. 1993).

To develop ICRISAT’s core collection, the entire peanut collection of 14,310 accessions was first stratified by botanical variety within subspecies, and then stratified by country of origin. Accessions of the same botanical variety from small and adjacent countries with similar agro-climates were then grouped together, resulting in 75 groups. The accessions within each group were then clustered using multivariate morphological analysis, and approximately 10% of the accessions in each cluster were randomly sampled to obtain the final core collection of 1,704 accessions (Upadhyaya et al. 2003).

In China, a core collection based on 6,390 accessions in the OCRI peanut collection was developed by Jiang et al. (2008). The entire collection was first classified into five main groups (botanical types), and then divided into 258 variety clusters using morphological characterization data. In each variety cluster, 5–10% was sampled randomly, resulting in a total of 576 accessions selected for the core collection, accounting for 9.01% of the entire collection. A comparison of the

diversity indices calculated within the botanical varieties in the entire collection and in the core collection, indicated that the diversity of the core collection well represents that found in the entire collection (Jiang et al. 2008; Barkley et al. 2016).

Based upon the proven utility of these core collections, Upadhyaya et al. (2002) followed the same logic of representative subsets, to postulate the development of “mini cores,” wherein approximately 10% of the core collection (or 1% of entire collection) is further subsampled to reduce the overall size of the sub-set while still representing the breadth of diversity present in the entire collection. This concept led to the creation of mini cores for the peanut collections at ICRISAT, OCRI-CAAS, and USDA, where they were found to be even more manageable and amenable especially for analyzing characters that are expensive to measure. The mini cores developed at ICRISAT and OCRI-CAAS were later compared with one another (Jiang et al. 2008, 2010b), and with the USDA mini core, producing interesting results from a global gene pool perspective in terms of the overall *Arachis* diversity conserved, and its distribution between these three large peanut collections. In this comparison, Jiang et al. (2014) noted that the Chinese mini core did not include examples of the botanical vars. *peruviana* or *aequatoriana*, but was abundant in accessions of var. *hirsuta*, which is not present in either the ICRISAT or USDA mini core collection. They concluded that there are significant differences in the proportions of botanical varieties and agro-morphological traits between the Chinese and ICRISAT peanut mini-cores, such that the Chinese and ICRISAT collections are complementary to one another. Using SSRs to measure differences in allelic richness between the Chinese and USDA mini cores, they found higher allelic diversity in the USDA mini core, likely a result of greater representation of the different botanical varieties in the USDA collection (Jiang et al. 2014).

### 3.3 Taxonomic and ecogeographic gaps in the collections

#### 3.3.1 Wild species

Wild *Arachis* species are valued for the broad range of genetic variability that can contribute to the improvement of the cultigen, *A. hypogaea*, as well as serving as potential forage and cover crops. Much of the genetic diversity present in wild species is contained at the population level. Thanks to the intensive efforts of plant explorers, the majority of known wild *Arachis* species have germplasm conserved *ex situ* in two or more genebanks around the world. However, a large number of wild *Arachis* accessions remain unidentified, and many species are represented by only a single or very few original germplasm accessions, which is clearly reflected in the number of accessions



(including duplicates) currently conserved in genebanks (Figure 3.1). Furthermore, several of those under-represented species are severely endangered or believed to be extinct in their native habitat (Jarvis et al. 2003). For that reason, collecting and conserving additional populations of key *Arachis* species, particularly those in the section *Arachis*, are of priority importance for the future of peanut improvement. Moreover, many species from sections of the genus pertaining to the crop's tertiary gene pool (e.g., *Trierectoides*, *Heteranthae*, *Extranervosae* and *Erectoides*) are also under-represented in *ex situ* germplasm collections and their potential contributions to peanut improvement, and/or use as forage, green manure or groundcover crops, have yet to be adequately studied or evaluated.

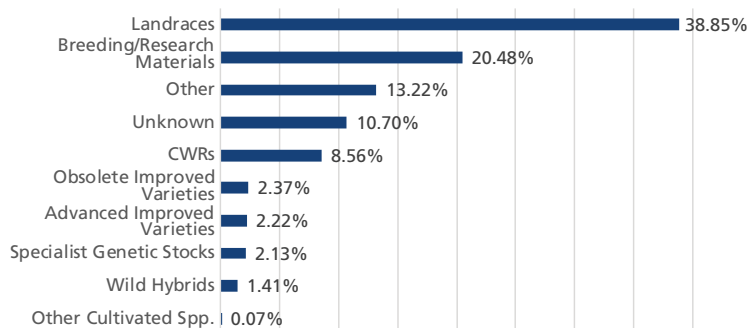
### 3.3.2 Cultivated peanut (*A. hypogaea*)

A similar predicament exists with regard to cultivated peanut landraces, which comprise the most genetically diverse part of the crop's (naturally occurring) primary gene pool (Isleib et al. 2001). While accessions of unimproved peanut germplasm are available for all six botanical varieties, the results of our survey reveal that there are many fewer representatives of the three least-commercialized varieties, i.e., vars. *hirsuta*, *peruviana* and *aequatoriana* (Figures 3.2, 3.3a, and 3.3b). The cultivation of these botanical varieties remains restricted to traditional farming communities in rural areas of northern South America, Guatemala and Mexico, and in the case of the var. *hirsuta*, to remote areas of China, SE Asia and Madagascar. Recent evidence indicates that unimproved landraces of the var. *peruviana* are also cultivated on various islands in Oceania (K. Williams, personal communication; L. Guarino, personal communication). The unique and potentially valuable genetic diversity present in these three botanical varieties is insufficiently described and it remains largely overlooked in current germplasm collections, genomic studies, and breeding programs.

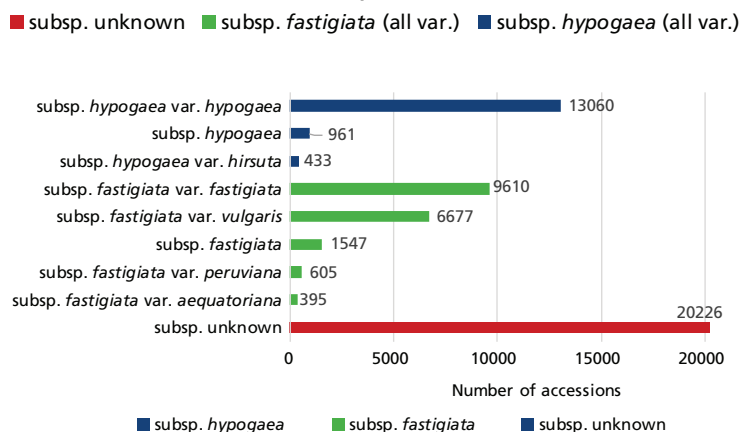
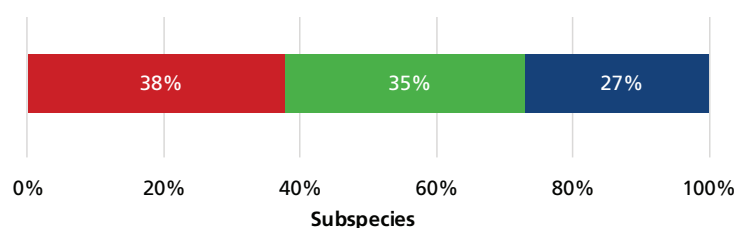
Like its wild counterparts, the cultivated peanut's primary gene pool is similarly endangered in areas of peanut diversity where local landraces are undergoing genetic erosion *in situ*. The frequent lack of recorded information regarding the diversity that existed in a particular locality in the past, can make it difficult to quantify the current loss of diversity in absolute terms (Houry et al. 2021). Nevertheless, a general consensus of visiting researchers and local

farmers supports the belief that peanut landraces are being lost at an increasing rate (Williams 1992, Loko 2020).

Gaps in the existing landrace collections are not only taxonomic but also ecogeographic. As noted previously, high levels of endemism are characteristic of peanut landraces (Krapovickas et al. 2009, 2013, 2021), meaning that unique diversity can be expected wherever peanuts have been cultivated for a very long time. A surprising amount of cultivated peanut diversity has been recently discovered in Mexico and Guatemala, while other countries in the crop's prehistoric range (e.g., Colombia, Venezuela, Guyana, Suriname, Belize, Honduras, Nicaragua, Costa Rica and Panama) have yet to be systematically explored for their indigenous peanut landraces. The same is true for



**Figure 3.2** Percentages of all biological germplasm types conserved *ex situ* as reported by the respondents to the online survey. Note the large proportion of “Landraces” (39%), followed by “Unknown” (11%) and “Other” (13%) unspecified types, which together represent nearly two thirds (63%) of the total accessions.



**Figure 3.3a** (top) and **3.3b** (bottom) Proportions and number of cultivated accessions conserved *ex situ* by the respondents to the online survey, as identified to subspecies and botanical variety. Note the large percentage of accessions (38%) reported with both subspecies and botanical variety identified as “unknown”, and the minute proportions (<1% each) representing the botanical varieties *hirsuta*, *peruviana* and *aequatoriana*.

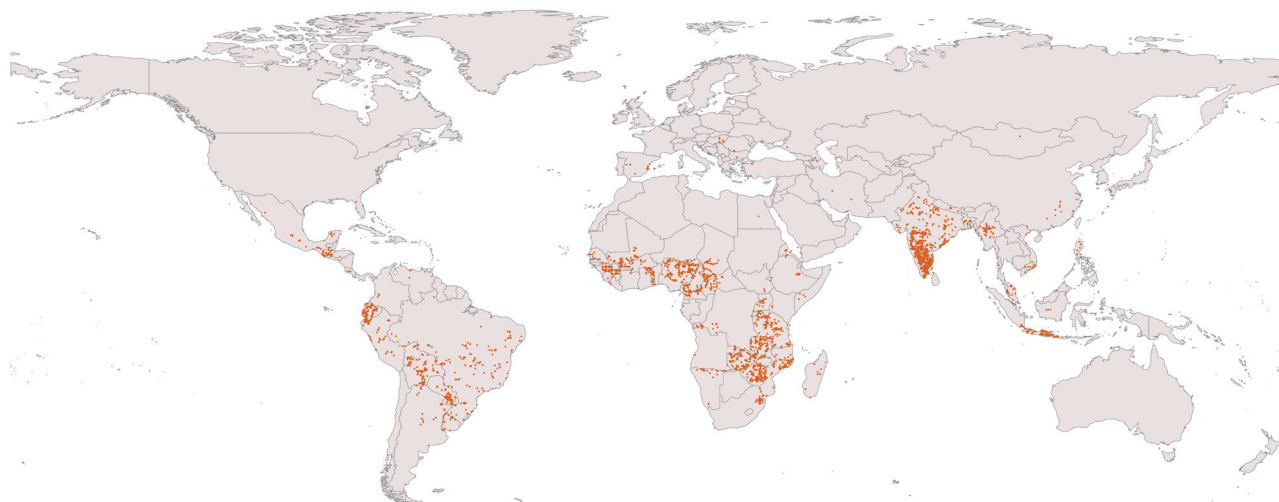
nearly the entire Amazon basin, where many unique and distinctive landraces are known to exist (Williams 1989, 1992; Nascimento et al. 2020), but large sectors remain entirely unexplored for native peanut varieties and relatively few Amazonian landraces are conserved *ex situ*.

Due to the peanut's early global dissemination in colonial times, independent secondary centers of landrace diversity developed in Africa, Asia and Oceania, but these local varieties have been scarcely described or conserved, and are likewise being rapidly displaced by improved cultivars. An interesting example is the spread of the botanical variety *hirsuta* in Asia (Krapovickas 1998). Known as "dragon" peanuts in China, this botanical variety was widely cultivated in prehistoric times from Argentina to as far north as Mexico. Today the variety *hirsuta* is rare in the Americas, cultivated only to a limited extent in a few, small and isolated places in northern Peru, Ecuador, Colombia, Guatemala and Mexico. However, in the mid-1600s, var. *hirsuta* landraces were evidently introduced – probably from Peru – into China, SE Asia, the Malay Archipelago, and India by early European traders. There, the newly introduced crop was rapidly adopted and diversified by the local farmers, who created novel landraces of "dragon" peanuts, never seen in the Americas. According to Sun (1998, cited by Barkley et al. 2016) in his account of peanut collecting activities in China, compared to other countries, more dragon-type landraces were collected than any other variety as these were the most extensively cultivated peanut variety in China until the early 20th century. The Oil Crops Research Institute of CAAS currently reports 375 accessions of *A. hypogaea* var. *hirsuta* in the Chinese national collection, while only 29 accessions of this botanical variety are conserved in the United States peanut collection, and the Global Peanut Collection at ICRISAT reports just 13 accessions. In West Africa, a significant diversity of local landraces

was recently described in cultivation by traditional farmers of various ethnicities in 33 villages in southern and central Benin (Loko et al. 2020). At present, these Beninese materials have not yet been identified to their botanical variety, are not conserved *ex situ* in any genebank under medium- or long-term storage conditions, but they continue to be valued and conserved by local farmers *in situ* (on-farm) as key components of their traditional seed systems.

### 3.3.3 Regional assessment of peanut landrace accessions

Based on passport data obtained from Genesys, WIEWS, USDA-GRIN, and ICRISAT databases, plus information obtained from the online survey, a general appraisal can be made regarding the geographic coverage and genetic diversity of the cultivated peanut accessions that are identified as landrace materials conserved *ex situ*. This information is presented in Figure 3.4, Tables 3.2, 3.3, 3.7, 3.8, and 3.9. Because many – if not most – cultivated peanut accessions are not identified as to their biological status (i.e., landrace, improved variety, breeding material, etc.) or to their botanical variety, it must be recognized that the simple quantity of accessions originating from a given country can serve only as an imprecise indicator of the actual presence and diversity of peanut landraces conserved *ex situ*. The raw numbers of accessions obtained from a given country can give a rough idea of the extent to which local peanut landraces may have been collected there, and can be useful for identifying outstanding *geographical* gaps in the existing germplasm collections. However, given the historic lack of attention given to peanut landraces in many countries, the quantity of locally collected accessions is often the only indicator we have for estimating *taxonomic* gaps in the collections, until those conserved materials can be duly characterized, named and described, and further germplasm collecting is done in the field.



**Figure 3.4** Origins of identified landrace accessions conserved *ex situ* and with coordinate data available. (Data sourced from Genesys, WIEWS, USDA-GRIN, and ICRISAT web portals. Only 45% of the 16,822 landrace accessions in this dataset have coordinate data.)

Taking into consideration the caveats described above, the following observations can be made regarding the likely *ex situ* coverage of landrace accessions from the following geographic regions.

### The Americas

#### Mexico, Central America, and the Caribbean

Significant peanut landrace diversity has been collected in Mexico, although the country has yet to be systematically explored for peanut landraces, and little characterization of the collected landraces has been carried out. USA016 currently holds 82 accessions, primarily from central Mexico and the states of Yucatan and Chiapas. Peanut landraces from Central American countries and the Caribbean are poorly represented in *ex situ* collections, with the exception being Guatemala, from where USA016 conserves a comprehensive sampling of 57 landrace accessions collected throughout the country. In our data, we found no accessions of peanuts collected in Nicaragua, El Salvador, and Panama, and only one accession each from Belize and Honduras. Similarly, there are extremely few landrace accessions from Caribbean countries, with the exception of Cuba.

### South America

#### Argentina

According to our survey, ARG044 and ARG1133 together hold more than 3,200 accessions of landraces, many of these collected regionally. Peanut landraces from Argentina are well represented *ex situ*, and are widely duplicated in other major genebanks.

#### Bolivia

We found that BOL316 holds a collection of about 1,000 landraces collected nationally, moreover USA016 holds about 500 landrace accessions from Bolivia, and IND001 holds 432 accessions. Based on passport data, at least part of the collection held at ICRISAT are duplicates of accessions held in USDA genebanks. The collection held in Bolivia is not characterized at subspecies level so it is not known how well the different subspecies and botanical varieties are represented. Krapovickas et al. (2009) formally named and described 62 distinct landraces for Bolivia, most of which are endemic.

#### Brazil

In our dataset, we found more than 6,500 accessions of cultivated peanut held in Brazil and, of these, at least 1,000 are landraces. Only 270 of these have geographical coordinates, so it is difficult to make precise estimates of the coverage of different regions of Brazil but, based on the data available, the northern states of Brazil, including the Amazon basin, are not well covered in *ex situ* collections (Table 3.2). Of the more than 400 accessions of landraces from Brazil held at IND001, the majority were donated by USDA and CENARGEN genebanks.

### Chile

In our dataset, we found only one landrace accession from Chile, and the other 11 accessions from Chile are of unknown biological status.

### Colombia

According to data in WIEWS we found only 24 accessions of cultivated peanut from Colombia. In our dataset, 9 are held at USA016 and 15 at VIR (RUS001), but none of these have information on biological type (landrace, improved variety, breeding material etc.). COL017 stores 211 accessions of cultivated peanuts but the information on the origin and the biological type of these accessions is missing. Based on the data available, we conclude that landraces from Colombia are currently not well represented *ex situ*.

### Ecuador

INIAP Ecuador currently conserves 448 accessions of cultivated peanut, and of these about 300 are landrace materials collected in Ecuador. USA016 also conserves 369 landrace accessions from Ecuador, which are likely to be duplicates from INIAP (as INIAP reported to have 374 accessions at safety-duplicated at USA016). Importantly, these collections include all the five botanical varieties expected in Ecuador (*var. aequatoriana*, *var. fastigiata*, *var. peruviana*, *var. hirsuta*, and *var. hypogaea*). Krapovickas et al. (2021) described 51 distinct landraces from Ecuador, nearly all of which are endemic.

### Peru

Landrace accessions from Peru are found at ICRISAT (289 accessions), USA016 (215 accessions) and PER773 (INIA, Peru, ca. 170 accessions), and USA520. Based on passport data, landrace accessions from Peru held at ICRISAT are mostly duplicates received from USA016 and USA520. In terms of the different botanical varieties, we found only 7 accessions of *var. peruviana* from Peru – its center of diversity. However,

**Table 3.2** Number of accessions, by state, for landraces collected in Brazil. Coordinate data are not available for many accessions, making impossible to determine the exact site of collection.

State	Accessions	State	Accessions
Rio Grande do Sul	77	Rondônia	7
Minas Gerais	69	Maranhão	6
São Paulo	57	Acre	5
Mato Grosso	48	Tocantins	3
Mato Grosso do Sul	34	Santa Catarina	3
Goiás	29	Amazonas	3
Bahia	19	Rio de Janeiro	2
Pernambuco	10	Distrito Federal	2
		Ceará	1

the majority of accessions collected in Peru have not been determined at the variety level. Krapovickas and colleagues (2013) described 47 distinct landraces from Peru, nearly all of which are endemic.

#### **Paraguay**

About 100 landrace accessions from Paraguay are stored in USA016 and about 100 at ICRISAT (IND002), which are mostly duplicated from USA016 and USA315. However, none of these accessions are identified as var. *vulgaris*, which is native to the Guaraní area of Paraguay, Argentina, and Brazil. Additionally, the Paraguayan genebanks that responded to the survey hold 137 landrace accessions, of which about 80% were collected in Paraguay, and about 23 of those are var. *vulgaris*.

#### **Uruguay**

URY003 (UDELAT) conserves 463 accessions of landraces collected in Uruguay. Smaller collections of landraces from Uruguay are held at USA016 (140 accessions) and ICRISAT (21 accessions). The collections held at URY003 are stored in medium-term storage and require urgent regeneration; only 50 accessions have safety duplicates (held at USA016).

#### **Venezuela, Suriname, Guyana and French Guiana**

In the data recovered from WIEWS, Genesys, USDA-GRIN, and the ICRISAT web portal, we found only 15 landrace accessions from Venezuela, 1 from Suriname, 3 from Guyana, and none from French Guiana.

#### **Africa**

##### **North Africa**

In our dataset, we found 435 landrace accessions obtained from countries in Northern Africa. Among these were 394 from Sudan, 28 from Egypt, 11 from Morocco, and 2 from Algeria.

##### **West Africa**

In our dataset, we found 1,977 landrace accessions from West African countries held *ex situ*. Among these, 661 are from Nigeria, 367 from Mali, 206 from Senegal, 184 from Guinea, 100 from Togo, 98 from Ghana, 95 from Niger, and 95 from Burkina Faso. Only 32 landrace accessions are recorded in our dataset from Sierra Leone although, according to a model of peanut landraces' potential geographic distribution produced as part of the work conducted by the CGIAR Genebank Platform (CGIAR Genebank Platform 2020), most of the area in Sierra Leone is suitable for peanut landraces. Therefore, landraces from Sierra Leone may be under-represented *ex situ*.

##### **East Africa**

In our dataset, we found 3,830 landrace accessions from East African countries held *ex situ*. Among these, 1,307 are from Zambia, 773 from Tanzania,

336 from Uganda, 279 from Mozambique, 150 from Kenya, 78 from Madagascar, and 63 from Ethiopia. We found only two potential landrace accessions from Rwanda, one from Burundi, and no accessions from South Sudan. Therefore, landraces from these countries may be under-represented *ex situ*. In the case of South Sudan, it is also possible that accessions collected in what is now South Sudan were recorded in the database as coming from Sudan, before South Sudan became independent in 2011. The relatively low number of peanut landrace accessions from Ethiopia suggests that a mission to collect local peanut varieties in that country would be worthwhile.

#### **Middle Africa**

In our dataset, we found 163 landrace accessions from Chad, 161 from Congo, 119 from Central African Republic, 109 from Cameroon, and 93 from Angola.

#### **South Africa**

In our dataset, we found 684 records of landrace accessions from Southern African countries, corresponding to 274 from Botswana, 252 from South Africa, 109 from Cameroon, and 49 from Namibia.

#### **Asia and Oceania**

In our dataset, we found 3,158 landrace accessions from Asian countries, and 2,279 of these were collected in India. Additionally, through our survey we learned that CHN003 holds 2,728 landrace accessions, and 65% of these (approx. 1,773 accessions) were collected in China.

#### **India and other South Asian countries**

In our dataset, we found 8,103 *Arachis* accessions from India stored at IND001, but it is difficult to know how many of these are landraces as the biological status of the accessions is missing for most of the accessions in the data available. We also found 1,697 accessions of landraces from India held at IND002, 380 at NER047 (most likely duplicates from IND002), and 189 at USA016. In our dataset, we also found 67 accessions of landrace peanuts from Bangladesh, 29 from Nepal, and 29 from Sri Lanka. The 772 peanut accessions reported by Pakistan (PAK001) are not determined to either botanical variety nor biological status, so the number of Pakistani peanut landraces conserved in their significant *ex situ* collections remains in question.

#### **China**

Reportedly, peanut landraces have been collected extensively in China and are mostly stored in CHN003. For more information on Chinese landraces, see the description of the OCRI-CAAS genebank in the following section on Key Collections. In our dataset, we found 148 landrace accessions from China conserved in genebanks outside of China, most of which are held at ICRISAT.

### South East Asia

In our dataset, we found accessions of landraces from South East Asian countries. Among these 228 from Indonesia, 88 from Myanmar, 67 from Malaysia, 64 from Vietnam, and 36 from the Philippines. The 1,732 peanut accessions reported by Thailand (THA300) are not determined to either botanical variety nor biological status, so the number of Thai peanut landraces conserved in their significant *ex situ* collections remains in question.

### Oceania

Little information on peanut landrace diversity – either *in situ* or *ex situ* – is currently available for Oceania. However, a number of unusual examples of local peanut varieties have been reported from various Pacific island nations (e.g., Papua New Guinea, Vanuatu, and the Solomon Islands) in recent years. It appears that Oceania may represent an important gap, not only in the international peanut collections, but also in our knowledge and understanding of the history and consequences of the peanut's introduction and dispersal in this region over the past five or six centuries – if not longer.

**Table 3.3** Global accessions of cultivated peanut (*A. hypogaea*) by host institution, subspecies, and botanical variety. Abbreviations: hyp = *hypogaea*; hir = *hirsuta*; aeq = *aequatoriana*; per = *peruviana*; vul = *vulgaris*; fas = *fastigiata*; NK = variety not known.

INSTCODE	<i>Arachis hypogaea</i>	subsp. <i>hypogaea</i>			subsp. <i>fastigiata</i>					Total
	subsp. NK	var. NK	var. hyp	var. hir	var. NK	var. fas	var. vul	var. per	var. aeq	
ARG1211	1,099	0	718	5	0	1,014	152	259	223	3,470
ARG1133	216	26	73	3	65	10	25	4	10	432
AUS167	0	0	0	0	0	0	0	0	0	0
AUS165	1,101	0	0	0	0	0	0	0	0	1,101
AZE003	7	0	0	0	0	0	0	0	0	7
AZE015	1	0	0	0	0	0	0	0	0	1
BENIN*	120	0	0	0	0	0	0	0	0	120
BGD028	50	0	0	0	0	0	0	0	0	50
BGR001	0	0	1,373	0	0	0	0	0	0	1,373
BOL316*	1,079	0	0	0	0	0	0	0	0	1,079
BRA002	2,070	23	104	1	25	305	4	2	2	2,536
BRA006	260	0	357	0	0	1,108	361	0	0	2,086
BRA003	1,478	0	19	0	0	112	0	0	0	1,609
BRA007	281	0	0	0	0	0	0	0	0	281
BWA015	417	0	0	0	0	0	0	0	0	417
CAN004	6	0	0	0	0	0	0	0	0	6
CHN003	2,268	0	2,256	375	0	2663	734	5	6	8,307
COL003	0	0	0	0	0	0	0	0	0	0
COL017	211	0	0	0	0	0	0	0	0	211
CRI001	2	0	0	0	0	0	0	0	0	2
CUB014	104	0	0	0	0	0	0	0	0	104
CUB284	23	0	0	0	0	0	0	0	0	23
DEU146	2	0	0	0	0	0	0	0	0	2
ECU023	37	11	19	7	228	73	0	41	68	484
ERI003	50	0	0	0	0	0	0	0	0	50
ESP004	18	0	0	0	0	0	0	0	0	18
ETH013	2	0	0	0	0	0	0	0	0	2
ETH065	63	0	0	0	0	0	0	0	0	63
GUY021	7	0	0	0	0	0	0	0	0	7
HUN003	82	0	0	0	0	0	0	0	0	82

INSTCODE	<i>Arachis hypogaea</i>	<i>subsp. hypogaea</i>			<i>subsp. fastigiata</i>					Total
	subsp. NK	var. NK	var. <i>hyp</i>	var. <i>hir</i>	var. NK	var. <i>fas</i>	var. <i>vul</i>	var. <i>per</i>	var. <i>aeq</i>	
IND002	125	0	6,806	13	403	2,334	5176	251	14	15,122
IND001	13,533	0	0	0	2	96		0	0	13,631
JPN183	1,135	0	0	0	0	0	0	0	0	1,135
KEN212	168	0	0	0	0	0	0	0	0	168
LKA036	60	0	0	0	0	0	0	0	0	60
MDG016	272	0	0	0	0	0	0	0	0	272
MEX006	7	0	0	0	0	0	0	0	0	7
MEX208	4	0	0	0	0	0	0	0	0	4
MMR015	655	0	0	0	0	0	0	0	0	655
MWI041	112	0	0	0	0	0	0	0	0	112
NAM06	18	0	0	0	0	0	0	0	0	18
NER001	42	0	0	0	0	0	0	0	0	42
NER047	6,131	0	0	0	0	0	0	0	0	6,131
PAK001	772	0	0	0	0	0	0	0	0	772
PER773**	250	0	0	0	0	0	0	0	0	250
PHL213	101	0	0	0	0	0	0	0	0	101
PRT001	0	0	0	0	0	0	0	0	0	0
PRY008	0	0	4	0	0	42	10	0	0	56
PRY027	11	0	4	0	0	26	0	0	0	41
PRY037	0	0	9	0	0	34	13	0	0	56
ROM021	0	0	0	0	0	0	121	0	0	121
RUS001	1,713	0	0	0	0	0	0	0	0	1,713
SDN002	274	0	0	0	0	0	0	0	0	274
SEN002	0	0	250	0	0	850	70	20	10	1,200
SWZ015	61	0	0	0	0	0	0	0	0	61
THA300	1,732	0	0	0	0	0	0	0	0	1,732
TWN001	28	0	0	0	0	0	0	0	0	28
TZA016	141	0	0	0	0	0	0	0	0	141
ZAF062	211	0	0	0	0	0	0	0	0	211
ZMB030	606	0	0	0	0	0	0	0	0	606
ZMB048	515	0	0	0	0	0	0	0	0	515
UGA132	313	0	0	0	0	0	0	0	0	313
UKR012	17	0	0	0	0	0	0	0	0	17
UKR048	29	0	0	0	0	0	0	0	0	29
URY003	0	0	0	0	463	0	0	0	0	463
USA016	6,992	160	533	29	363	1,149	130	23	62	9,441
USA158	62	10	3	0	2	1	0	0	0	78
USA317	159	741	554	0	0	2	2	0	0	1,458
USA520	5,238	0	0	0	0	0	0	0	0	5,238
<b>GRAND TOTALS</b>	<b>52,541</b>	<b>971</b>	<b>13,082</b>	<b>433</b>	<b>1,551</b>	<b>9,819</b>	<b>6,798</b>	<b>605</b>	<b>395</b>	<b>86,195</b>

Data sources:   =WIEWS + Genesys + GRIN-Global   =Online peanut survey   =ICRISAT website

†formal INSTCODE not yet assigned \*assumed to be equal to BOL317 \*\*assumed to be equal to PER031

### 3.3.4 Conclusions regarding peanut landrace conservation *ex situ*

- **Conclusion 1** – Peanut landraces from Central American and Caribbean countries, as well as from Northern South America (i.e., Colombia, Venezuela, Guyana, Suriname, and French Guiana) and Amazonian Brazil, are poorly represented in *ex situ* collections. In the Southern Cone, Uruguay and Chile have a smaller number of accessions of landraces conserved *ex situ* compared to other South American countries.
- **Conclusion 2** – In Africa, landrace materials from Sierra Leone, Rwanda and Burundi are not well represented in *ex situ* collections. This could also be the case with South Sudan, although it is also possible that the country of origin of accessions collected in South Sudan has not been corrected in passport data since its recent independence from Sudan.
- **Conclusion 3** – In Asia, the large majority of landrace materials were collected in China and in India, both of which may already be well represented *ex situ*. The numbers of landrace accessions reported from Bangladesh, Malaysia, Myanmar, Nepal, Philippines, Sri Lanka, and Vietnam appear lower than would be expected, and suggest that further collecting of local peanut varieties in those countries needs to be undertaken before the region's unique landraces become lost *in situ* through attrition, abandonment, or displacement by commercial varieties or other crops. The existence of unique peanut landraces in Pakistan and Thailand would be worth exploring with the collaboration of PAK001 and THA300. Similarly, further effort is needed to collect and conserve the unusual and undocumented peanut landraces reported from the Pacific Islands of Oceania.
- **Conclusion 4** – Determination of unidentified peanut accessions to the level of botanical variety, as well as to their **biological status** (i.e., landrace, improved variety, breeding material, etc.), is vitally important to have a better assessment of the geographical coverage and the genetic diversity of cultivated peanut accessions conserved *ex situ* in collections. Furthermore, additional collecting activities appear to be in order for many countries where local peanut landraces have been historically overlooked and undervalued as genetically diverse and locally adapted breeding materials. When collecting new accessions, it is important that the biological status as well as georeferenced (GPS) data be recorded at the collecting site to allow a more precise evaluation of the ecogeographic distribution and remaining gaps in landrace collections.

## 3.4 Key collections

The world's six largest collections of *Arachis* germplasm are currently maintained by: (1) the International Crop Research Institute for the Semi-Arid Tropics-ICRISAT (IND002) in India; (2) the Indian Council of Agricultural Research-ICAR (IND001) in India; (3) the US Department of Agriculture-USDA (USA016) in the United States; (4) the Oil Crops Research Institute of the Chinese Academy of Agricultural Sciences-OCRI-CAAS (CHN003) in China; (5) the Texas AgriLife Research Center of Texas A&M University-TAMU (USA520) in the United States; and (6) the Empresa Brasileira de Pesquisa Agropecuaria-EMBRAPA (BRA002) in Brazil. Together, these six collections maintain a total of more than 58,000 *Arachis* accessions, roughly two thirds of the global total. While it must be recognized that a large number of accessions are duplicated among these collections, a significant amount of unique material is also conserved in each.

Aside from these six largest *Arachis* repositories, a number of smaller but nonetheless important peanut collections exist in various countries around the world. Four of these smaller collections are also included here because they contain unique landraces, wild species, experimental research materials, and/or institutional research and conservation capacities that are not duplicated elsewhere and, therefore, also constitute strategic collections from a global conservation perspective. The germplasm holdings, conservation methods, challenges, and distribution policies of these 10 key collections are briefly described below in light of their potential roles in the implementation of a Global Peanut Conservation Strategy.

### 3.4.1 ICRISAT (International Centre for Research in the Semi-Arid Tropics) – Patancheru, India (IND002)

ICRISAT is one of the 14 International Agricultural Research Centers of CGIAR and, in this capacity and as part of its international mandate, it maintains a global collection for groundnut (peanut) research and improvement. ICRISAT's groundnut collection was established in 1976 and is now the largest collection of *Arachis* germplasm in the world. The collection presently contains a total of 15,622 accessions of *Arachis* germplasm, with more than 15,000 accessions of cultivated peanut (*A. hypogaea*) from 92 countries, and 480 accessions of 47 wild *Arachis* species from six countries.

The cultivated peanut collection includes 7,397 accessions of traditional cultivars/landraces, 982 accessions of improved cultivars, 5,000 breeding lines and research materials, and 1,729 genetic stocks. All six botanical varieties of *A. hypogaea* are represented and identified in the collection: var. *hypogaea* (6,806 accessions), var. *vulgaris* (5,176 accessions), var. *fas-*



ICRISAT's peanut collection is conserved for long-term storage in double aluminum foil packing at -20 degrees Celsius.  
Photo: Vânia Azevedo/ICRISAT



*tigiata* (2,334 accessions), var. *peruviana* (251 accessions), var. *hirsuta* (13 accessions), and var. *aequatoriana* (14 accessions), plus 403 accessions for which the botanical variety is unknown.

ICRISAT's peanut collection is conserved 95% in long-term storage, packed in vacuum-sealed foil pouches at -20°C; and 99.6% in medium-term storage, packed in aluminum cans at 4°C and 20% RH. Whole plants of *Arachis glabrata* (that do not produce seeds) are maintained in a glasshouse, representing 0.4% of the total collection. More than 75% of the collection has been evaluated for biotic stress, and more than 50% evaluated for abiotic stress. A comprehensive genebank management system and protocols are in effect. Standard operating procedures (SOPs) for conservation, regeneration, characterization, acquisition, distribution and safety duplication are in place. Germination testing is performed on every peanut accession that is regenerated and they are then stored under medium-term and long-term conditions. Regeneration of cultivated materials is almost completely up to date; but around 45% of the wild species collection needs urgent regeneration. Each regenerated peanut accession is sent to the plant quarantine unit for health testing. No serious diseases are currently restricting germplasm distribution, although Indian Peanut Clump Virus (IPCV) limits introduction of groundnut germplasm into the USA.

Accessions from the ICRISAT peanut collection are safety-duplicated in two long-term seed repositories: 14,259 accessions (more than 90% of the entire collection) at the Svalbard Global Seed Vault (SGSV) in Norway, and 2,006 accessions at ICRISAT's Regional Genebank, Niamey, Niger. There are currently constraints to duplicating the collection elsewhere outside of India without Indian Government approval. To date, permission has only been approved for sending safety-duplicate materials to SGSV; permission to send safety-duplicates to other CGIAR genebanks is still pending. No outside genebanks have safety-duplicate materials stored at ICRISAT. Similarly, ICRISAT does not have any *ex situ-in situ* conservation linkages or activities, due to Indian Government policy constraints.

ICRISAT's electronic database for the peanut collection is GIMS, which stores accession-level information on most major data categories. The stored information is publicly available, and accessible (partly) through the internet at [genebank.icrisat.org](http://genebank.icrisat.org), and on Genesys. ICRISAT is currently migrating its data management system to GRIN-Global.

Peanut germplasm samples falling under the provisions of Article 15 of the ITPGRFA are distributed with an SMTA. Domestic distribution of germplasm within India is 79% to academic researchers, 20% to public

sector breeders, and 1% to breeders in the private sector. Recent international distribution has been 33% to academic researchers, 53% to public sector breeders, 7% to private sector breeders, and 7% to other users. Sufficient quantities of about 88% of ICRISAT's seed and living plant materials are currently available for distribution. The average number of accessions distributed annually is: 1,400 nationally, 800 regionally, and 700 internationally. Adequate procedures are in place for phytosanitary certification, packaging, and shipping of germplasm samples, for which no fees are charged.

The collection has a good overall global coverage in terms of its genetic diversity, although significant taxonomic gaps have been identified for South American materials (see above). The identified gaps need to be filled as a priority through collecting missions. However, many South American countries currently restrict access to their plant genetic resources by outside institutes. Since those countries cannot presently share their materials with ICRISAT for distribution, actions are being considered to provide them with support so that they can collect and conserve rare or unique local materials in their national collections. Moreover, ICRISAT is open to discuss the possibility of providing those countries with "black box" storage services where back-up duplicates of their national collections can be safely kept under long-term conservation conditions.

The ICRISAT peanut collection's funding, staffing, donor interest, and the availability of genetic resources required by breeders, are all reported as adequate. However, active use of the collection by breeders, researchers and other users, and the requested feedback from them, is still lacking. Historically, ICRISAT scientists collaborated with and had personal participation in international *Arachis* collecting missions in South America, most notably R. Gibbons, J.P. Moss, V.R. Rao, A.K. Singh, and P. Bramel. Current collaboration with other genebanks or breeders on aspects of peanut germplasm management was not reported, nor was participation in any network of peanut germplasm holders or users.

The most important vulnerabilities and threats to the ICRISAT peanut collection are:

- The large gap between the availability of diverse materials, and its utilization in breeding and research
- The excessive use of a reduced number of closely related germplasm accessions
- The limited amount of available evaluation data
- The difficulty in filling remaining gaps in the collection with new accessions from the crop's center of origin

### 3.4.2 ICAR-NBPGR (National Bureau of Plant Genetic Resources) – New Delhi, India (IND001)

#### ICAR-DGR (Directorate of Groundnut Research) – Junagarh, India (IND025)

The Indian Council of Agricultural Research (ICAR) maintains two important national peanut collections in India. The largest of these is hosted by the National Bureau of Plant Genetic Resources (NBPGR) in New Delhi, where 13,755 total accessions are conserved (ICAR-NBPGR 2020), including 81 accessions representing 16 wild *Arachis* species (Table 3.4). The second of ICAR's peanut collections is hosted by the Directorate of Groundnut Research (DGR) located in Junagarh, where 97 accessions representing 43 wild species of *Arachis* are conserved, as well as two accessions each of *A. hypogaea* var. *hirsuta* and var. *aequatoriana*, and one accession of *A. hypogaea* var. *peruviana* (Table 3.5).

Unfortunately, no response to the online survey was received from ICAR other than the NBPGR response to survey Question 13 (Table 3.4), and a list of germplasm accessions held by the DGR (Table 3.5) which was sent as an email attachment, both of which are presented below. No further details were provided about the ICAR genebanks or their peanut genetic resources collections.

### 3.4.3 USDA (United States Department of Agriculture) – Griffin, Georgia, USA (USA016)

The USDA's National Peanut Collection was established in 1949 and is maintained at the Plant Genetic Resources Conservation Unit (PGRUC) in Griffin, Georgia. It is one of the largest and most comprehensive *Arachis* germplasm collections in existence, currently consisting of 9,753 active accessions, of which 9,194 are cultivated peanuts (*Arachis hypogaea*), and 559 are wild *Arachis* species.

Since 1936, USDA has conducted and/or supported an extensive series of international missions to collect both cultivated and wild *Arachis* germplasm in South America and other countries of Latin America and the Caribbean, the peanut's primary center of origin and diversity (Annex 6). The USDA collection is composed of *Arachis* materials collected in, or donated by, 102 countries around the world.

The 9,194 accessions of cultivated peanut include numerous unimproved landrace samples representing each of the six botanical varieties of peanut, as well as modern, improved and legacy cultivars, breeding materials, and genetic stocks.

The cultivated peanut materials are maintained entirely as seed accessions. Each seed accession is split into two samples which are stored at 4°C and

-18°C, respectively. The seed samples stored at 4°C are maintained at 25% relative humidity and are primarily used for distribution to requestors, whereas those stored at -18°C are packed in heat-sealed laminated foil bags used for long-term preservation. Over 95% of the USDA peanut collection is backed-up with security-duplicate samples in long-term cold storage at the National Laboratory for Genetic Resources Preservation (NLGRP) in Fort Collins, Colorado. Additionally, about 877 cultivated peanut and 116 wild species accessions are deposited in the Svalbard Global Seed Vault as a secondary security back-up.

The USDA collection of wild *Arachis* germplasm currently maintains 559 accessions, representing at least 65 different species (Annex 5). The maintenance of wild *Arachis* accessions is much more demanding than the cultivated peanut, because of the different reproductive physiologies and regeneration challenges of the wild species. Accessions of section *Rhizomatosae* (perennial peanut) and some wild *Arachis* species are maintained clonally as whole plants in the greenhouse, but most wild *Arachis* species accessions are stored as seed in 4°C and -18°C cold storage.

The US National Peanut Collection has an adequate and stable maintenance budget, and the management of the collection is not presently considered to be at risk. Staffing is currently limited to the curator and one full-time technician to assist the curator with peanut germplasm curation activities. The curator and the technician work together to maintain plants in the greenhouses with daily watering, periodical fertilization and chemical sprays. They also coordinate field planting, harvesting and post-harvest activities involving shelling, cleaning seeds, recording descriptor data, and filling vegetative requests for peanut germplasm. In addition, a part-time worker assists with postharvest activities and other general greenhouse tasks such as weeding, trimming and cleaning. Adequate greenhouse space which includes 3,400 square feet of greenhouse bench space, is available for the maintenance of perennial peanut germplasm and regeneration of other wild species. Additionally, a large screenhouse is available for peanut regenerations. Adequate field space and manual support is available for planting and managing the crop, and for harvesting operations. A full-fledged analytical laboratory is available for measuring total oil, fatty acid profiles and protein content of the peanut germplasm, and is also equipped with facilities to conduct basic PCR work (Tallury 2020).

One external concern that could potentially threaten the collection is the peanut smut disease caused by the soil-borne fungus, *Thecaphora frezii*. This disease is currently limited to Argentina, where present estimates indicate that all peanut production areas in

**Table 3.4** Wild *Arachis* species held by ICAR-NBPGR, New Delhi, India.

Q13. Please record each of the wild *Arachis* species in your collection, with the number of accessions conserved, and the percentage (%) of those accessions conserved by the different storage methods:

Species name	Accessions in Long Term Storage as Seeds	Accessions in Cold Storage as Seeds (%)	Accessions in Greenhouse (%)	Accessions in Field Plots (%)	Accessions in Tissue Culture (%)
<i>Arachis appressipila</i>	4				
<i>Arachis benensis</i>	2				
<i>Arachis cardenasii</i>	5				
<i>Arachis chiquitana</i>	14				
<i>Arachis dardani</i>	1				
<i>Arachis duranensis</i>	32				
<i>Arachis hoehnei</i>	4				
<i>Arachis kretschmeri</i>	1				
<i>Arachis kuhlmannii</i>	1				
<i>Arachis matiensis</i>	1				
<i>Arachis paraguariensis</i>	1				
<i>Arachis pusilla</i>	3				
<i>Arachis rigonii</i>	1				
<i>Arachis stenophylla</i>	1				
<i>Arachis stenosperma</i>	8				
<i>Arachis valida</i>	2				

**Table 3.5** *Arachis* species held by ICAR-DRG, Junagarh, India.

No.	Species	Number of Accessions	No.	Species	Number of Accessions
1	<i>A. benensis</i>	2	25	<i>A. archeri</i>	1
2	<i>A. burchellii</i>	1	26	<i>A. correntina</i>	1
3	<i>A. cardenasii</i>	5	27	<i>A. dardani</i>	1
4	<i>A. chiquitana</i>	2	28	<i>A. decora</i>	2
5	<i>A. dardani</i>	2	29	<i>A. diogoi</i>	1
6	<i>A. duranensis</i>	27	30	<i>A. duranensis</i>	1
7	<i>A. glabrata</i>	1	31	<i>A. glabrata</i>	2
8	<i>A. hagenbeckii</i>	1	32	<i>A. glandulifera</i>	1
9	<i>A. hermannii</i>	1	33	<i>A. hoehnei</i>	1
10	<i>A. hoehnei</i>	2	34	<i>A. hypogaea var. aequatoriana</i>	2
11	<i>A. kretschmeri</i>	1	35	<i>A. hypogaea var. hirsuta</i>	2
12	<i>A. kuhlmannii</i>	1	36	<i>A. hypogaea var. peruviana</i>	1
13	<i>A. major</i>	1	37	<i>A. ipaensis</i>	1
14	<i>A. marginata</i>	1	38	<i>A. kuhlmannii</i>	1
15	<i>A. matiensis</i>	2	39	<i>A. magna</i>	1
16	<i>A. monticola</i>	2	40	<i>A. oteroi (kuhlmannii)</i>	1
17	<i>A. pintoii</i>	2	41	<i>A. paraguariensis</i>	1
18	<i>A. prostrata</i>	2	42	<i>A. simpsonii</i>	1
19	<i>A. pusilla</i>	4	43	<i>A. stenosperma</i>	3
20	<i>A. stenosperma</i>	6	44	<i>A. sylvestris</i>	1
21	<i>A. sylvestris (pusilla)</i>	2	45	<i>A. triseminata</i>	1
22	<i>A. valida</i>	3	46	<i>A. valida</i>	1
23	<i>A. vallsii</i>	2			
24	<i>A. williamsii</i>	1			
				<b>TOTAL</b>	<b>102</b>

the country are infected (Rago et al. 2019, Wann et al. 2020). If this pathogen were ever to enter the US, it could potentially shut down the entire US peanut industry. It can be presumed that all current cultivars are highly susceptible to this pathogen and there is an urgent need to identify resistant sources to peanut smut. A cooperative research effort to combat peanut smut is underway between the USDA-ARS, the US peanut industry, and Argentine researchers to identify resistant sources and initiate crossing programs to develop resistant commercial varieties, and this collaboration has already produced encouraging results (Bressano et al. 2018, de Blas et al. 2019, Massa et al. 2021). Meanwhile, phytosanitary vigilance should be pursued through proper quarantine guidelines to prevent an accidental introduction of this pathogen into the US.

An established genebank management system is in place and its procedures and protocols are fully implemented. The routine germplasm regeneration program is essentially up-to-date, with a very low percentage of accessions in urgent need of renewal. Random samples in storage are tested regularly for viability. All regenerated samples are germination-tested before going into cold storage. Health testing is also done before accessions are placed in cold storage. In general, the health of the accessions is good, and does not represent a constraint for their distribution. The collection is 90% characterized agro-morphologically using USDA Peanut Descriptors, while just 2% of the collection has been characterized to date using molecular or genotypic characterization methods. Current research priorities for the collection include: 1) completing the safety duplication effort, and 2) continuing to genotype accessions.

Accession-level information on the peanut collection is publicly available on [USDA's GRIN-Global database](#). This online database is fully searchable for accession-level information on all major data categories, including full passport, characterization, evaluation, images and distribution data for many accessions. Some of the information on the USDA peanut collection can also be found on [PeanutBase](#).

The US National Peanut Collection serves the national and international communities by providing seeds and plant cuttings to requestors for research and education purposes. In the 15 years from 2003 to 2018, a total of 32,187 samples of cultivated peanut and related wild species were distributed to over 52 countries, with China, France, Pakistan, Turkey, Israel, Bolivia, and South Korea being the most frequent foreign requestors. In 2019 alone, 4,527 peanut accessions were distributed to domestic and international users. The uses for the requested germplasm vary widely, but include cytogenetic, molecular and

genomic studies, breeding for pest and disease resistance, drought tolerance, biochemical evaluation, restoration of heirloom varieties, and educational purposes, among others. Germplasm of most accessions is made available at no cost to legitimate users under the terms of the ITPGRFA, through an SMTA. User requests for germplasm can also be processed through the GRIN-Global website.

The US National Peanut Collection actively supports research collaborations with public and private entities by freely providing necessary germplasm to understand and develop knowledge about the collection for use by breeders and other researchers. Research collaborations are in progress for genotypic characterizations of cultivated as well as wild species accessions. In 2019, seed of 2,600 accessions of African origin and some samples of wild *Arachis* species were supplied, respectively, to two genotyping projects currently underway at the University of Georgia. At present, the collection is a collaborating partner in the PeanutBase genomic research network.

USDA plays an inadvertent role in conserving “national” collections of landraces and wild species from various Latin American countries in which collaborative collecting missions have been conducted in the past. Although the original samples collected during those missions were deposited in-country at the time of their initial collection, some of the countries experienced difficulties in conserving, maintaining and/or characterizing those accessions. In these cases, the duplicate set conserved by USDA effectively serves as a *de facto* security back-up, which can be – and in some instances has been – rematriated to their countries of origin along with the corresponding passport and characterization information.

#### **3.4.4 OCRI (Oilseed Crops Research Institute, CAAS) – Wuhan, China (CHN003)**

The National Genebank of *Arachis* species in China was established in 1950, and currently maintains a total of 8,600 accessions, including 8,307 accessions of cultivated peanut (*A. hypogaea* L.), 234 accessions of 37 wild *Arachis* species, and 123 accessions of wild species hybrids. The collection is considered to be partly unique as 65% of the accessions were collected in China, including heritage cultivars and indigenous landraces. All six botanical varieties of the cultigen are represented in the collection, including 375 accessions of var. *hirsuta*, 5 accessions of var. *peruviana*, and 6 accessions of var. *aequatoriana*.

A full genebank management system is in place, with established procedures and protocols for germplasm management. Eighty percent of the collection is conserved in long-term storage at -18°C; 95% of the collection is in medium-term storage at -4°C; and 5%

is conserved in short-term storage. Germination rates are required to be >85% and are tested annually. No urgent regeneration needs are reported. Accession-level information on the collection, including passport, taxonomy, characterization and evaluation data, is stored on a searchable database that is [publicly accessible online](#) (in Chinese). This information is not included in any other (external) databases.

The more important conservation research activities are: collecting diverse accessions, development of the core collection, and genotyping the core collection. The budget for the collection's maintenance and genebank operations is stable and adequate. The National Genebank collection is not safety-duplicated at another institution, nor does it maintain security-duplicate accessions from other institutions. The collection is not currently involved in any *in situ-ex situ* linkages or activities, nor are any germplasm management collaborations reported with any other peanut genebanks, breeders or networks.

Approximately 70% of the collection is currently available for distribution. An average of 700 accessions of *Arachis* germplasm are distributed domestically or regionally per year, using an institutional MTA or other bi-lateral agreement. Of the domestic distributions, approximately 80% are provided to public sector breeding programs and 20% to academic researchers and students. Adequate procedures are in place for phytosanitary certification, packaging and shipping of samples, and no cost is charged for these services. At present, germplasm from the National Genebank is not available for international distribution.

More *var. hirsuta* genotypes were collected in China compared to other botanical varieties as these were the main peanut landraces that were cultivated there until the early 20th Century. A List of Chinese Peanut Genetic Resources published in 1978 described 1,577 accessions. These were composed by the following types: 713 virginia, 481 spanish, 151 dragon, 44 valencia, and 25 intermediate types, and 160 introduced lines (Sun 1998; Barkley et al. 2016).

Since the late 1970s a major effort in collecting and characterizing peanut genetic resources in China was conducted by the Oil Crops Research Institute of the Chinese Academy of Agricultural Science (OCRI-CAAS) in Wuhan, in collaboration with other research institutions across the country (Sun 1998). As part of this effort, landraces were collected, breeding lines and improved cultivars were produced, and additional germplasm was sourced from other countries (Jiang and Ren 2006; Jiang et al. 2008b, 2010b, 2014; Liao 2014; Yu 2011). As a result, by 2013, 8,439 accessions of cultivated peanut were either collected or produced in China, and 4,638 of these are landraces from

22 Chinese provinces. Furthermore, ICRISAT's mini core collection was introduced into China's peanut collection (Jiang et al. 2008b, 2010a) and, since 1979, 246 accessions of wild *Arachis* were introduced from the USA and ICRISAT. Wild *Arachis* materials are conserved at OCRI and in a nursery in Nanning, Guangxi (Sun, 1998).

The National Crop Germplasm Genebank at the Institute of Crop Science of CAAS in Beijing conducts long-term conservation of crop germplasm, including peanut, while the active genebank at OCRI (Wuhan) was established to provide germplasm to breeders and researchers, as well as to conduct seed regeneration and facilitate the exchange of germplasm in China (Barkley et al., 2016; Yu 2011).

### **3.4.5 TAMU (Texas AgriLife Research Center, Texas A&M University) – Stephenville, Texas, USA (USA520)**

The peanut germplasm collection of Texas A&M University (TAMU) is maintained at the Texas A&M AgriLife Research Center in Stephenville, Texas. This collection conserves an estimated total of 6,500 accessions, including a wide array of peanut landraces from South America, and 954 accessions of wild *Arachis* corresponding to at least 76 species and subspecies, as well as over 300 wild species hybrids – making it one of the largest, most diverse and most comprehensive assemblages of *Arachis* genetic resources in existence. The collection was established in 1975 by Dr. Charles Simpson as a consequence of what would become his lifelong collaboration with Drs. Walton Gregory, Antonio Krapovickas, José Pietrarelli, José Valls, Tom Stalker, and other pioneers of modern peanut science. Dr. Simpson's involvement in this collaboration included his participation and leadership on a series of 24 *Arachis* collecting missions conducted in South America between 1977 and 2007, during which much of the germplasm conserved in this collection was obtained.

Dr. Simpson continues to curate the TAMU *Arachis* collection, upon which a profusion of taxonomic, agronomic, phylogenetic and genomic research has been based. The wealth of genetic diversity contained in this collection has proven to be of great value to peanut breeders. For example, numerous accessions have been successfully utilized by combining them with specific bridge species for incorporating genes from wild species into the development of improved cultivars that are resistant to some serious peanut pests and diseases. The mostly untapped potential of this collection is now assuming even greater importance as newly emerging genomic approaches and tools become increasingly effective in identifying compatible wild species with useful traits, and in transferring those traits to the cultivar.

The germplasm accessions are maintained under a combination of short-term (40%), medium-term (50%) and long-term (20%) storage conditions. Seeds are conserved in a cold-storage box and refrigerators kept at 5°C, 0°C, and -18°C. Most of the wild *Arachis* accessions are also maintained as whole plants in a greenhouse. Germplasm management procedures and protocols are *ad hoc* based on the curator's personal expertise. Currently, about 25% of the wild species and 100% of the cultivated peanut accessions require urgent regeneration, and some problems with local diseases could hinder the distribution of some materials. Passport data is available for 100% of the accessions. No searchable electronic database is used, although some of the accession-level data can be found on [GRIN](#) and [PeanutBase](#).

While the TAMU *Arachis* collection contains some accessions that are unique, many more have been distributed widely and are now duplicated in other collections (e.g. ICRISAT, USDA, EMBRAPA, IBONE, NCSU, INTA, etc.). The cultivated landrace accessions include good regional representation for Peru and Ecuador. Some remaining ecogeographic gaps in the collection are perceived in Brazil, Bolivia, Paraguay and Uruguay. The TAMU *Arachis* collection collaborates regularly with the US National Peanut Collection in Griffin, Georgia (since 1967); with EMBRAPA's Wild *Arachis* Collection in Brasilia, Brazil (since 1979); with IBONE in Corrientes, Argentina (since 1976); and with USDA's GRIN database managers to ensure the compatibility and accuracy of the accession data.

At the present time, none of the TAMU *Arachis* accessions are available for distribution due to insufficient seed quantities and a lack of resources, support personnel, or institutional approval to do so. Access to anyone outside the Texas A&M University System is restricted. Institutional funding for maintenance of the collection has long been insufficient. The principal vulnerabilities that are putting the collection at risk are: 1) a precarious financial situation, 2) inadequate germplasm maintenance facilities, 3) the curator's age and alternative options, 4) restrictive internal and external policies, and 5) a shortage of trained personnel. The cumulative weight of these risks is placing TAMU's historic living germplasm collection in imminent jeopardy of being lost forever. This plight notwithstanding, recent changes in local and higher-level administrators have led to a renewed interest in preservation and internal utilization of the collection that, coupled with external support, could change the present outlook in a favorable direction.

### 3.4.6 EMBRAPA (Empresa Brasileira de Pesquisa Agropecuária) – Brasília, Brazil (BRA002)

Brazil is recognized as the center of origin of the genus *Arachis* (Simpson et al. 2001). At least 64 species of wild *Arachis* are native to Brazil and 45 of these are endemic, more than any other country. Brazil is also the home of a significant diversity of cultivated peanut landraces, particularly of the valencia and virginia market types.

EMBRAPA is a state-owned agricultural research corporation affiliated with the Brazilian Ministry of Agriculture, and since 1981 has been active in peanut genetic resources exploration, conservation and use. EMBRAPA maintains extensive collections of both cultivated and wild peanut germplasm, currently conserving over 4,000 *Arachis* accessions in total.

#### Wild *Arachis* collections

EMBRAPA's collection of wild *Arachis* germplasm is the largest and most comprehensive in the world, with 1,559 accessions of 84 species, including 79 wild species published to date, plus five recently discovered taxa that are in the process of being described as new species (Table 3.6). This collection is maintained in the Wild *Arachis* Genebank at CENARGEN, in Brasilia. The accessions are conserved using a combination of three storage methods. Typically, two or more of these storage methods are employed simultaneously, depending upon the particular requirements of the individual species. The storage methods employed are: seeds in medium-term cold storage; whole plants growing in greenhouses, screenhouses or field plots; and three species (*A. pusilla*, *A. retusa* and *A. villosulicarpa*) are also conserved using slow-growth *in vitro* tissue culture.

In addition to the large Wild *Arachis* Genebank in Brasilia, an *Arachis* Forage Genebank was established by EMBRAPA in Rio Branco, Acre State, in the Amazon biome, to help restore ecological sustainability and productivity in degraded areas of monospecific African grass pastures that were established on deforested land several decades ago. The Forage *Arachis* Genebank currently manages 118 germplasm accessions that are exclusively of the Brazilian stoloniferous species *Arachis pintoii* (83 accessions) and *A. repens* (21 accessions), as well as the rhizomatous *A. glabrata* (14 accessions). These 118 forage accessions are maintained as plants in Rio Branco, where they are studied under greenhouse conditions and in field plots; and they are also conserved as seed in the Wild *Arachis* Genebank at CENARGEN in Brasilia.

#### EMBRAPA's cultivated peanut collections

EMBRAPA's collections of *Arachis hypogaea* germplasm conserve a total of 2,508 accessions (Table 3.7). These collections are currently maintained in four

**Table 3.6.** Wild *Arachis* accessions conserved in EMBRAPA genebanks (Survey Q.13)

13. Please record each of the wild *Arachis* species in your collection, with the number of accessions conserved, and the percentage (%) of those accessions conserved by the different storage methods:

Species name	Number of Accessions	Accessions in Cold Storage as Seeds (%)	Accessions in Greenhouse/ Screenhouse (%)	Accessions in Field Plots (%)	Accessions in <i>In Vitro</i> Tissue Culture (%)
<i>A. appressipila</i>	8	100.0	75.0	0.0	0.0
<i>A. archeri</i>	15	80.0	33.3	0.0	0.0
<i>A. batizocoi</i>	4	75.0	0.0	0.0	0.0
<i>A. benensis</i>	3	33.3	0.0	0.0	0.0
<i>A. benthamii</i>	20	55.0	35.0	0.0	0.0
<i>A. brevipetiolata</i>	6	33.3	33.3	0.0	0.0
<i>A. burchellii</i>	91	63.0	21.0	0.0	0.0
<i>A. burkartii</i>	42	7.1	26.1	0.0	0.0
<i>A. cardenasii</i>	2	100.0	50.0	0.0	0.0
<i>A. chiquitana</i>	1	0.0	100.0	0.0	0.0
<i>A. correntina</i>	8	37.5	0.0	0.0	0.0
<i>A. cruziana</i>	1	100.0	0.0	0.0	0.0
<i>A. cryptopotamica</i>	13	53.8	46.1	0.0	0.0
<i>A. dardani</i>	58	75.8	0.0	0.0	0.0
<i>A. decora</i>	37	78.4	0.0	0.0	0.0
<i>A. diogoi</i>	7	57.1	42.8	0.0	0.0
<i>A. douradiana</i>	7	57.1	42.8	0.0	0.0
<i>A. duranensis</i>	9	66.6	0.0	0.0	0.0
<i>A. giacomettii</i>	4	100.0	50.0	0.0	0.0
<i>A. glabrata</i>	152	6.6	48.0	9.2	0.0
<i>A. glandulifera</i>	2	100.0	0.0	0.0	0.0
<i>A. gracilis</i>	6	66.6	16.6	0.0	0.0
<i>A. gregoryi</i>	17	94.1	0.0	0.0	0.0
<i>A. guaranitica</i>	6	0.0	66.6	0.0	0.0
<i>A. hassleri</i>	1	100.0	100.0	0.0	0.0
<i>A. helodes</i>	16	75.0	50.0	6.2	0.0
<i>A. hermannii</i>	7	71.4	85.7	0.0	0.0
<i>A. hoehnei</i>	7	100.0	0.0	0.0	0.0
<i>A. interrupta</i>	1	100.0	0.0	0.0	0.0
<i>A. ipaënsis</i>	1	100.0	0.0	0.0	0.0
<i>A. jacobinensis</i>	3	66.6	66.6	0.0	0.0
<i>A. kempff-mercadoi</i>	7	85.7	28.6	0.0	0.0
<i>A. krapovickasii</i>	1	100.0	0.0	0.0	0.0
<i>A. kretschmeri</i>	10	70.0	40.0	0.0	0.0
<i>A. kuhlmannii</i>	58	82.7	55.2	0.0	0.0
<i>A. lignosa</i>	7	71.4	57.1	0.0	0.0
<i>A. linearifolia</i>	1	100.0	100.0	0.0	0.0
<i>A. lutescens</i>	34	58.8	8.8	0.0	0.0
<i>A. macedoi</i>	40	65.0	32.5	0.0	0.0
<i>A. magna</i>	15	100.0	0.0	0.0	0.0
<i>A. major</i>	16	50.0	50.0	0.0	0.0
<i>A. marginata</i>	5	100.0	40.0	0.0	0.0
<i>A. martii</i>	5	80.0	40.0	0.0	0.0
<i>A. matiensis</i>	31	70.9	12.9	0.0	0.0
<i>A. microsperma</i>	11	90.9	72.7	0.0	0.0
<i>A. monticola</i>	3	100.0	0.0	0.0	0.0
<i>A. nitida</i>	17	0.0	52.9	0.0	0.0
<i>A. oteroi</i>	27	48.1	18.5	0.0	0.0
<i>A. palustris</i>	7	85.7	0.0	0.0	0.0
<i>A. paraguariensis</i>	34	85.2	29.4	0.0	0.0
<i>A. pflugeae</i>	7	42.8	71.4	0.0	0.0

Species name	Number of Accessions	Accessions in Cold Storage as Seeds (%)	Accessions in Greenhouse/Screenhouse (%)	Accessions in Field Plots (%)	Accessions in In Vitro Tissue Culture (%)
<i>A. pietrarellii</i>	6	33.3	16.6	0.0	0.0
<i>A. pintoii</i>	178	53.9	55.0	46.6	0.0
<i>A. porphyrocalyx</i>	1	100.0	100.0	0.0	0.0
<i>A. praecox</i>	3	100.0	0.0	0.0	0.0
<i>A. prostrata</i>	100	39.0	26.0	0.0	0.0
<i>A. pseudovillosa</i>	14	7.1	35.7	0.0	0.0
<i>A. pusilla</i>	43	90.7	0.0	0.0	2.3
<i>A. repens</i>	42	33.3	54.7	50.0	0.0
<i>A. retusa</i>	30	60.0	50.0	0.0	3.3
<i>A. rigonii</i>	1	100.0	0.0	0.0	0.0
<i>A. schininii</i>	1	100.0	0.0	0.0	0.0
<i>A. seridoënsis</i>	1	100.0	0.0	0.0	0.0
<i>A. sesquijuga</i>	1	100.0	100.0	0.0	0.0
<i>A. setinervosa</i>	6	16.6	0.0	0.0	0.0
<i>A. simpsonii</i>	13	38.4	23.1	0.0	0.0
<i>A. stenophylla</i>	6	33.3	66.6	0.0	0.0
<i>A. stenosperma</i>	57	89.4	0.0	0.0	0.0
<i>A. subcoriacea</i>	4	50.0	50.0	0.0	0.0
<i>A. submarginata</i>	10	30.0	0.0	0.0	0.0
<i>A. trinitensis</i>	1	100.0	0.0	0.0	0.0
<i>A. triseminata</i>	20	65.0	40.0	0.0	0.0
<i>A. tuberosa</i>	11	18.1	36.3	0.0	0.0
<i>A. valida</i>	7	100.0	0.0	0.0	0.0
<i>A. vallsii</i>	2	100.0	0.0	0.0	0.0
<i>A. veigae</i>	77	79.2	1.0	0.0	0.0
<i>A. villosa</i>	12	75.0	33.3	0.0	0.0
<i>A. villosulicarpa</i>	11	100.0	0.0	0.0	27.2
<i>A. williamsii</i>	1	100.0	0.0	0.0	0.0
<i>A. sp. nov. (1)</i> [sect. Procumbentes]	5	0.0	80.0	0.0	0.0
<i>A. sp. nov. (1)</i> [sect. Extranervosae]	1	100.0	100.0	0.0	0.0
<i>A. sp. nov. (1)</i> [sect. Erectoides]	1	100.0	100.0	0.0	0.0
<i>A. sp. nov. (2)</i> [sect. Arachis]	2	100.0	0.0	0.0	0.0
<b>Total wild <i>Arachis</i> accessions</b>			<b>1,559 accessions of 84 species (79 described + 5 inedit.)</b>		

**Table 3.7** Cultivated peanut accessions conserved in EMBRAPA genebanks (Oct. 2020).

Scientific name	Peanut Genebank	Wild <i>Arachis</i> Genebank	EMBRAPA Long-term Genebank	Accessions conserved in Genebanks	Number of unique accessions
<i>Arachis hypogaea</i>	281	498	1,263	2,042	2,011
<i>Arachis hypogaea</i> L. subsp. <i>fastigiata</i>		25	-	25	25
<i>Arachis hypogaea</i> L. subsp. <i>fastigiata</i> var. <i>fastigiata</i>	-	246	59	305	246
<i>Arachis hypogaea</i> L. subsp. <i>fastigiata</i> var. <i>vulgaris</i>	-	4	-	4	4
<i>Arachis hypogaea</i> L. subsp. <i>fastigiata</i> var. <i>aequatoriana</i>	-	2	-	2	2
<i>Arachis hypogaea</i> L. subsp. <i>fastigiata</i> var. <i>peruviana</i>	-	2	-	2	2
<i>Arachis hypogaea</i> L. subsp. <i>hypogaea</i>	-	23	-	23	23
<i>Arachis hypogaea</i> L. subsp. <i>hypogaea</i> var. <i>hirsuta</i>	-	1	-	1	1
<i>Arachis hypogaea</i> L. subsp. <i>hypogaea</i> var. <i>hypogaea</i>	-	93	11	104	93
<b>TOTAL</b>	<b>281</b>	<b>894</b>	<b>1,333</b>	<b>2,508</b>	<b>2,407</b>



genebanks located at facilities with separate research objectives:

(1) A peanut genebank is located at the Cotton Research Station in Campina Grande, Paraíba State, and currently holds 281 accessions of mostly valencia and spanish market types.

(2) The Wild *Arachis* Genebank, located at the Centro Nacional de Recursos Genéticos (CENARGEN) in Brasília conserves a collection of 894 accessions of *Arachis hypogaea* in medium-term storage. This collection is comprised of samples, mostly duplicated elsewhere, obtained from historic plant explorations conducted in Brazil, Bolivia, Peru and Uruguay. About half of these accessions have been identified as to their botanical variety, all six of which are represented by at least one accession. Of the 894 accessions conserved here, at least 101 are duplicated in long-term storage at the COLBASE genebank (see no. 3, below), 436 are duplicated in the USDA collection, and 408 are duplicated in the ICRISAT collection. And from the 408 accessions that ICRISAT received from Brazil, 360 duplicate samples were deposited into the Svalbard Global Seed Vault in Norway.

(3) EMBRAPA's long-term genebank for its base collection (COLBASE) is also located at CENARGEN in Brasília, and currently maintains 1,333 accessions of *A. hypogaea* as seed under long-term conditions at -20°C. At least 101 of these accessions are security duplicates of cultivated-peanut samples from the Wild *Arachis* Genebank. Another 1,232 accessions were received from the IAC Peanut Genebank in Campinas as security duplicates for their long-term conservation, although many of these materials may have been accessions originally received by IAC from CENARGEN, but were shipped back with only IAC numbers, without complete passport data or original identifiers.

(4) A small collection of 28 peanut cultivars is maintained at EMBRAPA's Temperate Climate research station located in Pelotas, Rio Grande do Sul, where it is used for agronomic evaluation associated with a regional peanut selection program. The collection includes a number of commercial cultivars and some IAC breeding lines that are duplicated in other genebanks, as well as some local landraces collected in neighboring counties that may be unique. The accessions in this collection have not been registered on EMBRAPA's Alelo Platform for germplasm documentation, so it is not possible at this time to detect any duplication with accessions maintained elsewhere.

#### **Other peanut germplasm collections in Brazil**

In addition to EMBRAPA, the Agronomic Institutes of the states of Paraná (IAPAR, Londrina) and São Paulo (IAC, Campinas, BRA006) have their own peanut

(*A. hypogaea*) genebanks, linked directly to peanut-breeding programs. According to the national survey for the Second State of the World Report on Plant Genetic Resources for Food and Agriculture (FAO 2010), IAPAR has 240 accessions, while IAC maintains 2,000 accessions. The IAPAR collection is mainly for agronomic evaluation and selection of materials for local cultivation, involving some duplication of accessions originally from the IAC Genebank.

The IAC Genebank is associated with the most dynamic and persistent peanut breeding program in Brazil, and has a long tradition of researching *Arachis*, including wild species. Many of the accessions maintained by IAC were originally obtained by the Institute itself, over the course of a century-old history of peanut introduction, conservation, evaluation and breeding. Since 1981, there has been intense collaboration between IAC and EMBRAPA, including collecting missions where the materials collected have been consistently shared, at least until 2001. About 650 accessions were deposited over 25 years ago by IAC at EMBRAPA's base collection genebank for long-term conservation, including some materials that were originally provided by CENARGEN to IAC. So far, a total of 1,232 accessions have been sent by IAC for long-term conservation (-20°C) at EMBRAPA's base collection genebank (COLBASE), where IAC intends to eventually duplicate its entire collection.

The conservation of *Arachis* germplasm in Brazil is not presently at great risk or vulnerability, since most of the necessary activities are currently in the hands of well-trained people in the country's main institutions (EMBRAPA and IAC). Collecting activity for wild *Arachis* germplasm has been steady for decades but, since the year 2000, collecting of *A. hypogaea* landraces has been greatly reduced, due to regulatory barriers (and collectors' doubts) related to the potential access to traditional knowledge. In recent decades, the introduction and exchange of *Arachis* germplasm has not been ideal, also reflecting aspects of national and international legislation, as well as the fact that the genus *Arachis* is not included in Annex 1 of the Multilateral System of the ITPGRFA.

The initial and routine increase of wild accessions collected in nature is a regular practice, but is generally not sufficient to produce the quantities needed for characterization, maintenance, and long-term conservation. EMBRAPA's facilities for long-term conservation are adequate, and the entire collection of *A. hypogaea* at the IAC genebank will eventually be stored in the base collection at EMBRAPA-CENARGEN in Brasília. The regeneration of old accessions of *A. hypogaea* collected by CENARGEN, most of which have been duplicated in the past at IAC, USDA and ICRISAT, has not been accomplished for many years.

The documentation of the accessions is advancing at a good pace on the EMBRAPA Alelo Portal. Regular monitoring of germplasm health is not being carried out as would ideally be necessary. A reasonable number of Brazilian accessions, including cultivated peanuts, forage *Arachis* species, and a series of other wild accessions mainly those collected from 1980 to 2000, are duplicated in the USDA, ICRISAT and CIAT genebanks, and from those genebanks, duplicates have also been deposited at the Svalbard Global Seed Vault in Norway.

Institutional funding is available for routine genebank operations, while cytogenetic and molecular characterization research is conducted through projects, for which funding is eventually available from various donors. However, considering current and future trends, important activities such as field collecting and the regular increase of wild accessions are becoming seriously threatened due to the lack of replacement of trained personnel—including the curator himself who is still available and working full-time, but aging. At a time of intense environmental degradation in areas where wild *Arachis* species occur, and which also affects the traditional nuclei of landrace cultivation such as indigenous territories, the potential deterioration of field collecting activities would have grave repercussions for *Arachis* conservation and use, given that Brazil harbors the greatest number of wild *Arachis* species, and most of them are endemic. Without the replacement of trained staff, a subsequent decrease in institutional interest on the *Arachis* germplasm may shift the goals, infrastructure and human resources involved with characterization to more attractive crops, leading to the eventual neglect of Brazilian CWRs which would result in serious damage to the global research community and to *Arachis* conservation and use activities around the world.

### 3.4.7 INTA (Instituto Nacional de Tecnología Agropecuaria) – Manfredi, Argentina (ARG1211)

The INTA peanut collection was first established in 1944 at what is now the Estación Experimental Agropecuaria Manfredi, located in the heart of Argentina's extensive peanut production area in the province of Cordoba. The collection currently holds a total of 3,576 accessions: 3,470 of which are of cultivated peanut including 352 improved varieties and 61 breeding lines; as well as 106 accessions of wild *Arachis* representing 29 species. The collection of cultivated peanut contains a significant number of unique accessions, including over 3,000 landrace accessions, 7% of which are of national origin and 93% of foreign origin (54% Latin America, 46% rest of the world), including many original accessions of indigenous landraces from Argentina, Bolivia, Paraguay, Uruguay, Brazil, Peru, and Ecuador. As can be seen in Table 3.8, many of the landrace accessions have been

identified to their botanical variety, all six of which are represented in the collection. Studies conducted on the landrace materials in this collection formed the basis for the landmark monographs on the peanut landraces of Bolivia, Peru, and Ecuador (Krapovickas et al. 2009, 2013, and 2021, respectively).

The INTA-Manfredi genebank maintains the accessions as a working collection, 100% of the cultivated materials are stored as seeds, sealed in tri-laminated foil bags, and placed in medium-term cold storage at 4°C. The wild *Arachis* accessions (with the exception of *A. glabrata*) are also stored as seed under the same conditions, as well as being maintained as whole plants in field plots. The 13 accessions of *A. glabrata* are only maintained in field plots.

Practically the entire collection has been agro-morphologically characterized using IBPGR/ICRISAT Descriptors, and 4% of the collection has some molecular/genotypic characterization data. This information is stored on the dbGERMO database (INTA proprietary), which is not publicly accessible, nor available elsewhere, but can be requested from the curator. The whole collection is safety-duplicated in long-term storage at the INTA Centro de Investigación en Recursos Naturales (CIRN) in Buenos Aires.

Risk factors affecting the collection include insufficient funding for routine operations and maintenance, insufficient level of interest and feedback from users, and phytosanitary problems. Currently, 20% of the accessions are in need of urgent regeneration. There are 2,310 accessions currently available for distribution, although an infestation of peanut smut disease (*Thecaphora frezii*) is currently a limiting factor for exporting germplasm samples.

### 3.4.8 NCSU (North Carolina State University, Dept. of Crop and Soil Science) – Raleigh, USA (USA317)

The Department of Crop and Soil Sciences at North Carolina State University has a long and illustrious his-

**Table 3.8** INTA-Manfredi landrace accessions identified to botanical variety

<i>A. hypogaea</i> landraces, by botanical variety	No. accessions
<i>var. hypogaea</i>	718
<i>var. hirsuta</i>	5
<i>var. fastigiata</i>	1,014
<i>var. vulgaris</i>	152
<i>var. peruviana</i>	259
<i>var. aequatoriana</i>	223
<b>Total</b>	<b>2,371</b>

tory of peanut research and breeding activities. NCSU's *Arachis* germplasm collection was first established in the 1920s and has expanded over time, particularly as a consequence of peanut exploration activities of Prof. Walton C. Gregory in South America.

The NCSU peanut collection currently houses a total of 2,009 *Arachis* germplasm accessions. The collection includes over 1,000 breeding and research materials, genetic stocks and advanced improved varieties, as well as over 500 landrace accessions, about one-third of which are from South America and elsewhere outside the US. Also included in the collection are 600 accessions of 59 wild *Arachis* species, and 100 diploid wild species hybrids, 77 tetraploid wild species hybrids, two synthetic amphidiploids and 25 synthetic hexaploid plants in the greenhouse. Cultivated materials other than *A. hypogaea* are three accessions of commercial forage *Arachis* (Amarillo, Latitude 34, and UF Tito). About 1,100 accessions are currently available for distribution.

About 33% of accessions are maintained in short-term storage as whole plants in greenhouses or field plots, 40% in medium-term storage in cold rooms, and 60% in long-term storage in a freezer. About 60% of the conserved material have phenotypic characterization data; both USDA and institute-specific descriptors are used. About 20% of the accessions have molecular or genotypic characterization data, 40% have been evaluated for biotic stresses, and 10% for abiotic stresses.

No formal genebank management system or written procedures or protocols are currently employed, nor are any quality-control activities regularly conducted. Urgent regeneration is currently required for 21% of the wild species collection, everything else has good viability. There are no phytosanitary issues affecting the distribution of the germplasm. The current status of the collection is good or adequate with regard to risk, and that is not expected to change. Most accessions are safety-duplicated in the USDA collection, and many wild species are duplicated in the TAMU collection; breeding materials are not duplicated.

Microsoft Excel and Jupyter Notebook are the searchable platforms used to store and retrieve all categories of accession-level data, except for images and distribution information which is available from the curator upon request. About half the accessions are available for distribution, most are in sufficient quantities and available for distribution under an institutional MTA. About 50 accessions/year are typically distributed nationally, none regionally, and about 10 internationally. More accessions would be distributed if more requests were received. No fees are charged for accessions, packing or shipping. No restrictions are placed on who may receive materials, but the MTA must be signed.

The collection is regarded as having good global coverage, and there are no known or perceived gaps. The main vulnerabilities to the collection are: (1) freezers dying, (2) difficulty propagating and harvesting wild species, (3) lack of future funding to maintain wild species (staffing), (4) plants dying in greenhouses, and (5) lack of genotyping funds.

The NCSU genebank collaborates regularly with the USDA-ARS genebank in Griffin, GA; but it does not currently participate in any networks of peanut germplasm holders or users.

### 3.4.9 IBONE (Instituto de Botánica del Nordeste, UNNE-CONICET) – Corrientes, Argentina (ARG1133)

The Instituto de Botánica del Nordeste (IBONE) is a botanical research institute affiliated with the National University of the Northeast (UNNE) and the National Research Council (CONICET). The *Arachis* collection at IBONE was initiated in 1965 by Prof. Antonio Krapovickas, the institute's founding Director, who led and inspired generations of *Arachis* research and researchers. IBONE hosts a large herbarium (CTES) containing over 500,000 mounted specimens from around the world, focusing primarily on the flora of northern Argentina, Bolivia, Paraguay and Brazil. Among these are what is undoubtedly the world's most extensive herbarium collection of the genus *Arachis*, including numerous type specimens of wild *Arachis* species as well as type herbarium and fruit specimens of botanical varieties and landraces of *A. hypogaea*. All told, the IBONE herbarium hosts more than 2,000 voucher and type specimens of wild *Arachis* species and 3,300 voucher and type specimens of cultivated landraces, which document the original passport information of most of the *Arachis* germplasm accessions that were collected in South America and then distributed around the world.

Attached to the herbarium, IBONE also boasts a specialized botanical library containing some 20,000 volumes, including original editions of classic botanical works dating from the 18<sup>th</sup> Century that were part of Prof. Krapovickas' personal collection, as well as a trove of historical, archaeological, ethnographic and botanical references, and subscriptions to a host of current scientific journals. The Institute also houses specialized research laboratories for plant taxonomy, physiology, cytogenetics, genomics, and tissue culture studies. As an integral part of its botanical research program, IBONE edits and publishes the indexed scientific journal *Bonplandia*, now celebrating its 60th year, where many landmark articles on *Arachis* taxonomy and genetics have been and continue to be published.

The germplasm collection at IBONE currently maintains a total of 688 *Arachis* accessions. These include 216 accessions of cultivated peanut, plus 259 acces-

sions comprising 57 wild species (52 described, plus 6–8 new but still-undescribed species), and 213 accessions of wild species hybrids.

The germplasm collection has good coverage for the crop's region of origin and diversity (Argentina, Bolivia, Brazil, Ecuador, Paraguay, Peru, and Uruguay). Perceived taxonomic gaps that remain include wild species of the Sections *Trierectoides*, *Heteranthae*, *Extranervosae* and *Erectoides*. Remaining ecogeographic gaps include materials from Bolivia (Pantanal and Chaco), Paraguay (Chaco), and Brazil (Cerrado and Caatinga). Unique aspects of the collection include many new accessions recently collected from the wild, including several (6–8) undescribed (i.e. new) species. Many of these recent accessions represent potentially valuable diversity at the population level, with several samples obtained in each locality. Other unique accessions include numerous endemic heritage peanut landraces of Guaraní people with different culinary uses, some wild species that are now extinct from nature, and many experimentally produced hybrids between wild species that are useful for genomic studies and pre-breeding for improved varieties with agronomic traits important to maintain commercial crop production (such as resistance to peanut smut).

The accessions are maintained for multiple purposes, i.e., as a reference collection, a working collection, and a breeding collection. Approximately 80% of the materials are conserved under short-term storage conditions, the remaining 20% are in medium-term storage. Three different storage facilities are used: 1) A greenhouse of 150m<sup>2</sup> is used for conserving whole plants in short-term storage, with insect netting to control unwanted pollinators but no temperature or humidity control. 2) A refrigerator, kept at 10° C, is employed to conserve dried seeds in short- and medium-term storage, with no humidity control and no hermetic packaging. 3) A freezer, kept at -20° C, is also employed to conserve seeds in medium-term storage, with no humidity control and no hermetic packaging.

Written protocols are followed for the acquisition, regeneration, characterization, storage, and documentation of the germplasm accessions. Accessions are re-sown every 3–5 years to ensure continued high-germination rates. Between 40% and 60% of the accessions are currently in need of urgent regeneration. Electronic documentation of the accession-level information is stored using MS Excel and MS Access software. Most data fields are 80–100% complete. The accession-level information is not publicly accessible through the internet, but is available upon request from the curator. Information from the collection is partly available on other, external databases (GBIF, GRIN-Global, Argentinian National System for Biological Data, and JSTOR).

Some accessions are currently available for distribution. Accessions are distributed using an institutional MTA or bi-lateral agreements, but these agreements are not shared. In-country distribution is mostly to academic researchers and farmers, and a few breeders. One hundred percent of international distributions are sent to academic researchers and students.

The average annual distribution of accessions is 20 nationally, 5 regionally, and 5 internationally. Policy restraints limit the international distribution of many materials.

The main constraints affecting the genebank's management are: insufficient infrastructure, financial constraints, policy constraints, and lack of governmental awareness. The most important limiting factors affecting the use of the accessions are: promotion of conserved materials, constraints to access and exchange, limited interest by breeding programs in wild species or landrace materials, and difficulties increasing seed stocks.

The main vulnerabilities that place the collection at risk are: insufficient operational budget, shortage of trained permanent staff, inadequate characterization and evaluation of materials, and the lack of safety duplication. The institution does not provide adequate funding for recurrent maintenance costs for the collection, and the budget is decreasing. The difference is currently made up from researchers' and fellowships' own funds.

The IBONE *Arachis* genebank considers the promotion of *in situ* conservation of wild and cultivated *Arachis* to be one of its priority conservation research activities. Examples of their activities promoting linkages between *ex situ* and *in situ* conservation include:

- Survey conducted of peanut landraces currently maintained by local landholders in northeast Argentina, comparing those with the landraces that were first collected there 60 years earlier for *ex situ* conservation by IBONE.
- Development of local seed banks to facilitate re-adoption of local varieties
- Development of seed banks at schools in rural communities
- Documentation of biocultural patterns associated with local peanut landraces
- Outreach activities with local farmers' organizations and local governments to promote the cultivation, use, and on-farm conservation of local peanut landraces

Some of the obstacles encountered when enabling, managing or monitoring the *in situ* (on-farm) conservation of peanut landraces include:

- Low market value/income generated from landraces

- Loss of the biocultural patterns that actively maintain the interest in local landraces
- Financial constraints
- Lack of permanent staff adequately trained in *in situ* conservation and non-industrial production methods
- Lack of government awareness of the value and importance of on-farm conservation

Obstacles faced in promoting, managing or monitoring the *in situ* conservation status of wild *Arachis* populations:

- Financial constraints
- Lack of specialized staff trained in this topic
- Policy issues and constraints
- Lack of public and government awareness
- Changes in land use

The IBONE genebank currently collaborates with the following institutional partners:

- Herbario Martín Cárdenas, Cochabamba, Bolivia. 2007–every few years
- Herbario Nacional de Bolivia, La Paz, Bolivia. 2004–every few years
- Pairumani Experimental Station, Cochabamba, Bolivia. 2007–every few years
- Criadero El Carmen, General Cabrera, Argentina. Germplasm evaluation. 2010–present
- Facultad de Ciencias Agrarias, Universidad de Asunción, Paraguay. 2018–present
- EMBRAPA-CENARGEN, Brasilia, Brazil. –ongoing
- University of Georgia, Athens, Georgia, USA. –ongoing
- TAMU–Texas AgriLife Research Center. Stephenville, Texas, USA. –ongoing

The IBONE genebank currently participates in the following *Arachis* networks:

- Peanut Genome Initiative - (Global) - Partner in taxonomy, cytogenetic, genotyping, biogeographic data sharing. Providing genomic tools for utilizing the genetic variability in the *Arachis* genepool.
- Red Maní Argentino - (National) - Expertise in germplasm characterization and evaluation. Coordinate interinstitutional research and technical staff for attending the producers' and industrial demands on peanut research.

#### 3.4.10 CIAT (Centro Internacional de Agricultura Tropical) – Cali, Colombia (COL003)

The International Center for Tropical Agriculture (CIAT, from its Spanish initials) is one of the 14 specialized international agricultural research centers of CGIAR, and is based in Cali, Colombia. CIAT merged with Bioversity International in 2019 to form the Alliance of Bioversity International and CIAT. Best known for its important world collections of common beans (*Phaseolus*) and cassava (*Manihot*), CIAT's mandate

also includes a large collection of tropical forage species, all of which are managed by the center's Genetic Resources Unit. The CIAT Tropical Forages Collection was established in 1976 and currently conserves 22,694 accessions of more than 700 species, including 158 accessions of *Arachis*, with 29 wild species represented. CIAT's *Arachis* collection is reported as having good regional coverage for Brazil, Bolivia, Paraguay, Argentina, Uruguay and Costa Rica.

Seeds of the *Arachis* accessions are conserved in medium-term (12%) and long-term (65%) cold storage at -18°C, packed in vacuum-sealed foil pouches. The remainder of the accessions (23%) are conserved as whole plants in a greenhouse at 20–35°C and 70–90% RH. An established genebank management system and protocols are in place. About 10% of the *Arachis* accessions are in urgent need of regeneration, and there are some health issues with the live plants. The *Arachis* accessions are safety-duplicated at CIMMYT, in Mexico, and at the Svalbard Global Seed Vault, in Norway. Black-box storage is also provided by CIAT for 1 accession of forage *Arachis* received from the International Livestock Research Institute (ILRI), in Ethiopia.

Funding support, staffing, and donor interest in the *Arachis* collection is adequate and stable. On the other hand, demand for and use of the accessions by breeders, researchers and other users has been relatively poor. The main constraints reported regarding the *Arachis* collection are the current lack of a forage curator with the requisite taxonomic expertise to properly manage the collection, a limited capacity to obtain and curate historical data about the collection, and no capacity to evaluate the important agronomic traits of the accessions. Immediate threats to the collection include the potential loss of the greenhouse accessions due to an acute shortage of support staff as a result of the current COVID-19 restrictions; problems with seed viability, longevity and dormancy; lack of information about the species; and the lack of use of the accessions.

Accession-level information on the collection is stored in a Legacy Oracle database, to be eventually phased out, and the data will be migrating to GRIN-Global and Genesys. The collection data is publicly accessible and may be requested by users online at [CIAT](#) and [Genesys](#). The accession-level data includes good passport information, 51% of the accessions are georeferenced, and 95% are with high-quality images.

Currently, there are 30 *Arachis* accessions (19% of the collection) with sufficient material available for distribution as seed and/or live plants. Those accessions are available for distribution under CIAT's Article 15 agreement with the Governing Body of the ITPGRFA. CIAT has good existing capacity for phytosanitary

certification, packaging, and shipping of samples, for which no fees are charged.

CIAT is not currently engaged in *in situ-ex situ* linkages or other activities involving *in situ* or on-farm conservation of wild *Arachis* species. Similarly, CIAT does not currently collaborate with other partners on *Arachis* germplasm management activities, nor does it participate in any *Arachis* research, conservation, or utilization networks.

### 3.5 Global status of surveyed genebanks

A spreadsheet was created to assemble and analyze the information received from the 24 institutions with *Arachis* collections that completed the online survey, as well as from 3 others that only partially completed the survey questionnaire. The genebanks that contributed to this analysis include several of the largest peanut collections in the world, as well as some of the

smallest. Despite the vast differences in size and mandate of the institutions hosting these collections, there were many features, challenges and trends that are shared by nearly all of the genebanks surveyed. The results of the analysis of the data collected through the survey is presented here.

#### 3.5.1 Size and composition of the collections

The 25 genebanks that contributed to this analysis (24 that completed the survey, plus IND001) comprise six international or multinational research centers, 19 national (governmental) research organizations, including six universities. Together, these institutions currently conserve 72,108 *Arachis* germplasm accessions (Table 3.9), representing approximately 80% of the global total. The surveyed collections vary greatly in terms of their geographic and taxonomic coverage (e.g., cultivated botanical varieties, landraces, improved and obsolete cultivars, breeding and

**Table 3.9** Number of *Arachis* accessions maintained *ex situ* by surveyed institution and biological type of germplasm conserved.

INSTCODE	Landraces	Obsolete Improved vars.	Advanced Improved vars.	Breeding/ Research Materials	Specialist Genetic Stocks	CWRs	Other Cultivated spp.	Wild spp. Hybrids	Unknown	Other	Total
ARG1211	3,006	342	11	61	0	106	0	0	50	0	<b>3,576</b>
ARG1133	216	0	0	0	0	259	0	213	0	0	<b>688</b>
AUS167	0	0	1	0	0	43	11	1	0	0	<b>56</b>
BENIN*	52	0	2	0	0	0	0	0	0	0	<b>54</b>
BGR001	10	52	12	610	929	0	0	0	0	0	<b>1,613</b>
BOL316	1,079	0	0	0	0	0	1	0	0	0	<b>1,080</b>
BRA002	0	0	0	0	0	1,559	20	100	2,536	0	<b>4,215</b>
BRA006	481	422	44	32	0	0	0	1,107	0	0	<b>2,086</b>
CHN003	2,728	510	167	1,736	298	234	0	123	2,198	596	<b>8,590</b>
COL003	0	0	0	0	0	158	0	0	0	0	<b>158</b>
ECU023	300	0	3	94	0	0	1	0	6	0	<b>404</b>
IND001	6,010	15	200	1,777	191	81	0	0	4,762	719	<b>13,755</b>
IND002	7,397	0	982	5,034	0	480	0	0	0	1,729	<b>15,622</b>
PER773	0	0	0	0	10	0	0	0	0	240	<b>250</b>
PRT001	5	0	0	0	0	0	0	0	0	0	<b>5</b>
PRY008	56	0	19	19	0	0	0	0	0	0	<b>94</b>
PRY027	41	0	0	0	0	109	0	0	0	0	<b>150</b>
PRY037	0	0	0	0	0	0	52	0	0	0	<b>52</b>
SDN002	274	0	0	0	0	0	0	0	0	0	<b>274</b>
SEN002	1	0	35	1,147	0	10	0	7	0	0	<b>1,200</b>
TWN001	18	0	0	0	0	1	1	0	0	0	<b>20</b>
URY003	463	0	0	0	0	3	0	0	0	0	<b>466</b>
USA016	1,621	0	0	1,286	0	564	0	0	326	5,364	<b>9,161</b>
USA317	500	50	10	659	241	499	3	77	0	0	<b>2,039</b>
USA520	4,000	0	0	1,238	0	954	3	300	5	0	<b>6,500</b>
<b>Grand Total</b>	<b>28,258</b>	<b>1,391</b>	<b>1,486</b>	<b>13,693</b>	<b>1,669</b>	<b>5,060</b>	<b>92</b>	<b>1,928</b>	<b>9,883</b>	<b>8,648</b>	<b>72,108</b>

\*formal INSTCODE not yet assigned

research materials, and wild species). Most genebanks denoted their collections to be either fully unique (3), mostly unique (4), or partly unique (14), and most of those provided details on the kinds of unique materials conserved. Some genebanks reported significant numbers of accessions of “unknown” identity, or as “other” material. Only four institutions reported their accessions to be fully duplicated elsewhere. Other relevant observations on the data recovered through the online survey, as well as available expert knowledge on various specific topics, will be included in the discussions that follow.

### 3.5.2 Structure and management of the collections

All of the *Arachis* genebanks surveyed pertain to public institutions. Eighty percent of these institutions are the legal owners of their collections, and 20% are not. As for the stated purposes of the collections, roughly three quarters of the genebanks indicated their objectives as long-term conservation and medium-term working collections, 44% as breeding collections, and 30% as reference collections.

### 3.5.3 Storage methods

Conventional cold storage chambers and freezers are almost universally employed for long- and medium-term storage of *Arachis* seeds, both cultivated and wild, typically packaged in hermetically sealed foil packets. Only three genebanks reported conserving their seed collections in short-term storage at ambient temperature and humidity. Seven genebanks also maintain wild *Arachis* accessions as whole plants grown in greenhouses, screenhouses, or field plots. In a very few instances, slow-growth tissue culture is also used for medium-term conservation of some recalcitrant accessions of wild *Arachis*. There were no reports of *Arachis* germplasm being conserved using cryopreservation methods, nor as DNA samples.

**Quality control** – Most institutions have established some form of genebank management system, or follow written procedures and protocols for basic germplasm conservation, documentation and quality control processes (Figures 3.5 and 3.6).

**Regeneration** – The regeneration status of the collections (i.e., the percentage of accessions requiring urgent regeneration) varies greatly across the different institutions. Some of the better-funded genebanks report very few or no accessions in need of urgent regeneration. On the other hand, many other genebanks—including some of those with the larger and/or more unique collections—report that some specific categories of accessions, if not 100% of their collections, require urgent regeneration, indicating that these collections are already at significant risk of losing potentially unique sources of peanut genetic diversity.

### 3.5.4 Characterization and evaluation

The characterization, evaluation, and phytosanitary status of the collections also varies widely across the genebanks surveyed. As above, the better-funded collections have a high percentage of their accessions with characterization data (both phenotypic and genotypic), while most others indicate that a lack of adequate characterization and evaluation data is impeding the use of their collection, and resolving that deficiency remains a top research priority for them. The use of standardized descriptor lists is widespread, particularly the IBPGR/ICRISAT Descriptors for Groundnut, and the USDA Peanut Descriptors, as well as some institution-own descriptors. Molecular and genotypic characterization is much less prevalent, with three genebanks reporting molecular characterization data for 50% (ARG1133), 71% (ECU023) and 90% (SEN002) of their collections, respectively, and the remainder reporting percentages averaging between zero and 20%. Half of the collections reported having some evaluation data for biotic stresses, and less than a third of the collections reported having any eval-

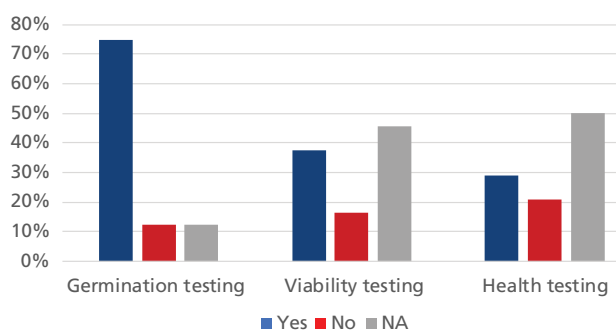


Figure 3.5 Genebank quality control activities. NA = not answered

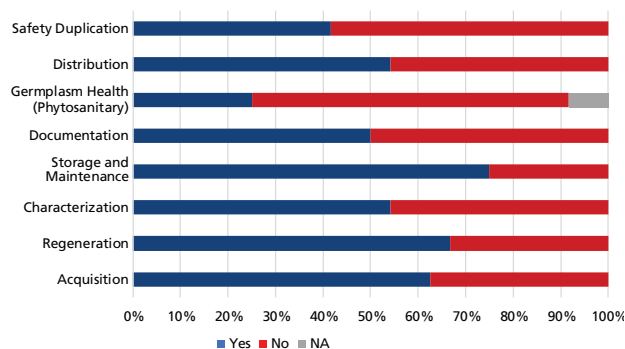


Figure 3.6 Genebank management systems or procedures in place for collections surveyed. NA = not answered

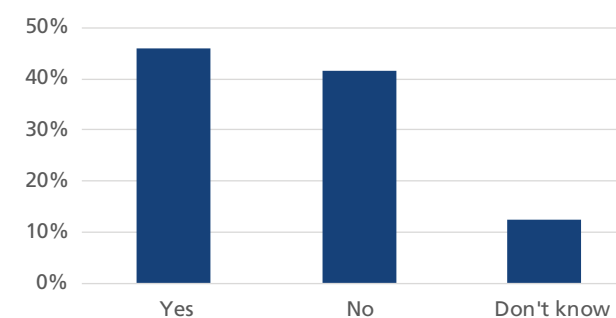


Figure 3.7. Surveyed genebanks with safety-duplicated accessions

uation data for abiotic stresses. Plant health issues affecting the ability to distribute germplasm from the collection were reported to exist to some extent by six genebanks.

### 3.5.5 Safety-duplication

Less than half (11) of the responding genebanks have a safety-duplicate of their collections deposited in another genebank (Figure 3.7). Most of those collections are safety-duplicated in base collections or other genebanks within their country, while three genebanks sent a second safety-duplicate to an international genebank, i.e., ICRISAT-Regional in Niger, CIMMYT in Mexico, and USDA-S9, and one genebank deposited an estimated 400 accessions as a safety-triplicate to ICRISAT in India. Duplicate *Arachis* accessions stored at the Svalbard Global Seed Vault, are mostly from ICRISAT, TWN006, and USA996 (Table 3.10). More than half (18) of the genebanks surveyed reported restrictions for sending duplicate accessions outside their countries for safety back-up conservation, citing national and international policy issues, lack of adequate seed stocks, and phytosanitary issues as the primary reasons. Three of the genebanks surveyed, i.e., CIAT (COL003), IPTA-CICM (PRY008) and FCA-UNA (PRY027), each reported storing a small number of safety-duplicate accessions received from other genebanks.

### 3.5.6 Collecting missions

A total of 350 *Arachis* germplasm collecting missions, beginning as early as 1932, were reported by 15 of the genebanks responding to this question. Although international collecting activities have become far less common in recent years, domestic missions to collect *Arachis* germplasm continue to be conducted at the national level. A summary of *Arachis* collecting missions reported by the institutions surveyed is presented in Table 3.11.

### 3.5.7 Priority conservation research

The most frequently reported conservation research activities as prioritized by the genebank managers surveyed were: (1) germplasm collecting missions, (2) genotyping accessions, (3) core subsets, (4) seed regeneration, (5) characterization, and (6) safety-duplication.

### 3.5.8 Constraints to genebank operations

The most frequently reported constraints affecting the successful operation of the genebank, as prioritized by the genebank managers surveyed were: (1) financial, (2) staffing, (3) facilities and infrastructure, (4) research capacity, (5) policy, (6) documentation, and (7) public and governmental awareness.

**Table 3.11** Summary of peanut collecting missions reported by surveyed genebanks.

WIEWS INSTCODE	Collection Period	No. of Missions	Accessions Collected
ARG1211	1947-1983	15	587
ARG1133	1959-2020	39	1,323
BENIN*	2019	1	120
BGR001	1956-1986	4	9
BOL316	2017-2018	2	27
BRA002	1980-2019	133	2,186
CHN003	1950-2020	8	8,516
ECU023	1995-2012	3	234
IND002	1976-1996	65	2,756
PRY027	2020	2	109
SDN002	2004-2018	8	1,984
SEN002	2019	1	1,049
TWN001	2001-2009	2	5
USA016	1932-2007	39	1,773
USA520	1977-2016	28	2,632

\*formal INSTCODE not yet assigned

**Table 3.10** *Arachis* accessions conserved at Svalbard Global Seed Vault and institute of origin. Source <https://seedvault.nordgen.org/>, data retrieved on 9 September 2021.

INSTCODE	Institute name	Acronym	Accessions
IND002	International Crop Research Institute for the Semi-Arid Tropics	ICRISAT	14339
TWN006	Taiwan Agricultural Research Institute	TARI	1540
USA996	National Plant Germplasm System	NPGS	1005
ZMB030	SADC Plant Genetic Resources Centre	SPGRC	66
COL003	Centro Internacional de Agricultura Tropical	CIAT	44
SDN002	Agricultural Plant Genetic Resources Conservation & Research Centre	ARC	16
AUS165	Australian Grains Genebank	AGG	14
KOR043	National Agrobiodiversity Center	NAC	10
CAN004	Plant Gene Resources of Canada	PGRC	3
ETH013	International Livestock Research Institute	ILRI	3
USA974	Seed Savers Exchange	SSE	1



### 3.5.9 Documentation and information sharing

Seventy-one percent of the genebanks surveyed use some form of searchable electronic database to store and retrieve their accession-level data (Figure 3.8). At least five of the genebanks report using GRIN-Global, another five are using proprietary database software, and the remainder report using MS Access or Excel spreadsheets. A few indicated that their data is also partly available on Genesys, or that they are in the process of migration to the Genesys platform.

In terms of the kinds of data stored in these databases, passport (90%), taxonomy (76%) and characterization (71%) data is recorded by most of the genebanks, with information on storage conditions (52%), evaluation data (43%), images (33%), genotype data (24%), and distribution data (24%) being less frequent (Figure 3.9). The accession-level information is made publicly available by 15 of the genebanks surveyed, while seven genebanks make their information available only upon request, and three genebanks keep their accession-level information private. Six of the surveyed genebanks make their accession-level information accessible to the public through the internet. Of the five genebanks that reported having much or part of their accession-level data available on other, external databases—four of them indicating Genesys, and the other PeanutBase.

### 3.5.10 Gaps and vulnerability of the collections

Seventeen genebanks responded to survey questions about known or perceived gaps in their *Arachis* collections. Regarding **genetic gaps** in their collections, answers were received from nine respondents. Three genebank managers reported that genetic diversity is incompletely represented in their collections, some mentioning that no collecting missions have taken place for many years, and that several wild species with positive attributes for crop improvement are represented by only a single accession, or by a small number of accessions. More accessions need to be collected to increase the genetic diversity conserved *ex situ*. Three other genebanks reported that their lack of characterization data limits their ability to identify genetic gaps, and indicated that characterization of their collections is urgently needed. The remainder of

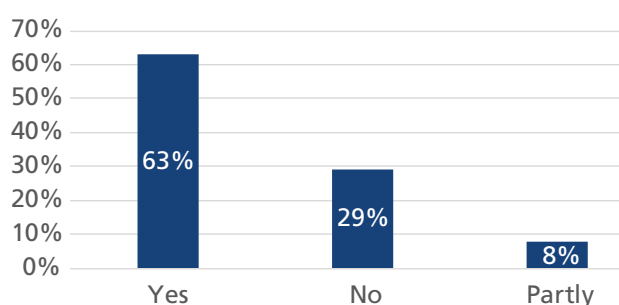


Figure 3.8 Percent of surveyed genebanks with electronic accession-level databases

the managers reported that they didn't know what genetic gaps existed in their collections, which very likely is also due to a lack of characterization.

Regarding known or perceived **taxonomic gaps** in their *Arachis* collections, answers were received from 12 genebank managers. EMBRAPA reported that there are three new *Arachis* species from Brazil to be described and others will certainly come to light as the collecting expeditions proceed; and their value as genetic resources needs to be assessed using modern technology. Six genebank managers cited gaps in wild *Arachis* species represented in their collections, some of whom mentioned specific sections of the genus that are currently under- or not represented, i.e. sections *Arachis*, *Trierectoides*, *Heteranthae*, *Extranervosae* and *Erectoides*. Other managers cited the lack of cultivated groundnut accessions from South America, some of whom mentioned specific market types or botanical varieties, i.e. runner type, var. *hirsuta*, var. *peruviana* and var. *aequatoriana*. Five genebank managers reported insufficient taxonomic expertise to be able to adequately assess the existing taxonomic gaps in their *Arachis* collections.

Regarding known or perceived **ecogeographic gaps** in their *Arachis* collections, 12 genebank managers responded. Five managers reported specific areas within their own country or other countries that represented ecogeographic gaps in their collections. Four managers were uncertain about potential gaps, citing insufficient ecogeographic data or know-how to conduct a gap analysis of their collection. One manager replied that their collection was simply lacking accessions from other countries.

As far as plans to fill the known or perceived gaps in their collections, managers most frequently mentioned the need to conduct plant collecting missions, or alternatively by requesting samples of unrepresented materials from other genebanks. Those that were unsure of the nature of their existing gaps

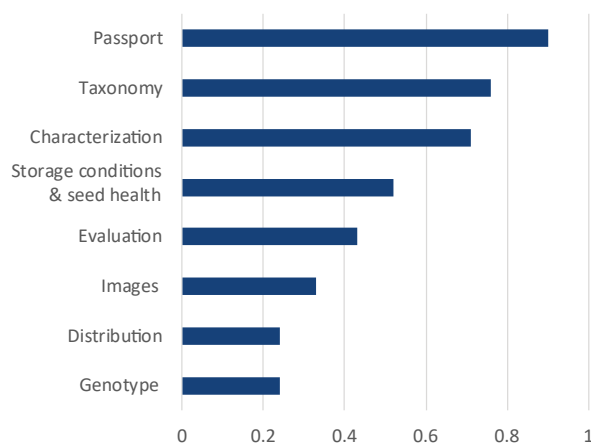


Figure 3.9 Types of accession-level data stored on surveyed collection databases

proposed, financial resources permitting, to undertake the morphological and molecular characterization of their collection, or recruit experts to properly classify the accessions they already have in their collection. One genebank manager said that technical assistance made available through the Seed Treaty's CAPFITOGEN tools would be used to help them define existing ecogeographic gaps.

Regarding the **most important vulnerabilities or threats** to their *Arachis* collections, genebank managers reported the following:

- Lack of trained, permanent staff (74%)
- Insufficient financial support (58%)
- Inadequate infrastructure, especially for long-term conservation (53%)
- Lack of interest in, or use of, the collection (42%)
- Restrictive policies on germplasm acquisition and distribution (32%)
- Lack of characterization and evaluation data (32%)
- Need for seed regeneration (32%)

In addition to the above vulnerabilities, a few genebanks also reported the following as important threats to their collections:

- severe climate events (2)
- phytosanitary issues (2)
- need for safety duplication (1)
- gaps in the collection (1)

Regarding the **institutional support** received for the maintenance of the germplasm collections, exactly half (12) of the 24 survey respondents indicated that the recurrent maintenance costs were mostly or entirely covered by their organization, and that their conservation budget had remained stable over the last five years. The other 12 genebank managers responded that recurrent maintenance costs were **not** sufficiently provided by their institutions, with 11 managers reporting their budgets to be steadily decreasing, and one that their conservation budget was increasing. Nine respondents commented on their sources of supplemental funds to compensate for the deficit in their conservation budget; these included, in three cases, the use of the managers' personal funds and researchers' own fellowship funds, funds solicited by the genebank from other branches of the government, and from breeding programs and international projects. One respondent reported that international

funding is no longer available for germplasm conservation, and another reported that their funding comes from national research and development corporations and not the federal government.

### Discussion on gaps and vulnerabilities

Overall, some great disparities are apparent among the genebanks with regard to known or perceived gaps in their respective collections. While nearly all collection managers reported some gaps, roughly half of the genebanks reported important shortages of information and capacity that are preventing them from identifying and addressing genetic, taxonomic and ecogeographic gaps

A very large disparity exists among peanut collections in terms of the institutional support they receive for basic genebank maintenance, with inadequacy and instability of funding presenting serious challenges for at least 50% of the genebank managers surveyed. This lack of institutional recognition and financial support for germplasm collections represents a significant threat to the viability and utility of their germplasm collections. Unfortunately, there are too many well-known cases that attest to the seriousness of this threat, where entire collections of unique materials, assembled at great expense and effort, were subsequently lost due to inadequate institutional support for basic genebank operations. This particular threat undercuts and exacerbates virtually all of the other vulnerabilities reported by the genebank managers surveyed, and must be addressed as a priority action item in the Global Peanut Conservation Strategy.

Another significant vulnerability from a global perspective is the fact that accessions of wild *Arachis* species are notoriously difficult to maintain and multiply *ex situ*, a constraint made worse by the fact that a number of these wild species are represented by only a single or very few original accessions, and foreign access to additional material is currently prohibited in most of the countries where these species occur. Large collections of wild *Arachis* species are maintained by only a few genebanks worldwide, half of which do not currently make their accessions available internationally. Similarly, large gaps exist in the *ex situ* collections with regard to the existing diversity of cultivated peanut landraces, which remain poorly studied or conserved in many countries. This is especially true in

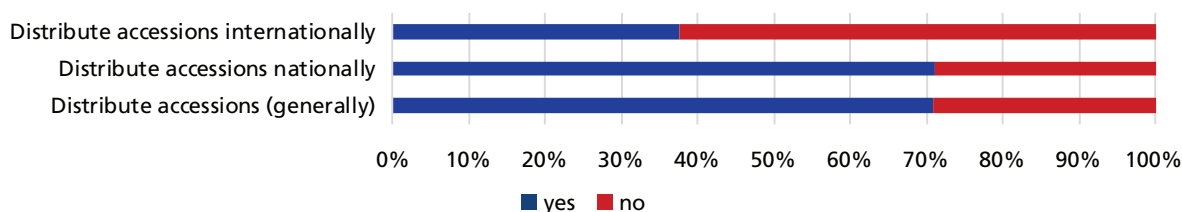


Figure 3.10 Germplasm distribution by surveyed genebanks.

many countries within the peanut's South and Central American range of prehistoric distribution, as well as in some African and Asian countries where locally adapted landraces have not been sufficiently documented or conserved *ex situ*. Peanut landraces everywhere are undergoing rapid genetic erosion as they become increasingly displaced by improved cultivars, without ever having been collected and conserved *ex situ*, resulting in the progressive extinction of unique sources of peanut diversity within the crop's primary gene pool.

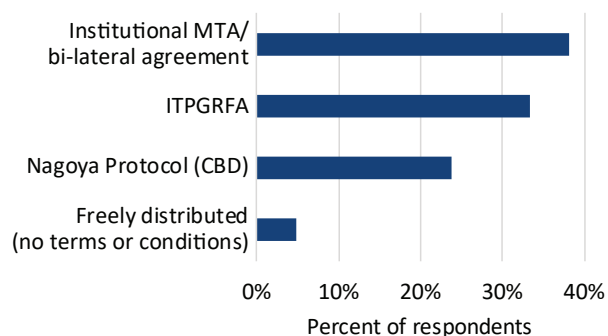
### 3.5.11 Distribution and use of genetic resources

When asked if they **distribute germplasm accessions**, 17 of the surveyed genebanks responded in the affirmative (Figure 3.10). Conversely, seven genebank managers responded in the negative, three of whom cited the following explanations: (1) they receive no request for germplasm, (2) they lack the resources and personnel to respond to requests, and (3) current institutional, national and international policies prevent them from distributing germplasm except to institutional collaborators.

For the 21 genebanks that reported involvement in germplasm distribution, their materials are made available to outside users, subject to the **terms and conditions** shown in Figure 3.11).

Of the 24 genebanks that responded to the question on distribution records, 16 reported that they keep records of their germplasm distributions, while eight indicated that they do not keep such records.

Regarding the kinds of **germplasm recipients** at the **national level**, genebank managers reported that academic researchers and students are by far the most frequent users of the collections, with public sector breeding programs a distant second place, followed by farmers, and other genebanks. Private sector breeding programs and NGOs were infrequent users of the collections.



**Figure 3.11** Terms and conditions applied to distribution by surveyed genebanks (n = 21; three respondents to which the question does not apply are not included).

Regarding the kinds of **germplasm recipients** at the **international level**, genebank managers reported a similar pattern as with their domestic distribution although to a much lesser degree. Academic researchers and students are by far the most frequent users of the collections, followed by public-sector breeders, private-sector breeders, farmers and NGOs.

When questioned about **expected changes in distributions** over the next 3–5 years, genebank managers responded that they expected to see the demand increase (61%) or remain stable (26%) at the national level; to increase (48%) or remain stable (29%) at the regional level; and to increase (38%) or remain stable (19%) at the international level. The proportion of genebank managers that were unsure about future distributions increased progressively from 13% at the national level, to around 24% at the regional level, climbing to almost 43% at the international level.

For those institutions reporting **no international distribution** of materials, genebank managers were asked the reason for this. Of the 13 genebanks that responded to this question, four cited institutional policy restrictions; three responded that no international requests were received; another three genebanks reported insufficient accession-level data; two reported insufficient seed stocks; and one indicated a phytosanitary problem with their collection. Moreover, at least three of the 11 genebanks that skipped this question are known to have institutional policies restricting the international distribution of their accessions.

When asked about their existing **capacity for distributing germplasm** samples, more than 60% of the 23 respondents reported adequate procedures in place for phytosanitary certification, packaging, and shipping of germplasm samples; while 30–40% of the genebanks reported not having such procedures or capacity available. Nearly all of the responding genebanks do not charge for the above-mentioned services; with one genebank charging the cost of the accessions, and five genebanks charging the shipment costs.

When asked to enumerate the three most important **factors limiting the use** of the materials maintained in the collections, the most frequently mentioned limiting factors were: insufficient seed quantity (13); lack of accession-level data (10); lack of user interest (7); inadequate finances and/or infrastructure (5); policy restrictions (3); staffing deficiencies (3); lack of diverse materials (2); and bureaucratic paperwork or phytosanitary issues (1 each).

### Discussion on distribution and use

At the global level, it can be said that the peanut genepool is reasonably well-known, the information is readily available online and in the scientific literature, and the germplasm is reasonably well-conserved, albeit in different genebanks around the world. The fact that the peanut is not included in Annex 1 of the Plant Treaty and its Multilateral System of Access and Benefit Sharing represents a persistent constraint to global distribution and exchange of *Arachis* germplasm. Germplasm remains accessible to users through bilateral agreements with other genebanks, with ICRISAT and USDA distributing the bulk of germplasm requested internationally. National and institutional policies on genetic resources were also frequently cited by collection managers as important constraints to germplasm access, distribution and use.

### 3.5.12 Networks and other collaborative initiatives

With regard to their participation in one or more networks of peanut germplasm holders or users, five genebanks reported participating in at least one network, and 19 reported having no network participation (Figure 3.12). The national peanut networks reported are: a project on Uruguayan Native Peanut Diversity; the Argentine Peanut Network; a Wild *Arachis* Genebank initiative in Brazil; and the National Center for Genetic Resources and Biotechnology (CENARGEN) in Brazil. Regional networks reported are: the Innovation and Plant Breeding Initiative in West Africa (IAVAO); and the Latin American Meeting of *Arachis* Specialists. International networks cited are: the International Peanut Genome Initiative (IPGI); and USDA's Germplasm Resources Information Network (GRIN-Global).

Regarding their involvement in any collaborations with other genebanks and/or breeders on aspects of peanut germplasm management (e.g., regeneration, characterization, evaluation, etc.), only 11 genebank managers answered in the affirmative, and 13 answered that they had no such collaborations (Figure 3.13). All 11 of the genebank managers reporting collaborations with other partners identified the partner, almost all of which are public institutions pertaining either to the national agricultural research system, national universities, or a CGIAR Center (ICRISAT). Out

of 20 collaborations listed (some participants listed more than the most frequent areas of collaboration were regeneration (20%) and characterization (35%) followed by evaluation (20%). The collaborations reported were 40% national, 35% regional, and 20% international in nature (5% did not specify the type of collaboration). Three respondents indicated only national collaborations. The durations of the collaborations were: constant (25%), frequent (30%), annual (15%), and occasional (25%). Six of the genebanks reported ongoing collaborations with two or more research partners.

### Discussion on networks and collaborative initiatives

In comparison with many other crops of global importance, there appears to be a paucity of pre-existing regional or global peanut networks. Of the few international collaborative networks reported, the most noteworthy is the International Peanut Genome Initiative (IPGI) and its data-sharing portal, [PeanutBase](#). With the exception of the Americas, nearly all of the Regional Crop Strategies and PGR network reports consulted make little or no mention of peanut. There are a number of isolated national and inter-institutional collaborations reported, e.g. with public-sector breeders and academia. Very few interactions were reported with NGOs, civil society groups, farmer organizations, conservationist groups, protected areas, etc.

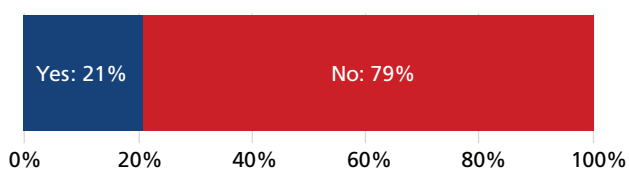


Figure 3.12 Percentage of surveyed genebanks engaged in *Arachis* germplasm networks.

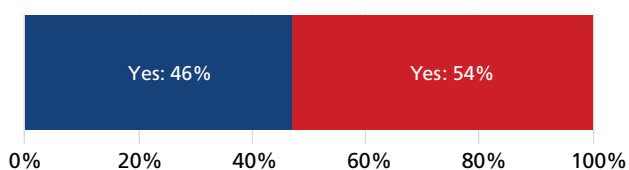


Figure 3.13 Percentage of surveyed genebanks collaborating with other genebanks or breeding programs.



## 4 IN SITU CONSERVATION AND ON-FARM MANAGEMENT OF CULTIVATED PEANUT AND ITS WILD RELATIVES

### 4.1 Introduction

The ultimate goal of genetic resources conservation is to ensure that the maximum amount of genetic diversity within a crop's genepool is safely maintained and kept available for use by farmers, breeders, researchers, and other germplasm users. The previous section has discussed in detail how the diversity of *Arachis* germplasm is conserved and managed in *ex situ* facilities (genebanks). In the case of peanut, a large proportion of the crop's genetic diversity exists *in situ*, that is, in the field, in those environments where it has evolved, continues to evolve, and where its distinctive characteristics have arisen. For wild *Arachis* species, *in situ* conservation takes place in natural populations occurring in protected areas or other relatively undisturbed ecosystems within the species' native range in South America, while for cultivated peanut landraces, *in situ* conservation occurs on-farm, in traditional agroecosystems under the management of rural farmers whose ancestors have been selecting for preferred traits and attributes over generations.

Perhaps the most noteworthy advantage of *in situ* conservation is that, in contrast to genebanks where germplasm accessions are essentially "frozen" in time, the genetic resources conserved *in situ* are subjected to natural and/or farmers' selection pressures and are continuously evolving and adapting to environmental and social changes. These ongoing evolutionary processes can give rise to new, more adapted traits important for ensuring the plants' sustainability within their natural and/or anthropogenic ecosystems. Another distinct advantage of the *in situ* approach is that the materials, both wild and cultivated, are typ-

ically conserved in populations that are considerably larger than the small quantities of seeds, plants or tissues that can be realistically managed in a genebank, thereby preserving a broader amount of within-population diversity, which can be significant.

On the other hand, an inherent weakness of the *in situ* approach is that the genetic diversity is often located in remote areas beyond the immediate control and access of researchers, where they may be vulnerable to fires, overgrazing, deforestation, mining, urbanization, or other catastrophic threats. The status of genetic resources conserved *in situ* must be monitored periodically by specialists to assess their conservation status, and samples need to be collected and incorporated into *ex situ* collections in order to document, characterize, and make them readily available to researchers and other users. These users may include native or traditional farmers who have inadvertently lost one or more of their ancestral landraces, or ecosystem restoration efforts for degraded lands or protected areas.

Consequently, the *in situ* conservation of wild *Arachis* species and the on-farm management of traditional peanut landraces are regarded as complementary to *ex situ* conservation methods that, together, represent the most effective strategy for ensuring the long-term preservation and use of the widest possible range of peanut genetic diversity. In order to take full advantage of this complementarity, the development of linkages between the two approaches and their eventual incorporation into an integrated conservation strategy is to be encouraged and pursued.

This section presents a review of the scientific literature as well as the country reports presented to the FAO and CBD on progress made by countries in surveys/inventories conducted regarding *in situ* conservation and on-farm management of *Arachis* genetic resources. In general, there has been a dearth of *in situ* and on-farm conservation efforts involving peanut landrace diversity in the Americas, Africa and Asia.

## 4.2 *In situ* conservation and on-farm management of peanut genetic resources

As mentioned earlier in Section 2, wild relatives of the cultivated peanut are native to South America and their center of origin and diversity extends across five countries, namely Brazil, Argentina, Bolivia, Paraguay, and Uruguay. While these countries comprise the target areas for *in situ* conservation of peanut wild relatives, the cultivated crop, *Arachis hypogaea*, is widely cultivated in many countries in South and Central America, Africa and Asia, where many traditional varieties are grown by local communities and should be the subject of on-farm conservation and management. The countries of origin recognize that they hold a rich diversity of *Arachis* spp. However, an analysis of the country reports of these countries to FAO and CBD shows that very few initiatives have been reported on the *in situ* and on-farm conservation of peanut genetic resources. Brazil reported that inventories of the conservation status of landraces and of crop wild relatives were conducted by EMBRAPA and by the National Institute for Amazonian Research (INPA) and coordinated by the Ministry of the Environment. These inventories included peanut genetic resources. Furthermore, some activities were aimed at fostering the conservation of these landraces and their wild relatives.

In Bolivia, institutions such as ANAPO and CIFP have developed *in situ* conservation programs involving *Arachis* species in the valleys and chacos of the eastern lowlands. The Friends of Nature Foundation (FAN – Fundación Amigos de la Naturaleza), based in Santa Cruz, Bolivia has also undertaken an inventory of the crop wild relatives (CWRs) in the valleys and altiplano regions. These projects have focused on public awareness of the wealth of crop diversity they are maintaining and their relationship to food security (Bolivia FAO Country Report, 2008). The Bolivian Ministry of Environment and Water – Vice Ministry of the Environment, Biodiversity and Climate Change (MMAyA-VMABCC) has undertaken different actions related to research and conservation of CWRs as a partner in the UNEP-GEF Global Project “*In Situ* Conservation of the Wild Relatives of Crops through the Strengthening of Information Management and its Application in the Field” during the period 2005–2009 (Hunter and Heywood, 2011). Within the framework of this project,

Bolivia published a Red Book of the crop wild relatives of Bolivia, prioritized research work, and generated considerable knowledge about the CWRs of 16 genera of food crops, including peanut, and developed a national information system on CWRs that integrates the information dispersed from the national institutions involved in the project. It also developed the capacities of national institutions to manage information on the CWRs for different purposes using spatial analysis tools such as GIS, among others. In Paraguay, 145 sites within the conservation units, private reserves and in the indigenous communities have been identified as important for *in situ* conservation of wild relatives of peanut and are permanently monitored by professionals from both the public sector and NGOs. In most countries, there have been few or no deliberate efforts to set aside special reserves or protected areas for wild *Arachis* species. It is often assumed that the wild relatives occur mostly in protected areas and are well-conserved, but there has been no action to document the occurrence of these species within existing protected areas and to validate if they are being adequately conserved.

In Latin America, *Arachis hypogaea* has been cultivated for millennia by local communities thereby generating diverse landraces, scores of which are still being cultivated and managed by native farmers (Freitas et al. 2007; Nascimento et al. 2020). Williams (2001) notes that collections of peanut landraces have been assembled in many countries within the crop’s prehistoric range, focusing on areas of highest diversity such as Bolivia, Peru, Ecuador, Brazil, Paraguay, Mexico and Guatemala. In Uruguay, national inventories of local varieties have been undertaken in the past and there is a recognition of the traditional landraces in family production systems. The Program of Responsible Production (PPR) of the Ministry of Livestock, Agriculture and Fisheries – with financing from the World Bank and the GEF – has promoted the conservation and sustainable use of plant genetic resources since 2005 (Uruguay FAO Country Report, 2007).

In a 1992 plant exploration in the highland states of Puebla and Guanajuato, Mexico, Sanchez-Dominguez and Williams (1993) studied the Peruvian-runner or ‘dragon’ type peanuts, locally known as ‘*cacahuates chinos*’ (*A. hypogaea* subsp. *hypogaea* var. *hirsuta*) that are highly valued by local farmers. The study found that landraces of ‘*hirsuta*’ peanuts are still cultivated using age-old labor-intensive planting and harvesting techniques, whose flavor is preferred over the introduced commercial varieties. In Ecuador and Guatemala, cultivated landraces have been mapped to identify key areas for on-farm conservation. A study led by IPGRI (now the Alliance of Bioversity International and CIAT), documented how and why Amerindian farmers maintained and managed a diverse

assemblage of peanut landraces and how the useful landraces were used in participatory breeding activities (Jarvis and Hodgkin 1998).

Cultivated species have been introduced and became established in West Africa and Asia in the 16<sup>th</sup> Century and local landraces quickly evolved and became widespread in rural farming communities. Nowadays, 95% of the global peanut area is in Africa and Asia, where it is cultivated under rainfed conditions with low inputs by resource poor farmers (Pasupuleti et al., 2013). Most of the cultivated peanuts were local landraces, but since the 20<sup>th</sup> Century improved varieties became established and displaced the local landraces, many of which, apparently, have suffered severe erosion since then.

For example, in China, peanut production by farmers was enhanced by the “Household Responsibility System” that was carried out in the early 1980s, which provided increased price incentives, partial privatization, increased use of specialized production and marketing (Yao 2004). This increase in peanut productivity was due to improved peanut varieties and improved package of cultivation practices which include deep tillage, balanced fertilizer, close planting, chemical control, and polythene mulching. There are no documented cases of on-farm management of local landraces in China, although Yao (2004) stated that China has had a long history of peanut cultivation.

In India, peanut was also introduced in the early 16<sup>th</sup> Century and became an important industrial crop in the states of Andhra Pradesh, Tamil Nadu, Gujrat, Karnataka and Maharashtra which accounts for about 90% of the peanut production in the country. Talawar (2003) gives a good overview of the history, production and utilization of peanuts. But no reference is made to traditional varieties, and improved ‘spanish’ varieties are the ones primarily cultivated in most states today. Although the peanut has been grown by smallholder farmers in India over the last five centuries and local varieties have undoubtedly been selected by them, there is no inventory or records made of these traditional varieties. Most of the reported research activities on peanut have focused on development and promotion of improved varieties (Ojeiwo et al. 2020; Pasupuleti et al. 2013; Talawar 2003), which has, in effect, led to the abandonment of local varieties by farmers, as it is a crop grown mostly for income generation rather than for food security.

In Africa, there are few documented examples of on-farm management of peanut genetic resources. A notable exception is the recent study of traditional varieties and their use in central and southern Benin (Loko et al. 2020). As in Asia, most of the local traditional peanut landraces have been displaced by

improved varieties for the oil-processing industry. For example, in Burkina Faso, improved peanut varieties were introduced in the early 1900s, mainly for oil processing. Farmers were encouraged to grow peanuts in many places, but most varieties grown were improved varieties (Konate et al. 2020). Jelliffe et al. (2018) however report that in Uganda between 84% and 90% of all crops including peanuts consist of landrace varieties from home-saved seeds and the Uganda National Agricultural Advisory Services (NAADS) helps to promote on-farm practices to enhance smallholder welfare.

#### 4.2.1 Threats

As mentioned above, the main threat to the myriad traditional landraces of peanut has been the expansion and intensification of improved varieties in Asia and Africa and Latin America, which has led to the abandonment of many traditional landraces (Williams 2001; Yao 2004; Konate et al. 2020; Loko et al. 2020). In Benin, for example, decreasing yields were mentioned as one of the main reasons for peanut varietal abandonment (Loko et al. 2020). With regard to wild *Arachis* species, many of them are currently endangered by rapidly expanding deforestation for mechanized agriculture and induced pasture, urbanization, and road and pipeline construction, among other changes in land use (Jarvis et al. 2003). The country reports to FAO on the status of *in situ* conservation also mention that key threats to wild populations include the advance of the agricultural frontier and/or realization or increase in building and road infrastructure, as well as by the establishment of hydroelectric dams. In Bolivia, the country report mentions that CWR are in danger, mainly due to habitat loss, the effects of climate change, the increasing industrialization of agriculture, inadequate soil and water management, slash-and-burn agriculture (*chaqueo*), and overgrazing. These threats have profound repercussions and lead to the genetic erosion of these resources. In Bolivia, the Red List assessment of wild relatives of peanut (VMABCC-BIOVERSITY 2009) revealed a number of key threats for the threatened wild peanuts species, which can be summarized as follows:

- Increase in mechanized agriculture
- Extensive cattle ranching and overgrazing
- Oil exploration
- Pipeline construction (gas pipeline)
- New human settlements
- Urbanization – accelerated growth of the cities (case for *A. benensis* and *A. williamsii*)
- Road improvement (case for *A. benensis*)
- Airport infrastructure (case for *A. benensis*)
- Deforestation
- Burning at end of season
- Climate change (for example, *A. kempff-mercadoi*, Jarvis et al. 2008)

#### 4.2.2 Landraces – conservation and management on-farm

The most detailed surveys of peanut landraces have been carried out by Krapovickas et al. (2009, 2013, 2021) in Bolivia, Peru and Ecuador, respectively, which include some of the most important centers of unique peanut diversity. In Bolivia (62), Peru (47), and Ecuador (51) distinct landraces have been identified and systematically described. In Bolivia, on-farm conservation of peanuts is carried out mainly by small farmers in the Andean valleys and lowland regions lacking irrigation, as well as areas with fragile soils and dry areas of the lower tropical region, where the use of traditional varieties and species is almost the only safe way to produce food of plant origin (Bolivia FAO country report, 2009). Bertioli et al. (2011) mention that many landraces of peanuts are cultivated by more isolated communities as companion planting with cassava and other native cultigens, in cropping systems practiced since pre-Colombian times. Many of these ancestral peanut landraces remain poorly characterized or are unknown to science and vulnerable to extinction, although they may have useful new traits of adaptation and resilience.

Alagirisamy (2016) noted that peanut landraces corresponding to the botanical varieties *hypogaea*, *hirsuta*, *fastigiata*, *vulgaris*, *peruviana*, and *aequatoriana* from Peru, Mexico, and Brazil showed high diversity and several characteristics of interest for breeding sustainable groundnut varieties. In Paraguay, there are traditional Guaraní peanut varieties such as '*manduví guaicurú*', '*manduví pytá*', '*manduví hui*' and '*manduví pytai*,' that have been adapted and selected over the years in agricultural localities, remain popular, and are linked to the culinary traditions of the population.

Williams (1989, 1991, 1992) documented a specialized peanut cropping system used by indigenous farmers in the Amazonian headwaters of Eastern Bolivia. These farmers plant a suite of dedicated peanut landraces on alluvial beaches and riverine sandbars that are exposed for a rather short period during the low-water season. Under this cropping system, the peanut plants are strongly selected for uniform germination and a short reproductive cycle as they must mature quickly and be harvested before the river rises again and inundates the growing area. As a result of these traditional farming practices, the local peanut landraces are well-adapted to produce abundantly in this highly specialized riparian agroecosystem.

Freitas et al. (2007) reported that the Kayabi Indians who inhabit the Xingu Indigenous Park, located in West Central Brazil have been cultivating great numbers of peanut landraces for a long time, and this germplasm shows large phenotypic diversity. Using

microsatellite markers, they detected high levels of genetic variation which clustered according to the villages where they were collected. The original study of the Kayabi landraces has been complemented by a recent molecular analysis (Nascimento et al. 2020) that also showed that these materials can be used to introduce new diversity into peanut-breeding programs.

In Benin, a detailed study of varietal diversity of local peanuts undertaken by Loko et al. (2020) revealed eight morphologically distinct landraces among 54 vernacular names given by the 10 ethnic groups involved in the study. This diversity is found to be lower than the 62 distinct landraces known to exist in Bolivia, but significantly higher than the four local varieties reported in Togo (Banla et al. 2018) and the eight local varieties reported in Tanzania (Daudi 2018). On average, four local varieties are grown per village, with a range of 1 to 11 local varieties. At the household level, peanut variety richness varied from 1 to 3 in the southern and 1 to 4 in the central part of Benin. The survey also documented the reasons for the abandonment of landraces. Five and fifteen farmers in the southern and central parts, respectively, abandoned the local landraces due to drop in yield, drought, drop in market price and lack of financial means (Loko et al. 2020).

#### 4.2.3 Constraints and obstacles

To the survey question relating to the most important obstacle that countries face in enabling, managing or monitoring *in situ* conservation of peanut landraces, the key obstacles listed by the respondents include the following:

- Low profit/income from landraces (Argentina IBONE)
- Loss of the biocultural patterns that actively maintain the interest in local races (Argentina IBONE)
- Financial/economic constraints (Argentina IBONE, Paraguay IPA-Choré; Paraguay UNA-FCA; Bolivia INIAF; Ecuador INIAP, Peru INIA; Benin)
- Human resources, permanent trained staff (Argentina IBONE, Paraguay IPA-Choré, Bolivia INIAF; Ecuador INIAP; Senegal; Australia)
- Agronomic staff and government awareness of the *in situ* conservation (Argentina IBONE)
- Public policy, lack of national policies for the conservation of germplasm (Paraguay IPA-Choré; Paraguay UNA-FCA; Bolivia INIAF)
- Lack of research interest (Paraguay UNA-FCA)
- Lack of public awareness (Paraguay UNA-FCA; Bolivia INIAF; Ecuador INIAP; Senegal)
- Contracting public services (Ecuador INIAP)
- Acquisition inputs (Ecuador INIAP)
- Local partners (Bulgaria)
- Lack of storage structures (Benin)



In Benin, Loko et al. (2020) studied the main constraints in landrace cultivation and concluded that the lack of labor, high seed price, decrease in yield and many pests including rats, partridge, centipedes, etc., were among the main limiting factors. Similarly, in Togo (Banla et al. 2018) and Tanzania, Daudi et al. (2018) identified pests and diseases, such as the late leaf spot, pod-sucking bugs, bruchids, and rust caused by *Puccinia arachidis*, as the most important constraints limiting peanut production.

#### 4.2.4 Crop Wild Relatives – conservation and management *in situ*

##### Checklists and inventories

There are over 82 species of wild *Arachis* and all are endemic to South America where their distributions are restricted to a variety of natural habitats in Brazil, Bolivia, Paraguay, Argentina, and Uruguay (Bertioli et al. 2011).

In Argentina, the competent authorities have carried out inventories of the vascular plants of Argentina and published a catalogue of the *Vascular Plants of Argentina and the Southern Cone*, which includes Uruguay, Paraguay and the southern parts of Bolivia and Brazil. Among these vascular plants, 23 species of wild *Arachis* are listed.

In Bolivia, the *in situ* conservation status of the crop wild relatives (CWR) of peanut was assessed during the implementation of the UNEP/GEF project “*In situ* conservation of crop wild relatives through information management and its field application” led by Bioversity International and executed by the Vice-Ministry for the Environment and Biodiversity and Climate Change (VMABCC) of the Ministry of the Environment and Water (MMA&A). An inventory of 20 wild species of which 11 are endemic were identified (*Arachis ipaënsis*, *A. trinitensis*, *A. williamsii*, *A. benensis*, *A. herzogii*, *A. kempff-mercadoi*, *A. cruziana*, *A. krapovickasii*, *A. batizocoi*, *A. cardenasii*, *A. simpsonii*, *A. diogoi*, *A. duranensis*, *A. glandulifera*, *A. matiensis*, *A. rigonii*, *A. chiquitana*, *A. magna*, *A. glabrata*, and *A. sp.*).

In Brazil, a survey concluded by Valls (2015), as part of a National Flora Checklist, has identified 63 native species of *Arachis*, and two only known under cultivation (*A. hypogaea* and *A. kempff-mercadoi*), providing data on ecological preferences, geographic distribution, and specimen citation and illustrations. This is now being updated in the Flora do Brasil 2020 Project, still under construction for the genus, where a morphological key to all Brazilian species was included, one new species (*A. jacobinensis*) was added, the old misused name *A. sylvestris* was replaced by *A. veigae*,

and herbarium information and illustrations have been expanded.

According to Vincent et al. (2013), 16 species of wild *Arachis* are prioritized for *in situ* conservation. Brazil (9 spp.) and Bolivia (8 spp.) are the two countries with the highest number of *Arachis* species prioritized for *in situ* conservation. Thirteen of the prioritized species have been reported to have either confirmed or potential uses for crop improvement, mainly for providing resistance to biotic stress (Stalker 2017) (Table 4.1). No data has been recorded on use in crop improvement for *A. helodes* and *A. herzogii*.

##### Threat assessment of peanut CWR

At the global level, only eight wild *Arachis* species have been assessed by the IUCN Red List (as of 21 April 2020) and they are all among the priority list of Vincent et al. (2013). These include five categorized as Near Threatened (62.5%), two as Vulnerable (25%) and one as Least Concern (12.5%) (Table 4.2).

As part of the UNEP-GEF project in Bolivia, mentioned earlier, the threat assessment of 20 CWR species was carried out and results were published in “The Red Book of Crop Wild Relatives in Bolivia” (VMABCC-BIOVERSITY, 2009). The book provides detailed information on the IUCN red list status for 17 threatened wild species of peanuts in Bolivia; the others are thought to be of least concern (*A. cruziana*, *A. simpsonii*, *A. glabrata*). Table 4.3 shows that there are two Critically Endangered (CR) species, six Endangered (EN) species, two Vulnerable (VU) species and seven Near Threatened (NT) species. In addition, the book provides information on the description of the CWR species, its geographical distribution and proposed conservation measures and actions. This provides a useful baseline information for the reassessment of the conservation status of wild relatives of peanuts in Bolivia.

In the case of *Arachis cruziana*, Jarvis et al. (2003) considered this species at risk of extinction based on the few existing records, the impacts of climate change, and the pressures on land use in the zone where it grows. However, in subsequent field visits carried out in 2007, relatively well-conserved populations of a few individuals were found, for which reason this species is considered as Near Threatened (NT).

*Arachis ipaënsis*, on the other hand, is listed as a Critically Endangered species, known only from its type locality, whose habitat is rapidly being degraded. It has not been collected since 1977, despite several subsequent expeditions to the collection site and surrounding areas from 1994 to 2007 to locate the species, all without success. The species was collected on the banks of the Taihuate Ravine, which are con-

stantly eroding due to the fragile substrate composed of yellow sandstone. Moreover, the habitat has been completely modified by expansion of the nearby village and the settlement of small farmers along the river bank. This species, widely accepted as one of the progenitors of the cultivated peanut, is now believed to be extinct in the wild. The location where this species was collected is outside of the Serranía del Aguaraque National Park and Natural Area of Integrated Management, but is very close to the eastern limit of this park.

The situation is similar for *Arachis rigonii*, which was originally collected in 1958 along an unpaved street just 400 meters from the central square of Santa Cruz

de la Sierra. In the ensuing years, Santa Cruz experienced rapid growth and is now Bolivia's largest city, with a vibrant metropolitan sprawl encompassing 2.5 million inhabitants and extending outward for kilometers. The species is known only from the type locality and has not been re-collected since 1959. Several subsequent attempts to locate other populations have been unsuccessful and it is feared that *A. rigonii*, like *A. ipaënsis*, may now be extinct. Seeds of *A. ipaënsis* and *A. rigonii* are conserved in the germplasm banks in Brazil, Argentina and the USA.

In the cases of *Arachis brevipedunculata* and *A. martii*, both of which were considered at risk and only known at the time from their type localities by Krapovickas

**Table 4.1** Confirmed and potential uses for 13 of the prioritized wild *Arachis* species with available information. Confirmed uses are in bold and potential uses are in regular text. Data source: Stalker (2017), with genepool adjustments (see Table 2.2).

Species	Genepool Level	Type of Use	Confirmed or Potential Use
<i>A. appressipila</i> Krapov. & W.C. Greg.	Tertiary	Biotic stress	<b>Early Leaf Spot resistance</b> ; Groundnut Rosette disease resistance; Rust resistance
<i>A. batizocoi</i> Krapov. & W.C. Greg.	Tertiary [ <i>Arachis</i> sect., K genome]	Biotic stress	<b>Root Knot Nematode Resistance; Rust resistance; Fertility Trait</b> ; Bud Necrosis disease resistance; Early Leaf Spot resistance; Late Leaf Spot partial resistance; Peanut Mottle Potyvirus resistance; Rust resistance; Stem Rot resistance
<i>A. cardenasii</i> Krapov. & W.C. Greg.	Secondary	Biotic stress	<b>Early Leaf Spot resistance; Late Leaf Spot partial resistance; Leaf Miner tolerance; Potato Leafhopper resistance; Root Knot Nematode resistance; Rust resistance; Southern Corn Rootworm resistance; Tobacco Caterpillar tolerance</b> ; Groundnut Rosette Disease resistance; Peanut Stunt Virus resistance; Thrips resistance
<i>A. correntina</i> (Burkart) Krapov. & W.C. Greg.	Secondary	Biotic stress	Peanut Stunt Virus resistance; Potato Leafhopper resistance, Rust resistance, Thrips resistance
<i>A. diogoi</i> Hoehne	Secondary	Biotic stress	<b>Late Leaf Spot partial resistance; Rust resistance; Root Knot Nematode resistance</b> ; Early Leaf Spot resistance, Groundnut Rosette Disease resistance
<i>A. duranensis</i> Krapov. & W.C. Greg.	Secondary	Biotic stress	Late Leaf Spot partial resistance; Rust resistance; Bud Necrosis disease resistance; Early Leaf Spot resistance; Groundnut Rosette Disease resistance; Peanut Mottle Potyvirus resistance; Potato Leafhopper resistance; Rust resistance; Stem Rot resistance; Thrips resistance
<i>A. hoehnei</i> Krapov. & W.C. Greg.	Tertiary [ <i>Arachis</i> sect., genome undet.]	Biotic stress	<b>Late Leaf Spot partial resistance; Rust resistance</b>
<i>A. kempff-mercadoi</i> Krapov., W.C. Greg. & C.E. Simpson	Secondary [ <i>Arachis</i> sect., A genome]	Biotic stress	<b>Early Leaf Spot resistance; Late Leaf Spot partial resistance; Rust resistance</b> ; Potato Leafhopper resistance
<i>A. linearifolia</i> Valls, Krapov. & C. E. Simpson	Secondary	Biotic stress	Early Leaf Spot resistance; Late Leaf Spot partial resistance; Rust resistance
<i>A. magna</i> Krapov. & W.C. Greg. & C.E. Simpson	Secondary	Biotic stress	Late Leaf Spot partial resistance; Rust resistance
<i>A. monticola</i> Krapov. & Rigoni	Primary	Agronomic trait	Yield improvement
<i>A. paraguariensis</i> Chodat & Hassl.	Tertiary	Biotic stress	<b>Early Leaf Spot resistance</b> ; Late Leaf Spot partial resistance; Peanut Stunt Virus resistance; Potato Leafhopper resistance; Rust resistance
<i>A. villosa</i> Benth.	Secondary	Biotic stress	<b>Late Leaf Spot Partial Resistance</b> ; Early Leaf Spot resistance; Groundnut Rosette Disease resistance; Rust resistance

& Gregory (1994), have been relocated and rescued in Brazil, including several natural populations now maintained as living plants and seeds at the Embrapa Wild *Arachis* Genebank. Some new populations of *A. brevipetiolata* were discovered over 500 km away from the original collection site, while some new populations of *A. martii* were found in the urban area of the fast-growing city of Campo Grande but have already been overcome by urban development. Both species are difficult to maintain under cultivation, but seeds germinate well, and the option of bringing local soil for use in greenhouse pots, something only possible when road expeditions are carried out from Brasília, guarantees the subsequent increase under controlled conditions. The use of soil brought from the collection sites is also responsible for a considerable part of the success achieved in the conservation of species of sect. *Extranervosae*, such as *A. marginata* (J.F.M. Valls, personal communication).

#### Conservation of wild *Arachis* species within protected areas

Very few records of wild *Arachis* species are shown to occur in existing protected areas established by the five countries in which these species are endemic. Jarvis et al. (2003) used 2,175 georeferenced observations of wild *Arachis* species to assess their *in situ* conservation status, and to biologically and geographically prioritize future conservation actions. That study showed that only 48 (or 2.2%) of the 2,175 observations, representing just nine *Arachis* species, were located within national parks. The same trend can be

observed in a more recent study in Brazil, as shown in Figure 4.1. Similar circumstances of under-protection of wild *Arachis* populations in protected areas also exist in the other four countries where the species occur. Although accurate data may be lacking in many cases, it seems clear that natural populations of nearly all wild peanut species are poorly conserved *in situ* within their host countries' systems of protected areas.

Wild *Arachis* populations remain under threat from a variety of factors as discussed above, and a greater effort to protect their hotspots of diversity is needed. However, the above figures on natural occurrence may be somewhat skewed due to restrictions placed on the collection of germplasm and herbarium specimens in conservation units. Hence, the floristic inventories of existing protected areas may not accurately reflect the possible presence or absence of wild *Arachis* species in such environments. Moreover, collection of wild *Arachis* species by non-specialists is a rare event in floristic surveys, just as *Arachis* specimens in general are typically scarce in herbaria. Most botanists tend not to collect plants on which they do not see fruits, and whose flowers remain turgid for only a few hours a day (Valls et al. 1995).

#### Constraints and obstacles

Of the five countries that harbor wild *Arachis* populations (Argentina, Bolivia, Brazil, Paraguay and Uruguay), all responded to the survey question on this topic. They unanimously indicated that the major constraints include the lack of financial and quali-

**Table 4.2** The IUCN Red List categories of priority peanut wild relatives (IUCN, 21 Apr. 2020).

Genus	Species	Authors	IUCN Red List Status
<i>Arachis</i>	<i>cardenasii</i>	Krapov. & W.C. Greg.	Least Concern (LC)
<i>Arachis</i>	<i>hoehnei</i>	Krapov. & W.C. Greg.	Vulnerable (VU)
<i>Arachis</i>	<i>diogoi</i>	Hoehne	Near Threatened (NT)
<i>Arachis</i>	<i>paraguariensis</i>	Chodat & Hassl.	Near Threatened (NT)
<i>Arachis</i>	<i>villosa</i>	Benth.	Near Threatened (NT)
<i>Arachis</i>	<i>magna</i>	Krapov., W.C. Greg. & C.E. Simpson	Near Threatened (NT)
<i>Arachis</i>	<i>helodes</i>	Krapov. & Rigoni	Near Threatened (NT)
<i>Arachis</i>	<i>cruziana</i>	Krapov., W.C. Greg. & C.E. Simpson	Vulnerable (VU)

**Table 4.3** Threatened *Arachis* species from Bolivia (VMABCC-BIOVERSITY 2009).

IUCN Red List Status	<i>Arachis</i> species
Critically Endangered (CR) [extinct from type locality]	<i>A. ipaënsis</i> , <i>A. rigonii</i>
Endangered (EN)	<i>A. benensis</i> , <i>A. chiquitana</i> , <i>A. krapovickasii</i> , <i>A. simpsonii</i> , <i>A. trinitensis</i> , <i>A. williamsii</i>
Vulnerable (VU)	<i>A. herzogii</i> , <i>A. matiensis</i>
Near Threatened (NT)	<i>A. batizocoi</i> , <i>A. cruziana</i> , <i>A. cardenasii</i> , <i>A. duranensis</i> , <i>A. glandulifera</i> , <i>A. magna</i> , <i>A. kempff-mercedoi</i>

fied human resources, lack of national policies and awareness among public and government. In addition, Argentina mentioned land-use changes, while both Paraguay and Uruguay indicated the lack of research interest as a major constraint for *in situ* conservation of wild *Arachis* diversity in their countries. These constraints are more or less similar to those cited for on-farm conservation of peanut landraces.

- Financial (Argentina, Bolivia, Paraguay, Uruguay)
- Lack of enough specialized staffing (Argentina, Bolivia, Brazil, Paraguay, Uruguay)
- Lack of national policies, or policy constraints for *in situ* conservation of germplasm (Argentina, Bolivia, Brazil, Paraguay)
- Public and government awareness (Argentina, Bolivia, Brazil, Paraguay, Uruguay)
- Land use change (Argentina)
- Lack of research interest (Paraguay, Uruguay)
- Lack of local partners (Uruguay)
- Lack of eco-physiological knowledge to recommend best management practices (Brazil)

#### 4.2.4 Complementarity with *ex situ* conservation

Although the importance of adopting a complementary approach with regard to *ex situ* and *in situ* on-farm conservation is well recognized in the literature (Maxted et al. 1997; Williams 2001; Hunter and Heywood 2011; Engels et al. 2009; Dulloo et al. 2017),

there is very limited evidence of any linkages between *ex situ* and *in situ*/on-farm conservation activities for peanut genetic resources. In response to the survey question on the involvement of the genebanks to promote, enable, manage or monitor *in situ* (on-farm) conservation of peanut landraces, only a handful of genebank respondents described any such activities. The few activities mentioned include:

- Survey of landraces maintained by local holders in NE Argentina, after 60 years of collecting for the *ex situ* conservation of peanut germplasm (Argentina IBONE)
- Development of local seed banks for re-adoption of local varieties (Argentina, Senegal)
- Development of seed banks at schools in rural communities (Argentina IBONE)
- Record of the biocultural patterns associated with local races of peanut (Argentina IBONE)
- Association with local organizations of farmers and local governments to promote the peanut cultivation and maintenance of local races (Argentina IBONE)
- Seed fairs (Ecuador, Paraguay, Uruguay)
- Participatory breeding, characterization and evaluation (Benin, Ecuador, Paraguay, Senegal, Uruguay)
- Community registers (Ecuador, Uruguay)
- Repatriation of accessions (Ecuador)
- Regeneration and multiplication (Ecuador)

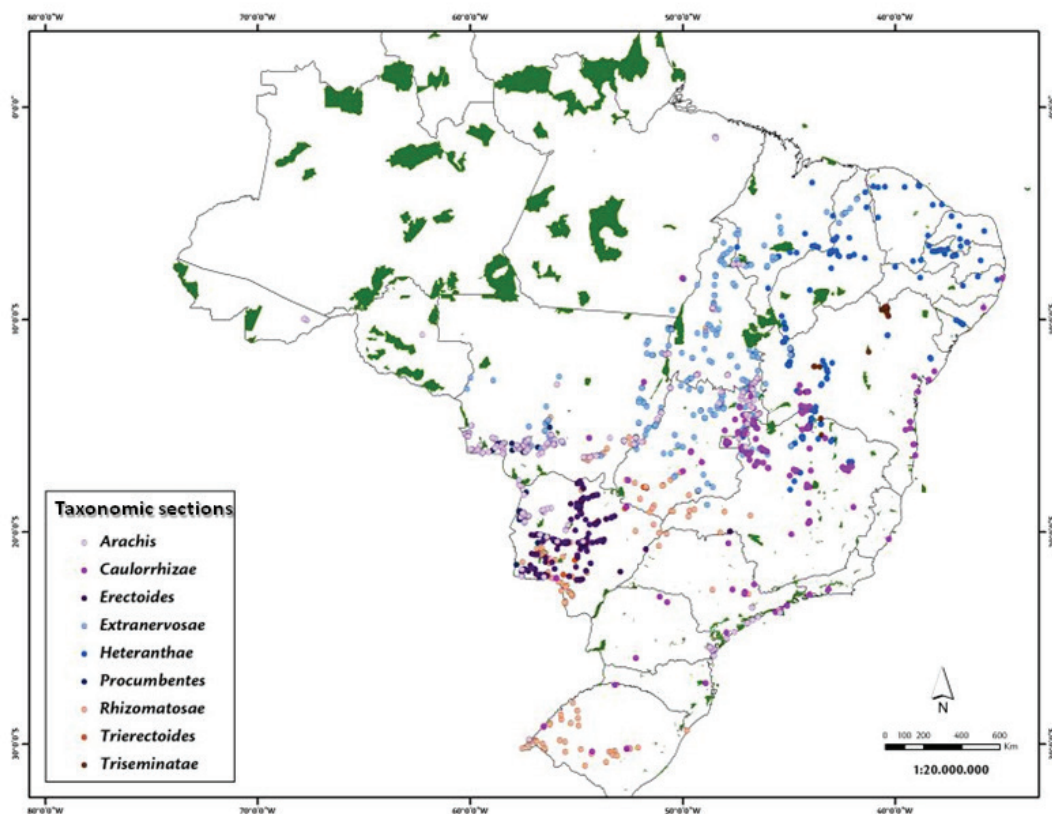


Figure 4.1 Distribution of protected areas and wild *Arachis* species, by taxonomic section, in Brazil. (Figure provided by J.F.M. Valls, March 2021)



# 5 A GLOBAL STRATEGY FOR THE CONSERVATION OF PEANUT DIVERSITY

## 5.1 Introduction

A strategy is understood as a systematic means of solving a complex problem, resulting in a carefully devised plan for successfully achieving a particular goal, usually over a long period of time. For stakeholders engaged in solving a complex problem, a well-designed strategy will enhance their chances of success by providing them with a road map for conducting a thorough diagnosis of the problem, a blueprint for shaping their guiding policy, and a master plan for coordinating the actions needed to reach the desired goal.

The intended purpose of this section is—based on a careful analysis of the information presented in the preceding sections—to lay out the key elements, opportunities and challenges that will be addressed by a prioritized action plan, and constitute the framework of a viable global strategy to conserve peanut diversity. The resulting global strategy should underpin and formalize critical partnerships and facilitate a degree of international collaboration that will enable the optimal preservation and use of *Arachis* genetic resources in the context of a global system. These are laudable but ambitious goals, and the purpose of the Global Peanut Conservation Strategy is to provide a roadmap of how to achieve them. As such, this Strategy can be considered as a “living document” that can be periodically updated and further developed.

## 5.2 Strategic challenges

Our analysis of the survey responses together with the literature review, revealed a number of scientific,

institutional, and policy challenges that constitute important constraints to the effective study, conservation and use of peanut genetic resources at the global level.

### 5.2.1 Key collections

Addressing the important challenges currently facing the key collections should be among the objectives of the Global Peanut Conservation Strategy. There are a few large *Arachis* germplasm collections with adequate infrastructure and research capacity to either lead or help underpin a global system of peanut conservation and use. There are also a number of other collections of key importance – some of which are seriously underfunded and suffer from inadequate infrastructure and minimal staffing – that nonetheless contain unique germplasm accessions and world-class scientific capacity. The unique materials conserved in these underfunded key collections are invaluable and imminently threatened, and could easily become lost in the foreseeable future.

At the present time, neither the relevant CGIAR Centers, nor the large (and small) national programs with key peanut collections, appear able to absorb, support, or otherwise assume responsibility for the unique and threatened collections referred to above. Some of the reasons for this situation may include a lack of information about the threatened materials, a lack of testing for quarantine pests and diseases, and limited resources – both monetary and personnel – available to address the specific needs.

ICRISAT, as the CGIAR center with a global mandate for peanut genetic resources, considers it important to support, backstop, and help protect threatened national collections. However, the severe restrictions currently imposed by national legislation in many countries for collecting, sharing and/or distributing germplasm make it difficult if not impossible for ICRISAT to provide the support required. Until such policy issues can be resolved, ICRISAT remains open to bilateral discussions with countries who wish to deposit a security duplicate of their collections at ICRISAT under long-term black-box storage conditions (V. Azevedo, personal communication).

If those underfunded key institutions could be integrated into a formalized global system of germplasm conservation and use, they would get the international recognition they deserve. Accordingly, their participation in the global system could greatly facilitate their efforts to leverage the additional support they require to sustain their collections and continue making vital contributions to *Arachis* conservation, research and use.

### 5.2.2 Taxonomic and ecogeographic gaps

**Cultivated peanut** – Peanut landraces and their botanical varieties require further attention to better quantify, manage and access the existing genetic diversity within the crop's primary genepool. While there is considerable duplication of materials across the key germplasm collections, there are also many key taxa, including some botanical varieties of *A. hypogaea* in particular, that are not widely available. These taxonomic gaps are apparent in many studies of the cultigen's infraspecific diversity in which very few or no examples are included of the less-common botanical varieties, especially vars. *hirsuta*, *peruviana* and *aequatoriana*, thereby weakening the scope of the analyses. Good numbers of accessions of each of these botanical varieties are being conserved in different collections, but they are evidently not widely shared among genebanks, or are not requested by researchers. Also, landrace accessions in many of the collections, including some of the larger ones, have never been thoroughly characterized or even identified to their respective botanical variety. These landrace materials need to be characterized, first phenotypically, and then genotypically, to gain a more complete understanding of the diversity already present within the crop's primary genepool, as well as to clarify the taxonomic and phylogenetic relationships among the botanical varieties.

Major ecogeographic gaps in the international peanut collections still exist, particularly regarding landraces from many parts of the crop's prehistoric range of distribution. Landraces from Colombia, Venezuela, Guyana, Suriname, French Guiana, Trinidad & Tobago, Panama, Costa Rica, Nicaragua, El Salvador, Honduras,

Belize, and Mexico are very poorly represented *ex situ* (Figure 3.4). Also, the entire Amazon Basin – and especially the northern and western parts – has yet to be comprehensively explored for peanut landraces. In Africa, there appears to be a significant lack of landrace peanut accessions from many countries where peanut is a longstanding traditional crop (Figure 3.4). Recent studies in Benin, Burkina Faso and other countries indicate that dozens of traditional peanut landraces continue to be cultivated by local farmers there, but the available evidence suggests that traditional landraces from many African nations are not well-represented in *ex situ* germplasm collections. Landraces of the botanical variety *hirsuta*, despite its widespread diffusion, are quite limited in most international collections and should be actively sought from across their known range of historic distribution, particularly Colombia, China, SE Asia, the Malay Archipelago, India, Sri Lanka, and Madagascar. The diverse peanut landraces from Oceania are also severely underrepresented in the international collections.

**Wild *Arachis* species** – In contrast with the situation described above for the cultigen, accessions of many wild *Arachis* species, including those most closely related to the cultigen, seem to be available and fairly well distributed to researchers worldwide. National specialists in Argentina, Bolivia, Brazil, and Paraguay are collaborating and conducting systematic, ongoing explorations to discover and collect new populations of wild *Arachis*, and a number of recently collected materials are already in the process of being described and published as new species. For the time being, germplasm of these new accessions is being conserved *ex situ* in the host countries' respective national genebanks, but not distributed internationally.

Nevertheless, numerous wild species are represented in *ex situ* collections by only a single or very few accessions, and nearly all are endangered to some degree as their natural habitats succumb to accelerating development activities and changes in both land-use and climate. The prime example of this is *A. ipaënsis*, one of the two diploid progenitors of the cultivated peanut. All germplasm accessions of *A. ipaënsis* are derived from just two germplasm samples (K 19455 and K 30076) collected at the type locality by Krapovickas et al. (in 1971 and 1977, respectively). No further specimens have or can be obtained as the species is now considered to be extinct in the wild. The scope of genetic diversity contained in the extant populations of wild *Arachis* species cannot be recovered once it is lost. Although permission for foreign access to germplasm is currently restricted in most countries where these species occur, it remains urgent that additional populations be identified, collected and conserved *ex situ* before they are lost. Wherever possible, *in situ* conservation measures should also be put

in place to preserve viable wild *Arachis* populations in their native habitats.

### 5.2.3 Documentation and information sharing

Without question, the sharing of germplasm within the peanut conservation community is to be encouraged for enhancing its use and for security duplication. Historically, large numbers of accessions have been widely distributed by several of the larger collections, whose recipients have in turn shared these same materials with other genebanks, and so forth, resulting in a large but unquantified amount of duplication of accessions currently existing across genebanks. From a global perspective, the widespread and large-scale duplication of commonly held materials may not be the most effective practice in light of the limited capacity—especially of smaller genebanks—to maintain, manage, distribute, and utilize excessively large numbers of accessions.

Collaborative research efforts typically imply the shared use of germplasm, yet these collaborations are often plagued by the replacement of identifiers, from one place to another. Most genebanks use independent documentation systems, and when germplasm is received from another genebank, the source information and original identifiers (e.g., original collector numbers, passport data, original accession numbers) are not always incorporated into the host genebank's database when the new, institution-own accession numbers are assigned. When the accessions' original passport and accession data are not transferred with the germplasm, the providing genebank and the germplasm collectors themselves soon lose track of the characterization, evaluation, and breeding results obtained and published on the accessions they provided. The resulting proliferation of unlinked accession identifiers can quickly make prior accession-level data inaccessible to other users.

Such documentation inadequacies often result from a failure to transfer – or record – existing accession numbers, passport information and/or characterization data associated with the germplasm received. A big advantage of retaining the original collector's number as a synonym for each accession typically using conventional collector prefixes (e.g. K or G standing for A. Krapovickas or W.C. Gregory, respectively) is that they often link to important information regarding the native habitat, climate and soils to which the germplasm is adapted. If, for example, the ICG (ICRISAT) numbers had been faithfully retained as synonyms for all of the wild *Arachis* accessions distributed by ICRISAT to Old World collections and genebanks, many of those distributed accessions could be easily traced back to the original collectors' numbers and be readily identified to the species level. Having the original collectors' information also permits the easy

link to an expanding number of freely available virtual herbarium databases which now include high-resolution photographic specimens that can be examined online to resolve morphological doubts concerning accession identifications.

Another consequence of the proliferation of unlinked accession identifiers is the large number of germplasm accessions held in genebanks that are identified only as "*A. hypogaea*," or the botanical variety listed as "unknown," or with wild species reported simply as "*Arachis* sp." (see Tables 6 and 12). Other manifestations of this problem include accessions that are misidentified or identified with invalid names, or have suffered cross pollinations, all of which make it difficult if not impossible to compare with, or take advantage of, the results of any investigations done on those same materials by different institutions.

When the original accession identifiers and other associated data are not retained in the receiving institution's database, the thread of each accession's identity is broken, and it becomes very difficult to trace the source(s) of the shared germplasm. That means that the degree of germplasm duplication, both across and within collections, cannot be determined. It also becomes impossible for the provider of the shared materials to consider them as being security duplicated. The cost burden of *ex situ* conservation assumed by the receiving genebank is increased when the accession identifiers are replaced by new, in-house identifiers without being duly cross-referenced to their original source identifiers including original collector records, associated passport information, and taxonomic determinations, as well as any pre-existing characterization and evaluation data, which often end up being replicated with expensive experiments.

The widespread duplication of *Arachis* accessions, the proliferation of unlinked accession numbers across genebanks, and the large number of taxonomically unidentified or uncharacterized accessions, has created a situation that significantly undermines the efficiency and utility of many germplasm collections, and impedes the progress of peanut research worldwide. From a global perspective, it is strategically important that these persistent documentation issues be addressed. There are two interrelated approaches through which these documentation deficiencies and information-sharing issues can be resolved, and both should be undertaken simultaneously:

The **first** approach is to promote the development and adoption of updated documentation standards for *Arachis* accessions that improve record keeping, enhance data compatibility, reveal duplications, and facilitate data analysis within and among collections.

Updated documentation standards and descriptors for *Arachis* germplasm characterization need to be developed and universally adopted to ensure the continuity of accession-level information, avoid inadvertent duplications of accessions and research efforts, and enhance the use of the conserved materials. The new documentation standards must include not only updated agro-morphological descriptors, but also valid taxonomic identification and cytogenetic, molecular, and genomic characterization data for each accession. Training activities in the application of the new standards will then need to be conducted to ensure the widespread adoption of the new standards and their incorporation into genebank documentation protocols (see section on Training needs, below).

To address the need to track accessions, identify unique materials, and detect duplicate accessions, the Secretariat of the International Treaty on PGRFA and its Governing Body have proposed the use of a “unique identifier” such as the DOI (Digital Object Identifier) system. By using the DOI to refer to genebank accessions, there is a possibility to automatically and correctly detect any corresponding data and publications where the specific genebank accession is cited. This must be done manually when using any other identifier. However, under the existing DOI system, whenever a germplasm accession is received from another researcher or genebank, or distributed by the recipient to a third researcher or genebank, a new DOI is automatically assigned to the material. According to some experts (including the lead author of this strategy), this feature could produce further confusion without the consistent linking of new DOIs to the original collector or accession numbers which remain constant and unique.

Most *Arachis* germplasm can still be accurately traced back to the original collector number—providing the opportunity to obtain, record and take advantage of the original passport data for much of the peanut diversity conserved *ex situ*. Institutions can continue to use their local identifiers and DOIs as required, but it remains crucial that the DOI system also retains the original identifiers as synonyms in open databases, thereby averting the loss of the vitally important original records.

The **second** way to enhance peanut germplasm documentation and information sharing is through the adoption of a **common web-enabled database platform**. For the benefit of the entire *Arachis* research and conservation community worldwide, access to the passport and characterization data of conserved germplasm accessions is essential. Adoption of a shared documentation platform will not only assist collection managers in curating and managing critical

information on their collections, it will also facilitate the many advantages and opportunities derived from their active participation in a global system of peanut germplasm conservation and use. To that end, a centralized, readily accessible and periodically updated online database of peanut genetic resources needs to be assembled at the global level.

One such global database, the online Catalog of *Arachis* Germplasm Collection, was published in 2001 on ICRISAT’s website (Stalker et al. 2002), and listed the passport data of more than 3,000 original specimens of wild *Arachis* species collected as either plants, seeds, or herbarium specimens up until the year 2000. Regrettably, the resources required to maintain this valuable online registry proved unsustainable in the long-term and, as a consequence, it was abandoned.

Existing global germplasm data-sharing platforms—some of which are inter-compatible—include [WIEWS](#), [Genesys](#), [GRIN-Global](#), [PeanutBase](#), the [Legume Information System](#), and [Alelo](#). These platforms are currently supported by large institutions or consortia with long-term commitments to their maintenance and accessibility.

At this writing, Genesys is the closest thing to a database platform addressing the current need for sharing accession-level germplasm information, and it already covers many of the functions called for above. Currently, Genesys hosts data on more than 35,000 germplasm accessions of cultivated and wild *Arachis* spp., and 10,000 of these are georeferenced. Genesys also maps species names to [GRIN Taxonomy](#) and the currently accepted names, which permits standardization of the botanical nomenclature used by different data providers. It also provides a “find similar accessions” function that can facilitate the detection of duplicates – both intentional and inadvertent.

Widespread adoption of a standardized, inter-compatible data-sharing platform or platforms will be an essential condition for the success of an eventual global system of peanut germplasm conservation and use. While a growing number of genebanks with *Arachis* collections are already making their accession information available on global platforms, a few of the larger key genebanks, such as IND001 and CHN001, have not yet joined in this effort.

If the current documentation and information-sharing difficulties can be addressed through an effective protocol for standardizing passport and characterization data and through the adoption of a common web-enabled database platform, such as Genesys, the progress of *Arachis* research, conservation and use at the global level will be greatly facilitated and enhanced.



#### 5.2.4 Training needs

The lack of adequately trained personnel was an almost universal problem reported by the genebank managers and curators. Moreover, an entire generation of global *Arachis* experts is currently in, or close to, retirement, and a window of opportunity is closing for their unique legacy of personal experience and technical expertise to be passed along to the upcoming generations of peanut researchers. Training of young professionals in *Arachis* taxonomy, specialized peanut-collecting methods, and standardized procedures for germplasm conservation, characterization and evaluation is critically important, particularly for genebanks in developing countries.

#### Taxonomic and agro-morphological characterization standards

Due to the often-enigmatic morphological characteristics of wild *Arachis* species and cultivated peanut landraces, their taxonomic identification can be challenging, even with taxonomic keys. Moreover, the standard morpho-agronomic descriptor lists for peanut/groundnut have not been revised in nearly 30 years (IBPGR/ICRISAT 1992, Pittman 1995). To facilitate the documentation of unidentified or misidentified accessions, a set of updated descriptors need to be developed that include the identification and characterization of wild *Arachis* species as well as the botanical varieties of *A. hypogaea*. The updated standards should include comprehensive photographic records for wild *Arachis* species, experimental hybrids, commercial cultivars, and botanical varieties of *A. hypogaea*. The availability of high-resolution photo-documentation of correctly identified living plants and herbarium specimens would be a boon to collection managers around the world, to help them resolve the many unidentified or misidentified materials that are currently maintained – unused – in their genebanks.

#### Cytological, molecular and genomic characterization standards

Remarkable progress has been made in the past three decades in the fields of cytology, molecular genetics and genomics, which has had a large impact on our understanding of the anatomy, phylogeny, evolution and inheritance of *Arachis* genetic diversity. Such information is key to germplasm users and genebank managers and, when available, needs to be documented using updated and standardized characterization methods. From a policy standpoint, the sharing of Digital Sequence Information on Genetic Resources (DSI) remains a controversial topic that is—for some countries—intrinsically intertwined with the ongoing discussions on access and benefit sharing (ABS) under the CBD (see section on International policy issues, below). Irrespective of the outcome of the current debate over access to DSI, the importance of documenting this information in a standardized format

remains essential to the efficient management and utilization of the germplasm, and should be promoted and implemented at the national level in any case.

#### Training capacity

Many of the institutions hosting the larger peanut collections are well positioned and equipped to provide the technical training and facilitate the transfer of expert knowledge, and this is already taken place in many instances. From the perspective of a Global Peanut Conservation Strategy, the training role of the larger genebanks will need to be revitalized and/or expanded to rectify the current shortage of trained technical staff at the smaller peanut collections, thereby elevating the smaller institutions' effectiveness and enhancing their capacity to participate in, contribute to, and benefit from the global system of peanut conservation and use.

As a rule, any existing legislative restrictions to international distribution of germplasm need in no way prejudice the possibility of providing training internships to scientists and technicians from foreign research institutions, and particularly in countries where wild *Arachis* species occur, which could include trainees' active participation in field expeditions to observe the behavior of the wild species in nature. In the past, international training collaborations like these have been a rewarding and formative experience for host country researchers, as well as for the trainees from other countries. Such international training collaborations and interactions should be encouraged and pursued, and now with added urgency due to the fact that many of the most knowledgeable and experienced *Arachis* specialists are ageing and, in many cases, without a clear chain of succession.

#### 5.2.5 Networking

Regular collaborations with other genebanks or participation in peanut-related networks were reported by relatively few of the surveyed genebanks, and many reported no collaborative partnerships or network activities whatsoever. Eight Regional Conservation Strategies for plant genetic resources were also consulted, i.e., The Americas; West and Central Africa; Eastern Africa; Southern Africa; West Asia and North Africa; Central Asia and the Caucasus; South, South-east and East Asia; and The Pacific. These regional crop conservation strategies were commissioned by the Crop Trust between 2005 and 2008, and can be downloaded from the [Crop Trust website](#).

Of the eight regional strategies, only two – Southern Africa, and the Americas – mention peanut in their reports. The Southern Africa Strategy scarcely mentions (in a table) that a total of 1,675 peanut accessions were maintained in the germplasm collections of

the 12 SADC member states. The Hemispheric Strategy for the Americas is the only report containing any substantive mention of peanut genetic resources, ranking it among the 20 most important crops in the region. The three sub-regional PGR networks in the Americas (i.e., REGENSUR, NORGEN and CAPGERNET) identified the national *Arachis* germplasm collections of Argentina, Bolivia, Brazil, Paraguay, Uruguay, USA, and the Caribbean nations, to be of highest importance from a regional perspective.

It is surprising to note that the remaining six regional strategies made no mention whatsoever of peanut (or groundnut), especially when one considers that the countries of South Asia, Southeast Asia and East Asia, together with those of Eastern Africa, produce over 80% of the world's peanut crop.

Overall, these results reflect the current dearth of regional or international peanut networks. Nevertheless, a few precedents do exist for collaborative activities and networks that could serve as models to emulate or build upon to foster more international collaboration, enable greater communication between peanut conservation and utilization communities, and facilitate the implementation of the Global Strategy for the Conservation of Peanut Diversity.

In the United States, the American Peanut Research and Education Society (APRES) has a large and active membership, and produces the refereed and indexed professional journal *Peanut Science*. APRES is supported largely by membership dues, and contributions from the peanut breeding, producing, processing, and marketing communities, including the American Peanut Council, The Peanut Foundation, and the National Peanut Board which have provided some limited support to germplasm management activities.

An active peanut research network that could be considered as a potential partner or model for the implementation of the Global Strategy for the Conservation of Peanut Diversity is the International Peanut Genome Initiative (IPGI). The IPGI has a widespread global membership and receives generous funding from a variety of sources. With support from the American Peanut Council, IPGI hosts the PeanutBase web portal. PeanutBase provides accession-level information on *Arachis* germplasm and is an effective mechanism for networking and sharing the results of genetic and genomic research, with the stated objective of enabling rapid crop improvement in peanut. The IPGI's Strategic Plan 2017–2021 (IPGI 2016) includes a number of strategic goals and milestones for the conservation and use of global *Arachis* genetic resources that coincide closely with the objectives of the present Global Strategy for the Conservation of Peanut Diversity.

### 5.2.6 International policy issues

The fact that the peanut (and its wild relatives) are not included on the list of crops in Annex 1 of the Multilateral System of the ITPGRFA represents a serious obstacle for the international exchange of peanut genetic resources, and constitutes a fundamental threat to the development and eventual implementation of a Global Strategy for the Conservation of Peanut Diversity. At present, the doors of a number of the largest peanut genebanks in the world are tightly closed to foreign access. This complicates the ability of those key institutions to participate in and support a conventional network of genebanks. Moreover, a number of countries in the crop's primary and secondary centers of diversity do not currently have the in-house capacity to conserve the full range of genetic diversity existing within their borders, either *ex situ* or *in situ*, and without international collaboration these unique peanut genetic resources are at serious risk of extinction. Mutually beneficial activities and incentives may be identified to strengthen the research and conservation capacity of those countries, and encourage their international collaboration on aspects unconnected to germplasm exchange, such as technical training, technology transfers, joint research activities and analyses, as has already been demonstrated by participants in the Peanut Genome Consortium.

Discussions are already underway between the Secretariat of the Convention on Biological Diversity (CBD) and national and international stakeholders regarding the use of Digital Sequence Information on Genetic Resources (DSI), and Access and Benefit Sharing (ABS) under the CBD (EU-China Workshop on ABS and DSI, 2020). The CBD Secretariat recognizes that open access to scientific data is a key component of scientific cooperation and the smooth functioning of science globally, and has important value to the implementation of the CBD's objectives. However, open access may restrict options to address benefit-sharing, and the challenge is to generate a different approach that maintains the efficiencies of the current model in delivering societal monetary and non-monetary benefits arising from activities within the current system while also responding to the calls for benefit-sharing in the context of the CBD. A lack of clarity on ABS regulations in both Provider and User countries hinders compliance by users with those regulations. An Ad-Hoc Technical Expert Group was formed to explore the issues and has generated its report.

Open access to DSI is a complex issue and large disagreements exist among the Parties. For example, the legal management of ABS in the EU is more focused on compliance with the CBD, while China puts more emphasis on access and benefit sharing requirements. The United States has indicated its strong opposition to placing any regulations or restrictions on DSI, but

it appears doubtful that many other CBD members would be willing to share their genetic and genomic research results on PeanutBase without some sort of monetary or non-monetary benefit. Developing a positive solution to the problems raised by DSI is an important part of the CBD's post-2020 Framework. Both China and the EU have expressed interest in setting up a process that will engage Parties and other stakeholders with different views to seek a solution acceptable for all. The *Arachis* research community should provide constructive inputs to this process, as international policy decisions on this topic will have a significant impact on the scope and effectiveness of any and all global *Arachis* networking initiatives.

### 5.3 Recommendations for priority action

The strategic challenges outlined above need to be addressed through priority actions designed to resolve or otherwise mitigate the existing constraints through targeted and prioritized activities leading to the development of a more rational, efficient, and mutually beneficial global system of peanut genetic resources conservation and use. The outstanding challenges and constraints that surfaced during the development of the Strategy form the basis for the recommendations provided here, to help orient and initiate the implementation process, and be expanded upon, fine-tuned, and pursued further by the stakeholders themselves.

#### 5.3.1 Priority Action 1 – Documentation standards and a common information platform

The current global system of peanut conservation and use is constrained by the lack of standardized, updated, and readily accessible information about existing genetic resources conserved *ex situ*. The development and adoption of updated documentation standards and protocols would greatly facilitate the exchange and use of standardized accession-level data, help identify inadvertently duplicated accessions, and bring to light unique accessions, many of which are maintained with extreme difficulty in their countries of origin, but not yet distributed. Disclosure of this information in a common database can raise the community's awareness of potential opportunities for exchange, collaboration, and conservation.

Documentation standards for *Arachis* germplasm need to be thoroughly updated or developed *de novo*, and their adoption should be widely promoted through training materials and events. The updated documentation standards should include new phenotypic, molecular, and genomic descriptors, standardized protocols for germplasm identification and characterization, as well as uniform guidelines for preparing and citing herbarium voucher specimens, and photo-documentation of *Arachis* accessions. The updated *Arachis* documentation standards should, in turn, facil-

itate and be conducive to the international adoption of a common, web-accessible information platform (or platforms).

The establishment of an updated, online, global catalog of peanut germplasm is a prerequisite to an effective global system of *Arachis* conservation and use. Hence, it is essential that the global peanut conservation and use community arrive at a consensus to adopt a suitable platform (or platforms) through which they share their accession-level data and other information.

The three most viable and currently available options that could satisfy the international peanut conservation community's need for a common data platform are Genesys, GRIN-Global, and PeanutBase. The Genesys and GRIN-Global platforms, while distinct in some respects, are also highly inter-compatible. In fact, some national genebanks that use GRIN-Global software to manage their internal accession-level information, can also make their data externally available on Genesys without entailing any additional effort. The PeanutBase platform is also designed to share accession-level information among a community of users, but is more focused on the documentation of data generated by genetic and genomic studies, which are becoming increasingly valuable for the management and use of *Arachis* germplasm. So, after carefully evaluating these options, it is conceivable that the global peanut conservation and use community may opt for a combination of inter-compatible platforms to satisfy the documentation requirements of a common global system.

To initiate the process of developing updated characterization and documentation standards, a few *ad hoc* committees of relevant experts could be formed to make recommendations on:

- standard protocols for molecular and genomic characterization of *Arachis* accessions, including the manner in which these data should be recorded
- updated descriptor lists for phenotypic and agro-morphological characterization, for *Arachis hypogaea* as well as for wild *Arachis* species, including the format in which these data should be recorded
- guidelines for assigning or obtaining correct taxonomic determinations for unidentified germplasm accessions
- guidelines for assigning or obtaining appropriate geographic coordinates for germplasm accessions lacking such information
- guidelines for making standardized high-quality photo-documentation of germplasm accessions and herbarium voucher specimens, including the manner in which these images should be composed, labeled, and stored

To expedite the global adoption of a common documentation platform (or platforms) for sharing accession-level information, an *ad hoc* group of relevant experts should be formed to:

- evaluate the pros and cons of the available database options in the context of a global system
- determine whether any of the existing options is suitable for direct adoption as a platform by the global peanut community
- evaluate the inter-connectivity and/or inter-compatibility of the available options, and the possibility that more than one database could readily contribute to a single global platform for the global peanut community
- canvas key genebank managers and other stakeholders in the global peanut conservation community to assess their individual documentation needs and preferences, and any concerns or pre-conceptions that might affect their willingness to participate in the global information platform, to aid the committee in their recommendation
- make their recommendation on the best way to arrive at an information platform that will address and satisfy the existing needs and facilitate the development and effectiveness of a global system of peanut genetic resources conservation and use

Additionally, as responsible and active members of the global genetic resources community, *Arachis* genebank managers should be encouraged to provide periodically updated accession information to the WIEWS database, as information from this database is widely used by international policy and decision makers to define global priorities and assign resources.

### 5.3.2 Priority Action 2 – Regenerating, characterizing and evaluating “unknown” accessions

To enhance the overall worth and utility of the collections, it is necessary to address the many genebank accessions that lie unused for various reasons, particularly the large number of accessions reported as lacking basic passport information, taxonomic identification, phenotypic or molecular characterization, and/or are in urgent need of regeneration and multiplication. The immediate benefits of addressing these deficiencies in accession-level documentation include:

- genebank database is current, allowing a more comprehensive analysis and more efficient use of the entire collection (e.g., development of a core collection)
- viability of the regenerated accessions is high, with seed quantities sufficient for distribution and study
- detailed information available on the accessions’ individual characteristics and traits for breeding and direct use

- identification of potentially unique or intrinsically valuable accessions
- detection of remaining taxonomic gaps
- detection of superfluous duplicates

As the retrieval or generation of this sort of information can involve considerable expense, sources of additional funding – either internal or external – will probably be required. Given the widespread need to undertake this important work, the capture of external funding for national genebanks may be more successful if pursued collectively in the context of a regional or even global project to fully document, revitalize, and mobilize the “hidden” genetic diversity contained in national peanut collections. For example, a recent global project on crop wild relatives provided strong technical and financial support to numerous national programs for similar kinds of research, and served as an incentive to their participation in an international effort aimed at achieving a shared conservation goal.

Among the ways that could be pursued to promote and support the taxonomic identification, regeneration and characterization of “unknown” *Arachis* accessions in genebanks, the IAG and individual genebanks may consider the following courses of action:

- promote a round of expert taxonomic identification of wild species and cultivated landrace accessions which, in many cases, can be verified through the revision of original passport data and/or information contained in institutional records of germplasm exchange, quarantine, regeneration, or characterization processes.
- coordinate the taxonomic identification, phenotypic and molecular characterization, georeferencing, and photo-documentation of the regenerated accessions with the application of the updated documentation standards and protocols (Priority Action 1) and their associated training events and activities (Priority Action 5)
- invite genebanks with similar or complementary interests in addressing this issue to pool their collective expertise and resources to carry out the needed work together
- engage graduate students willing to assume specific aspects of this work (e.g., conduct seed regeneration and characterization, develop a core collection, etc.) as the basis of their dissertation research
- prepare a proposal for a regional or global initiative to document and mobilize the “hidden” genetic diversity contained in national peanut collections, for submission to the Crop Trust
- prepare national and/or regional proposals to address the outstanding accession-level data needs, for submission to the Plant Treaty’s Benefit Sharing Fund

### 5.3.3 Priority Action 3 – Filling existing taxonomic, genetic and ecogeographic gaps in collections

Important gaps in the existing collections need to be identified and filled to enhance the overall comprehensiveness and collective utility of the collections. Once gaps are identified in accordance with the particular goals and purposes of the individual genebanks, targeted actions to fill those gaps need to be taken, either through transfer of material from other genebanks, or through collecting missions. For gaps that exist at the global level (i.e., material that is absent or severely underrepresented in *ex situ* collections everywhere), an urgent priority should be given to collect germplasm of those taxa to ensure their *ex situ* conservation.

Resources should be sought to sponsor targeted international collecting missions for cultivated landraces and wild *Arachis* species, in close collaboration with national scientists and authorities of the host country. The international collecting missions should be designed with a dual purpose: i.) fill the identified germplasm gaps, and ii.) help strengthen the host countries' capacity to conserve, study and use those materials at the national level. These international collecting activities deserve urgent attention, not only to secure the conservation of unique sources of diversity, but also to enable the direct transfer of expert knowledge through the participation of senior *Arachis* germplasm collectors, many of whom are aging. Upcoming collecting missions should always be combined with training activities for national personnel who will be carrying on this vital collecting work in the future (Priority Action 5).

Priority areas for germplasm collecting identified in this strategy are:

- Wild *Arachis* species with less than 10 populations currently represented in genebanks (see Table 2.2, Figure 3.1)
- Landraces from northern South America and Amazonia (Colombia, Venezuela, Guyana, Suriname, French Guiana, and Brazil)
- Wild *Arachis* species that may exist in geographical areas not previously explored by peanut germplasm collectors.
- Landraces from Central American and Caribbean countries (Belize, Honduras, El Salvador, Nicaragua, Panama, Haiti, the Dominican Republic, and Trinidad and Tobago)
- Landraces from Benin, Sierra Leone, Rwanda, Burundi, and Madagascar, among others
- Landraces from Pakistan, Nepal, Bangladesh, Sri Lanka, Myanmar, Vietnam, Thailand, Malaysia, Philippines, and Oceania

Partners with relevant expertise that, together with the corresponding national partners, could help coordinate peanut germplasm collecting (and training) activities include:

#### Americas

- IBONE (Argentina)
- INTA (Argentina)
- EMBRAPA-CENARGEN (Brazil)
- USDA-ARS (United States)
- TAMU-AgrLife Research (United States)

#### Africa

- ICRISAT (Zimbabwe)
- ICRISAT (Niger)
- ISRA Senegalese Institute of Agricultural Research (Senegal)
- SADC-SPGRC Southern African Development Community, Plant Genetic Resources Centre (Zambia)

#### Asia/Pacific

- ICRISAT (India)
- SPC-PAPGREN Secretariat of the Pacific Community, Pacific Plant Genetic Resources Network (Fiji)

### 5.3.4 Priority Action 4 – Ensuring security-duplication of unique accessions and collections

**4.a)** All unique accessions or collections currently without security back-ups need to be identified, prioritized, and targeted for security duplication.

Based on the data collected for this strategy, CHN003, BGR001, SEN002 and ARG1133 have the largest number of accessions with no safety duplicates and should be prioritized for safety duplication. Furthermore, other genebanks, that did not respond to our survey and hold significant collections that may not be safety duplicated, can be identified through further polling and personal contact with the genebank managers.

**4.b)** Identify suitable host institutions and negotiate appropriate storage agreements for depositing security-duplicates of all unique *Arachis* accessions and collections at partner locations within the current system of active genebanks where long-term, black-box conservation services can be provided. The host genebank need not necessarily have their own peanut collection, as long as they can provide the necessary space and the basic conditions of temperature and humidity required for long-term conservation of peanut germplasm. Where a suitable host institution can be identified, it would be most efficient to adopt a regional approach, with one major genebank acting as a security back-up repository for national collections in the region, as is the case with the SADC Plant Genetic Resources Centre (SPGRC), in Zambia. If a regional back-up solution is not possible, bilateral

agreements for security storage services should be made between genebanks in neighboring countries, or even within a country. These bilateral security storage agreements between genebanks can also be reciprocal—for mutual benefit and reduced costs.

For the long-term objectives of the Global Strategy for the Conservation of Peanut Diversity, additional samples of all unique materials (i.e., security-triplicate samples) should also be deposited in the Svalbard Global Seed Vault (SGSV). To this end, it makes sense to consult the list of current *Arachis* accessions stored at SGSV, freely accessible on the [SGSV web portal](#), when planning to deposit new accessions, to avoid deposit of redundant duplicates, and to help target unique materials that remain unrepresented at Svalbard.

### 5.3.5 Priority Action 5 – Training for peanut curators and technicians in developing countries

To address the shortage of skilled technical staff and the generational turnover of *Arachis* specialists, training events at key national and international centers of excellence should be organized for young professionals in priority topics such as *Arachis* taxonomy, peanut germplasm collecting methods, and germplasm characterization, evaluation and conservation methods and protocols. Such *Arachis*-specific training is critically important—particularly for strengthening genebanks with peanut collections in developing countries—to enhance their effectiveness and capacity to participate in and benefit from a global system of peanut conservation and use.

A global training strategy and plan should be developed to address this urgent need. One of the purposes of a global training plan is to make sure that relevant training activities are organized and implemented in conjunction with the abovementioned Priority Actions on: documentation standards (Priority Action 1), germplasm regeneration and characterization (Priority Action 2), and gap filling/collecting (Priority Action 3), where the training needs are most acute.

As soon as possible (when, post-COVID, international travel is once again safe), two regional training workshops should be organized (one in Latin America and another in Africa and/or Asia) on the topics of wild and cultivated peanut taxonomy, genomics, and conservation methods. These training workshops should be conducted by leading experts in these subjects, and aimed at younger and mid-career professionals working at national genebanks in developing countries with *Arachis* collections. Key partners for organizing these regional workshops include those listed above for collecting activities in Priority Action 3, among others.

### 5.3.6 Priority Action 6 – Initiating constructive international policy dialogue on peanut ABS

A constructive dialogue should be initiated by the global peanut scientific community with the ITPGRFA Secretariat to better understand the causes behind the exclusion of peanut from Annex 1 of the Plant Treaty's Multilateral System (MLS) of access and benefit sharing (ABS), and to discuss available options to help resolve this international policy deadlock. The ultimate objective of this Priority Action is to promote and facilitate the addition of peanut and its wild relatives (*Arachis* spp.) to the Plant Treaty's list of Annex 1 crops.

The global peanut community should offer its collaboration with the Treaty Secretariat—such as providing specific examples of the harmful consequences of the current policy, and illustrations of missed or unrealized benefits and opportunities—that could help inform, educate, and encourage the pertinent authorities of relevant national governments to reconsider their reservations on including peanut along with the other major crops in Annex 1. In return, the Treaty Secretariat may be able, through the MLS benefit-sharing mechanism, to offer valuable non-monetary benefits such as expert training, facilities, research support, and capacity-building activities to strengthen those countries' own *in situ* and *ex situ* peanut genetic resources conservation and management efforts.

It is a matter of some urgency that the current ABS policy impasse be sorted out, not only because it is an obstacle for international exchange and use of peanut germplasm, but it also directly threatens the long-term survival – both *ex situ* and *in situ* – of unique and endangered genetic resources of a major world crop. It should be emphasized that if the current restrictions had existed in the past, there wouldn't be any global collections of peanut germplasm conserved in genebanks around the world, as there are now. The availability of a broad array of *Arachis* genetic resources will be needed to underpin the significant increase in peanut production and consumption that is projected to occur in developing countries in the coming decades, and therefore has a direct impact upon global food security. As such, the success of this activity constitutes a basic requirement for the implementation of the Global Strategy for the Conservation of Peanut Diversity and the establishment of an effective global system for peanut conservation and use.

The International Advisory Group, in *bona fide* representation of peanut researchers, breeders and conservationists worldwide, working in concert with the Plant Treaty Secretariat and relevant national governments, should assume a proactive role in providing comprehensive scientific information about threatened peanut genetic resources in support of a dip-

lomatic solution to this unfortunate and deleterious policy stalemate.

### 5.3.7 Priority Action 7 – Integrating complementary *ex situ* and *in situ* conservation approaches

Peanut collection managers should be encouraged and supported – whenever possible and wherever appropriate – to incorporate complementary *in situ* conservation activities as part of an integrated conservation strategy for peanut genetic diversity. These *in situ* conservation approaches, which may include on-farm management of traditional landraces, should be initiated, promoted and overseen by the genebanks, and be directly linked to and complementary with the *ex situ* conservation of those same materials in the genebank. One important role that genebanks play in this regard is the *ex situ* conservation, characterization, and eventual rematriation (restoration) of those materials to native or traditional farming communities should they become lost on-farm. A similar integrated approach can be applied to wild species in terms of the discovery and/or restoration of natural *Arachis* populations *in situ* through productive interaction between genebank staff and managers of natural conservation areas. Such an approach would facilitate prospective searches in protected areas by trained *Arachis* collectors, which could improve the present knowledge of the species' distribution in natural conservation units.

Ample scientific literature is available describing the rationale, methods, and case studies that illustrate the effectiveness, mutual advantages, and ecosystem and social services that can be derived from an integrated *in situ-ex situ* approach to genetic resources conservation. (See the following section on Priority Actions for *In Situ* Conservation of *Arachis* Genetic Diversity.)

## 5.4 Priority actions for *In Situ* conservation of *Arachis* genetic diversity

As mentioned above and in Section 4, the *in situ* conservation of wild *Arachis* species and the on-farm management of traditional peanut landraces are regarded as **complementary to *ex situ* conservation methods**.

To take full advantage of this complementarity, the development of linkages between the two approaches – and their eventual incorporation into an integrated *ex situ-in situ* conservation strategy – is to be encouraged and pursued as the most effective means for ensuring the long-term preservation and use of the widest possible range of peanut genetic diversity. The following five priority actions were determined based on the assessment of the major constraints and obstacles identified by the survey respondents for the *in situ* conservation of peanut genetic diversity:

### 5.4.1 *In Situ* Priority Action 1: Inventory of peanut landraces and associated knowledge

One of the main threats to traditional landraces of peanut is their replacement by improved varieties. There is a dearth of information on the varietal diversity of peanuts and only a few studies have reported on the diversity of peanut landraces in selected countries and regions (Williams 1989, 1991, 1992; Freitas et al. 2007; Krapovickas et al. 2009, 2013, 2021; Banla et al. 2018; Daudi et al. 2018; Loko et al. 2020). Thus, systematic country-wide surveys of landraces are required to comprehensively describe, document and monitor their existence, *in situ* conservation status, and associated traditional knowledge. Once the occurrence, distribution, cultural contexts and conservation status of peanut landraces are inventoried at the country level, priority areas of landrace diversity can be identified and appropriate activities implemented. Appropriate *in situ* actions include, for example, education modules for the promotion and preservation of biocultural patterns and practices associated with the continued maintenance and use of the targeted landraces. At the same time, representative germplasm samples of each landrace should be deposited into the national peanut collections for long-term *ex situ* conservation, and serve as a deliberate security back-up for local farmers should they inadvertently lose their seed of a traditional variety.

In most cases, this work should be led by the genebank manager or genetic resources leader of the national agricultural research institute, in close coordination with local farmer organizations, indigenous groups, rural development NGOs, and national universities, as appropriate. The recommended methodology for identifying, describing and cataloging peanut landraces is explained by Krapovickas et al. (2009).

### 5.4.2 *In Situ* Priority Action 2: Capacity building on *in situ* conservation methods

The online survey responses and FAO country reports indicated a general lack of research interest for peanut genetic resources, and this may be due to the limited human and financial resources available for work in this area. Because traditional landraces are often poorly known and typically overlooked by breeding programs, and as there is little experience in promoting their conservation on-farm, it is not surprising that the capacity to address these aspects is lacking in most countries. Capacity building activities are closely associated with, and complementary to, public awareness raising activities, described below (*In Situ* Priority Action 5).

Our assessment also suggests that few species of wild *Arachis* are found within protected areas, although this information is liable to be biased as it relies mostly on floristic surveys that rarely yield reliable results concerning the cryptic *Arachis* species. Where wild *Arachis* populations do occur in protected areas, the awareness of their existence and importance should be brought to the attention of the managers of those areas so that they are included in the corresponding management plans. For populations occurring outside protected areas, awareness of landowners where wild species are found must be raised, together with that of the local communities and conservation organizations. Similarly, the capacity of national universities and environment offices needs to be developed so they can, for example, offer their own courses on *in situ* conservation and conduct research projects at the postgraduate level.

Strengthening the capacity of national partners on *in situ* conservation methods can begin with the preparation and distribution of relevant information materials and training courses, targeting the various kinds of stakeholders including: researchers, university students, landowners, conservation professionals, policy makers, community leaders, farmers, and rural development workers. A detailed training guide for *in situ* conservation of agricultural biodiversity on-farm was prepared by Jarvis et al. (2000). To some extent, standard capacity-building information tools and courses can be either applied directly or otherwise adapted for use in multiple countries. In the case of Latin America—the peanut’s primary region of diversity—practically all of the countries have either Spanish or Portuguese as their national language, which greatly facilitates the sharing or easy adaptation of training materials from one country to the next. Similarly, regionally organized training courses can take advantage of shared languages and historical, cultural and ecogeographic characteristics to broaden the scope and impact of capacity-building efforts.

Abundant additional training materials and courses on *in situ* conservation of agricultural biodiversity—some in multiple languages—are available for downloading at [Bioversity International’s Crop Wild Relatives Global Portal](#), as well as on [Bioversity International’s Training Materials webpage](#).

#### **5.4.3 *In Situ* Priority Action 3: *In situ* conservation of wild *Arachis* diversity**

Considering that only a very small number of observations of the wild *Arachis* species are located within existing protected area systems, it has become necessary to devise *ad hoc* approaches that afford sufficient protection to the wild *Arachis* populations in farmlands, rangelands, as well as in other private or otherwise unprotected natural areas in their countries

of origin. Concrete examples of *in situ* conservation activities focused on wild *Arachis* species are mostly anecdotal and undocumented. It is clear that more deliberate and extensive actions ensuring the *in situ* conservation of wild *Arachis* populations need to be urgently developed and implemented by the corresponding national partners and authorities, on a country-by-country basis. This priority action is closely associated with, and largely dependent upon, the enabling policies addressed, below, in *In Situ* Priority Action 5.

Wherever possible, key hotspot areas defined by *in situ* conservation planning exercises (e.g., Jarvis et al. 2002, 2003; Ferguson et al. 2005) should be designated as special reserves areas for peanut genetic resources. However, major changes in land use, additional collecting efforts, newly described species, and the advances in GIS-based technologies and georeferenced datasets that have occurred in the two decades since the aforementioned studies were conducted, imply that those ecogeographic studies will need to be updated to accurately reflect the current *in situ* conservation status of wild *Arachis* in South America. In areas where existing populations of wild *Arachis* are threatened or in imminent danger of becoming lost, it may become necessary to establish new *in situ* populations of those species, using either seed or vegetative propagules obtained directly from nearby populations, or germplasm accessions from earlier collecting missions conserved *ex situ*. The new populations should be established in nearby protected areas or other areas with similar habitats but where they will be less threatened and can continue to self-propagate and evolve as a population under relatively natural conditions. Certainly, the most pervasive threat to wild *Arachis* populations is the expansion of large-scale, mechanized agriculture, including the establishment of cultivated pastures and the associated use of herbicides in their areas of natural occurrence.

#### **5.4.4 *In Situ* Priority Action 4: Impact assessment**

Land-use changes including agricultural expansion, deforestation, urbanization, road and pipeline infrastructures, and the establishment of hydroelectric dams are among the greatest threats to many wild *Arachis* species. In this context, a priority would be to help ensure that any future or ongoing development activities should be subjected to an environmental impact assessment that takes account of potential threats to biodiversity in general, and to the wild populations of *Arachis* in particular. While it can be expected that any appeals for environmental impact assessments will likely encounter intense opposition from developers, politicians, and even local communities, it is important to make evident the impending risk of destroying irreplaceable crop genetic resources,



and see that this aspect is included along with the other social and environmental impacts that will be enumerated by conservation groups already engaged in informing decision makers and the general public regarding the impact of the proposed or ongoing development activities. To this end, the updated eco-geographic studies recommended above (*In Situ* Priority Action 3) can serve as tangible scientific evidence to support the inclusion of wild *Arachis* populations when conducting impact assessments of development projects planned in areas where these species are known to occur.

#### 5.4.5 *In Situ* Priority Action 5: Public awareness and enabling policies

This cross-cutting recommendation applies to the previous Priority Actions for both *in situ* and *ex situ* conservation approaches. The aforementioned scarcities of information, capacity and support for *in situ* conservation of wild species, on-farm management of landraces, and *ex situ* maintenance of peanut genetic diversity in general, is often due to insufficient understanding of the importance of conserving these resources by different stakeholder groups, including policy makers, managers of protected areas, farmers, traders, local communities and local authorities. There is a particular need of strong advocacy to policy makers for creating an enabling environment for the implementation of conservation activities aimed at peanut genetic resources. Developing information, education and communication tools appropriate for each stakeholder group is strongly recommended to enhance their awareness and stimulate their engagement in the conservation and utilization of peanut genetic diversity. This work is closely related to the capacity building activities discussed, above, in the *In Situ* Priority Action 2.

### 5.5 The way forward

The next step in implementing this global strategy will be the establishment of a global coordination committee with the participation of some of the key institutions and individuals who contributed to the strategy's development. It is recommended that this committee be formed—at least initially—by the International Advisory Group, in provisional representation of the entire global community of stakeholders for whom this strategy is intended to serve.

The original International Advisory Group (IAG) should be mobilized to promote the adoption and initiate the implementation of the Global Peanut Conservation Strategy. The members of this select group of *Arachis* experts (see Annex 1) have been engaged in the development of this strategic undertaking since its inception in 2020, and have contributed to the compilation of the present document. As managers and curators

of many of the most important germplasm collections in the world, the IAG members are already *de facto* leaders and key stakeholders in the present and future global system of *Arachis* genetic diversity conservation and use. As the initiating body for the implementation of the Global Peanut Conservation Strategy, the IAG should assume leadership of the Strategy's operation, and expand its membership to encompass key stakeholders from other geographic regions and sectors.

A series of virtual consultation meetings should be organized within the next few months to initiate the mobilization of the IAG. These virtual consultations should focus on building consensus on the top priority actions, develop an implementation plan with estimated costs, and identify who will be involved. The Crop Trust could facilitate the initial virtual consultations, which could be held regionally to deal with differences in time zones and languages.

Recommended agenda items for the virtual consultation meetings include:

- Selection of an interim chairperson, define a set of general objectives and responsibilities, and adopt some broad operational guidelines for the 'new' IAG.
- Nominations for a small number of expert stakeholders ( $n \leq 6$ ) to be formally invited to join the IAG for the purpose of strengthening the Group's geographic, institutional and scientific representation.
- Discussion on the key issues, opportunities and recommendations for priority action that emerged during the development of this Strategy, and any other topics or concerns pertinent to the Group.
- Calendar of upcoming IAG meetings and other related events (virtual and otherwise).
- Organization of a global, in-person meeting of the IAG—to be held within the next 12 months—that will include the expanded membership and other key stakeholders. This global meeting will serve to inaugurate the implementation of the global strategy, and provide the expanded IAG with an opportunity for direct personal interaction and a space to discuss, debate and define in greater detail the priority actions of the strategic plan, and define the roles, responsibilities and commitments that the IAG and its partners will assume. Participants in this meeting should also include managers of the 27 genebanks that participated in the strategy development, as well as other important peanut collections that did not respond to the survey. The global meeting could also include a one- or two-day regional training workshop for peanut genebank professionals, according to the location of the meeting venue and perceived training needs.

### 5.5.1 Lead institutions

The following is a list of institutions with the capacity to assume leadership roles in various aspects of the implementation and governance of the Global Peanut Conservation Strategy:

#### The Americas

- EMBRAPA – Empresa Brasileira de Pesquisa Agropecuária
- IBONE – Instituto de Botânica del Nordeste
- INTA – Instituto Nacional de Tecnología Agropecuaria
- CIAT – Centro Internacional de Agricultura Tropical
- USDA – United States Department of Agriculture
- NCSU – North Carolina State University
- UGA – University of Georgia
- TAMU – Texas A&M University, Texas AgriLife Research

#### Asia/Pacific

- ICRISAT – International Crop Research Institute for the Semi-Arid Tropics
- OCRI-CAAS – Oil Crops Research Institute, Chinese Academy of Agricultural Sciences
- SPC-PAPGREN – Secretariat of the Pacific Community, Pacific Plant Genetic Resources Network
- SARDI-APG – South Australian Research and Development Institute, Australian Pastures Genebank

#### Africa

- ICRISAT – International Crop Research Institute for the Semi-Arid Tropics
- CORAF – West and Central Africa Council for Agricultural Research and Development
- SADC-SPGRC – Southern African Development Community, Plant Genetic Resources Centre

#### Global

- CGIAR – Research Program on Grain Legumes and Dryland Cereals
- IPGI – International Peanut Genome Initiative

### 5.5.2 Potential donors

The following is a provisional list of donors that may be considered for funding various aspects and activities of the Global Peanut Conservation Strategy:

- ITPGRFA Secretariat – Benefit Sharing Fund
- CGIAR Research Program on Grain Legumes and Dryland Cereals
- USDA-ARS National Plant Germplasm System – Plant Exploration Grants
- The Global Crop Diversity Trust
- National Geographic Society – Exploration Grants Program
- Bill & Melinda Gates Foundation
- McKnight Foundation – Collaborative Crop Research Program, Cross-Cutting Theme: Agrobiodiversity
- MacArthur Foundation
- Gordon and Betty Moore Foundation
- National Academies of Science, National Agricultural Research Institutes, Universities

### 5.5.3 Conditions for success for the Global Peanut Conservation Strategy

The following conditions are among those that may be considered essential for the successful implementation of the Global Peanut Conservation Strategy:

- Lead institutions are willing and able to assume the management and governance of the Global Peanut Conservation Strategy's implementation, including the promotion of its research goals and achievements to stakeholders and the general public.
- Key institutions and stakeholders are aware of the Strategy, and are committed to contributing to—and perceiving the benefits of—a more rational and effective global system of peanut genetic resources conservation and use.
- Sources of funding are identified and engaged in supporting the implementation of the Strategy's priority actions.
- The ITPGRFA Secretariat provides guidance and facilitation of constructive policy dialogue and negotiations that will lead to an eventual endorsement from the Plant Treaty's Governing Body in support of positive changes in the Multilateral System—such as including *Arachis* spp. on the list of Annex 1 crops—that will enable greater international access, conservation, and use of peanut genetic resources, and the equitable sharing of the benefits thereby derived.

# 6 REFERENCES

- Alagirisamy, M. 2016. Groundnuts. Chapter 5, pages 89–134 *In: Gupta S.K. (Ed.), Breeding Oilseed Crops for Sustainable Production: Opportunities and Constraints.*
- Alva, W., and C.B. Donnan. 1993. Royal Tombs of Sipan. Fowler Museum of Cultural History, University of California, Los Angeles.
- Angelici, C.M.L.C.D., A.A. Hoshino, P.M. Nobile, D.A. Palmieri, J.F.M. Valls, M.A. Gimenes, and C.R. Lopes. 2008. Genetic diversity in section *Rhizomatosae* of the genus *Arachis* (Fabaceae) based on microsatellite markers. *Genetics and Molecular Biology* 31(1): 79–88.
- Arachis* in Flora do Brasil 2020 (em construção). Jardim Botânico do Rio de Janeiro. Available online. Accessed 17 Feb. 2021
- Azêvedo, H.S.F.S.; A.C.B. Sousa, K. Martins, J.C. Oliveira, R.B.T. Yomura, L.M. Silva, J.F.M. Valls, G.M.L. Assis, and T. Campos. 2016. Genetic diversity of the forage peanut in the Jequitinhonha, São Francisco, and Paranã River valleys of Brazil. *Genetics and Molecular Research* 15 (3): gmr.15038601.
- Banla, E.M., D.K. Dzidzienyo, I.E. Beatrice, S.K. Offei, P. Tongoona, and H. Desmae. 2018. Groundnut production constraints and farmers' trait preferences: a pre-breeding study in Togo. *Journal of Ethnobiology and Ethnomedicine* 14: 75.
- Badami, V.K. 1936. *Arachis hypogaea* Linn. Groundnut or peanut—Original habitat and its distribution in the world. *Journal of Mysore Agriculture Experiment Union* 15(4): 141–154.
- Barkley, N.A., R.E. Dean, R.N. Pittman, M.L. Wang, C.C. Holbrook, and G.A. Pederson. 2007. Genetic diversity of cultivated and wild-type peanuts evaluated with M13-tailed SSR markers and sequencing. *Genet. Res., Cambridge*. 89: 93–106. doi:10.1017/S0016672307008695
- Barkley, N.A., H.D. Upadhyaya, B. Liao, and C.C. Holbrook. 2016. Global resources of genetic diversity in peanut. Chapter 2, pages 67–109 *In: Stalker, H.T., and R.F. Wilson (Eds.), Peanuts: Genetics, Processing, and Utilization.* Academic Press and AOCS Press. ISBN: 9781630670382
- Bentham, G. 1841. On the structure and affinities of *Arachis* and *Voandzeia*. *Trans. Linn. Soc. London* 18(2): 155–162.
- Bentham, G. 1859. *Leguminosae*. *In: C. Martius, Flora Brasiliensis* 15(1): 86–87.
- Bertioli, D.J., G. Seijo, F.O. Freitas, J.F.M Valls, S.C.M. Leal-Bertioli, and M.C. Moretzsohn. 2011. An overview of peanut and its wild relatives. *Plant Genetic Resources: Characterization and Utilization* 9(1): 134–149.
- Bertioli, D.J., S.C. Leal-Bertioli, and H.T. Stalker. 2016. The peanut genome: the history of the consortium and structure of the genome of cultivated peanut and its diploid ancestors. Chapter 5, pages 147–161 *In: Stalker, H.T. and R.F. Wilson (eds.), Peanuts: Genetics, Processing and Utilization.* Academic Press and AOCS Press. ISBN: 9781630670382.
- Bertioli, D.J., S.B. Cannon, L. Froenicke, G. Huang, ... S.A. Jackson, R. Michelmore and P. Ozias-Akins. 2016. The genome sequences of *Arachis duranensis* and *Arachis ipaënsis*, the diploid ancestors of cultivated peanut. *Nature Genetics*, 22 Feb. 2016.
- Bertioli, D.J., J. Jenkins, J. Clevenger, O. Dudchenko, D. Gao, J.G. Seijo, ..... B.E. Scheffler, J. Grimwood, P. Ozias-Akins, S.B. Cannon, S.A. Jackson, and J. Schmutz. 2019. The genome sequence of segmental allotetraploid peanut *Arachis hypogaea*. *Nature Genetics* 51: 877–884.
- Bertioli, D.J., B. Abernathy, J.G. Seijo, J. Clevenger, and S.B. Cannon. 2020. Evaluating two different models of peanut's origin. *Nature Genetics* 52: 557–559.
- Bertioli, D.J., D. Gao, C. Ballen-Taborda, Y. Chu, P. Ozias-Akins, S.A. Jackson. C.C. Holbrook, and S.C.M. Leal-Bertioli. 2021. Registration of GA-BatSten1 and GA-MagSten1, two induced allotetraploids derived from peanut wild relatives with superior resistance to leaf spots, rust, and root-knot nematode. *Journal of Plant Registrations* 15: 372–378. DOI: 10.1002/plr2.20133
- Bertioli, D.J., J. Clevenger, I.J. Godoye, H.T. Stalker, S. Wood, J.F. Santos, C. Ballén-Taborda, B. Abernathy, V. Azevedo, J. Campbell, C. Chavarro, Y. Chu, A.D. Farmer, D. Fonceka, D. Gaon, J. Grimwood, N. Halpin, W. Korani, M.D. Michelotto, P. Ozias-Akins, J. Vaughn, R. Youngblood, M.C. Moretzsohn, G.C. Wright, S.A. Jackson, S.B. Cannon, B.E. Scheffler, and S.C.M. Leal-Bertioli. 2021. Legacy genetics of *Arachis cardenasii* in the peanut crop shows the profound benefits of international seed exchange. *Proceedings of the National Academy of Sciences*, September 2021. Vol. 18(38) DOI: 10.1073/pnas.2104899118
- Bonavia, D. 1982. Prececerámico Peruano. Los Gavilanes. Mar, Desierto y Oasis en La Historia del Hombre. Corporación Financiera de Desarrollo and Instituto Arqueológico Alemán.

- Branch, W.D., D.E. Williams, and E.J. Williams. 1997. Inheritance of black-pod color in peanut. *Journal of Heredity* 88(2): 156–158.
- Bressano M., A.N. Massa, R.S. Arias, F. de Blas, C. Oddino, P.C. Faustinelli, S. Soave, J.H. Soave, A.P. Maria, V.S. Sobolev, M.C. Lamb, M. Balzarini, M.I. Buteler, and J.G. Seijo. 2019. Introgression of peanut smut resistance from landraces to elite peanut cultivars (*Arachis hypogaea* L.). PLoS ONE 14(2): e0211920.
- Burow, M.D., C.E. Simpson, J.L. Starr, and A.H. Paterson. 2001. Transmission genetics of chromatin from a synthetic amphidiploid to cultivated peanut (*Arachis hypogaea* L.): Broadening the gene pool of a monophyletic polyploid species. *Genetics* 159: 823–837.
- Burow, M.D., M.G. Selvaraj, H. Upadhyaya, P. Ozias-Akins, B. Guo, D.J. Bertioli, S.C.M. Leal-Bertioli, M.C. Moretzsohn, and P.M. Guimarães. 2008. Genomics of peanut, a major source of oil and protein. Chap. 17 *In*: P.H. Moore and R. Ming (eds.), *Genomics of Tropical Crop Plants*, pp. 421–440. Springer.
- Burow M.D., C.E. Simpson, W. Faries, J.L. Starr, and A.H. Paterson. 2009. Molecular biogeography study of recently described B- and A-genome *Arachis* species, also providing new insights into the origins of cultivated peanut. *Genome* 52: 107–119.
- CGIAR Genebank Platform. 2020. Global assessment of landrace collection gaps and coverage for all CGIAR mandate crops. CGIAR Genebank Platform. Global Crop Diversity Trust, Bonn, Germany.
- Chu, Y., H.T. Stalker, K. Marasigan, C.M. Levinson, D. Gao, D.J. Bertioli, S.C.M. Leal-Bertioli, C.C. Holbrook, S.A. Jackson, and P. Ozias-Akins. 2021. Registration of three peanut allotetraploid interspecific hybrids resistant to late leaf spot disease and tomato spotted wilt. *Journal of Plant Registrations* 2021: 1–11.
- Custodio, A., J.G. Seijo, and J.F.M. Valls. 2013. Characterization of Brazilian accessions of wild *Arachis* species of section *Arachis* (Fabaceae) using heterochromatin detection and fluorescence *in situ* hybridization (FISH). *Genetics and Molecular Biology* 36: 364–370.
- Dash, S., E.K.S. Cannon, S.R. Kalberer, A.D. Farmer and S.B. Cannon. 2020. PeanutBase. Accessed 02 November 2020.
- Daudi, H., H. Shimelis, M. Laing, P. Okori, and O. Mponda. 2018. Groundnut production constraints, farming systems, and farmer-preferred traits in Tanzania. *Journal of Crop Improvement* 32(6): 812–828.
- de Blas, F.J., M. Bressano, I. Teich, M.G. Balzarini, R.S. Arias, M.M. Manifesto, B.P. Costero, C. Oddino, S.J. Soave, J.A. Soave, M.I. Buteler, A.N. Massa, and J.G. Seijo. 2019. Identification of smut resistance in wild *Arachis* species and its introgression into peanut elite lines. *Crop Science* 59(4): 1657–1665.
- Dillehay, T.D., J. Rossen, T.C. Andres, and D.E. Williams. 2007. Pre-ceramic adoption of peanut, squash, and cotton in northern Peru. *Science* 316: 1890–1893.
- Dubard, M. 1905. Une étude sur l'origine de l'arachide. *Bulletin National d'Muséum d'Histoire Naturelle (Paris)*, 5: 340–344.
- Dutra, W.F., Y.L. Guerra, J.P.C. Ramos, P.D. Fernandes, C.R.C. Silva, D.J. Bertioli, S.C.M. Leal-Bertioli, and R.C. Santos. 2018. Introgression of wild alleles into the tetraploid peanut crop to improve water use efficiency, earliness and yield. PLoS ONE 13(6): e0198776.
- EURISCO.
- FAO. 2010. The Second Report on the State of the World's Plant Genetic Resources for Food and Agriculture. Commission on Genetic Resources for Food and Agriculture, Rome. 370 pp.
- FAO. 2021. FAOSTAT. Consulted January 2021.
- FAO. 2020. WIEWS groundnut/peanut/Arachis. Early Warning System on Plant Genetic Resources for Food and Agriculture (WIEWS), Food and Agriculture Organization of the United Nations (FAO).
- Fávero, A.P., C.E. Simpson, J.F.M. Valls, and N.A. Vello. 2006. Study of the evolution of cultivated peanut through crossability studies among *Arachis ipaënsis*, *A. duranensis*, and *A. hypogaea*. *Crop Science* 46: 1546–1552.
- Fávero, A.P., J.G. Pádua, T.S. Costa, M.A. Gimenes, I.J. Godoy, M.C. Moretzsohn, and M.D. Michelotto. 2015. New hybrids from peanut (*Arachis hypogaea* L.) and synthetic amphidiploid crosses show promise in increasing pest and disease tolerance. *Genetics and Molecular Research* 14 (4): 16694–16703.
- Fávero, A.P., A.R. Custodio, N.B. Dinato, I.J. Godoy, J.G. Seijo, and M.D. Michelotto. 2020. Transference of multiple resistance to peanut through the development of cross-compatible complex hybrids of wild *Arachis*. *Genetics and Molecular Biology* 43(2).
- Ferguson, M.E., P.J. Bramel, and S. Chandra. 2004. Gene diversity among botanical varieties in peanut (*Arachis hypogaea* L.). *Crop Science* 44: 1847–1854.
- Ferguson, M.E., A. Jarvis, H.T. Stalker, D.E. Williams, L. Guarino, J.F.M. Valls, R.N. Pittman, C.E. Simpson, and P.J. Bramel. 2005. Biogeography of wild *Arachis* (Leguminosae): distribution and environmental characterisation. *Biodiversity and Conservation* 14(7):1777–1798.
- Fernández, A., and A. Krapovickas. 1994. Cromosomas y evolución en *Arachis* (Leguminosae). *Bonplandia* 8(1–4): 187–220.
- Fonceka, D., H.-A., Tossim, R. Rivallan, H. Vignes, E. Lacut, F. Bellis, I. Faye, O. Ndoye, S.C.M. Leal-Bertioli, J.F.M. Valls, D.J. Bertioli, J. Glaszmann, B. Courtois and J. Rami. 2012. Construction of chromosome segment substitution lines in peanut (*Arachis hypogaea* L.) using a wild synthetic and QTL mapping for plant morphology. PLoS ONE 7(11): e48642.

- Freitas, F.O., M.C. Moretzsohn, and J.F.M Valls. 2007. Genetic variability of Brazilian Indian landraces of *Arachis hypogaea* L. *Genet. Mol. Res.* 6 (3): 675–684.
- Fuson, R.H. (translator). 1987. *The Log of Christopher Columbus*. Ashford Press Publishing, 252 pages.
- Gao, D., A.C.G. Araujo, E.F.M.B. Nascimento, M.C. Chavarro, H. Xia, S.A. Jackson, D.J. Bertioli, and S.C.M. Leal-Bertioli. 2021. ValSten: a new wild species derived allotetraploid for increasing genetic diversity of the peanut crop (*Arachis hypogaea* L.). *Genetic Resources and Crop Evolution*, 03 January 2021.
- Genesys.
- Grabiele, M., L. Chalup, G. Robledo, and G. Seijo. 2012. Genetic and geographic origin of domesticated peanut as evidenced by 5S rDNA and chloroplast DNA sequences. *Plant Systematics and Evolution* 298: 1151–1165.
- Gregory, M.P, and W.C. Gregory. 1979. Exotic germplasm of *Arachis* L. interspecific hybrids. *Journal of Heredity* 70: 185–193.
- GRIN-Global. United States Department of Agriculture, Germplasm Resources Information Network (USDA-GRIN)
- Grosso, N.R., A. Krapovickas, J.R. Pietrarelli, and C.A. Guzman. 1994. Las proteínas seminales del maní (*Arachis hypogaea*, Leguminosae) y su relación con las categorías infraespecíficas. *Bonplandia* 8(1–4): 221–233.
- He, G.H., and C.S. Prakash. 2001. Evaluation of genetic relationships among botanical varieties of cultivated peanut (*Arachis hypogaea* L.) using AFLP markers. *Genetic Resources and Crop Evolution* 48: 347–352.
- Halewood, M., et al. 2020. Germplasm acquisition and distribution by CGIAR genebanks. *Plants* 2020 9(10): 1296.
- Halward, T.M., H.T. Stalker, and G. Kochert. 1993. Development of an RFLP map in diploid peanut species. *Theoretical and Applied Genetics* 87: 374–384.
- Hammons, R.O. 1973. Early history and origin of the peanut. Chapter 2, pages 17–45 *In*: C.T. Wilson (ed.) *Peanuts – Culture and Uses*. Am. Peanut Res. and Educ. Soc., Stillwater, OK.
- Hammons, R.O. 1982. Origin and early history of the peanut. Pages 1–20 *In*: H.E. Pattee and C.T. Young (eds.) *Peanut Science and Technology*. Amer. Peanut Res. Educ. Soc., Yoakum, TX.
- Hammons, R.O., D. Herman, and H.T. Stalker. 2016. Chapter 1 – Origin and early history of the peanut. *In*: Stalker, H.T. and R.F. Wilson (eds.), *Peanuts: Genetics, Processing and Utilization*. Academic Press and AOCs Press. ISBN: 9781630670382.
- Harlan, J.R., and J.M.J. de Wet. 1971. Toward a Rational Classification of Cultivated Plants. *Taxon* 20(4): 509–517.
- Hernandez-Garay, A., L.E. Sollenberger, C.R. Staples and C.G.S. Pedreira. 2004. ‘Florigraze’ and ‘Arbrook’ rhizome peanut as pasture for growing Holstein heifers. *Crop Science* 44: 1355–1360.
- Ho, Ping-Ti. 1955. The Introduction of American Food Plants into China. *American Anthropologist*, New Series, Vol. 57, No. 2, Part 1, pp. 191–201.
- Holbrook, C.C., W.F Anderson and R.N. Pittman. 1993. Selection of a core collection from the U.S. germplasm collection of peanut. *Crop Science* 33: 859–861.
- Holbrook, C.C., P. Timper, A.K. Culbreath, C.K. Kvein. 2008. Registration of ‘Tifguard’ peanut. *J. Plant Regist.* 2: 92–94.
- Husted, L. 1936. Cytological studies on the peanut, *Arachis*. II. Chromosome number, morphology and behavior, and their application to the problem of the origin of the cultivated forms. *Cytologia* 7: 396–422.
- IBPGR. 1990. *International Crop Network Series. 2. Report of a Workshop on the Genetic Resources of Wild Arachis Species*. Including Preliminary Descriptors for *Arachis*. International Board for Plant Genetic Resources, Rome.
- IBPGR/ICRISAT. 1992. *Descriptors for Groundnut*. International Board for Plant Genetic Resources (IBPGR) and International Crops Research Institute for the Semi-Arid Tropics (ICRISAT). 125 pp.
- ICAR-NBPGR. 2020. *Annual Report 2019*, ICAR-National Bureau of Plant Genetic Resources, New Delhi, India. 239 pp.
- IPGI. 2016. Strategic Plan for 2017 to 2021: Integration of Germplasm & Genomic Resources. International Peanut Genomic Research Initiative (IPGI), downloaded 30/11/2020.
- Isleib, T.G., C.C. Holbrook, and D.W. Gorbet. 2001. Use of plant introductions in peanut cultivar development. *Peanut Science* 28: 96–113.
- Isleib, T.G., S.R. Milla-Lewis, H.E. Pattee, S.C. Copeland, M.C. Zuleta, B.B. Shew, J.E. Hollowell, T.H. Sanders, L.O. Dean, K.W. Hendrix, M. Balota, and J.W. Chapin. 2011. Registration of ‘Bailey’ peanut. *J. Plant Regist.* 5: 27–39.
- IUCN. 2021. The IUCN Red List of Threatened Species. Version 2020–3. International Union for Conservation of Nature and Natural Resources. ISSN 2307–8235
- Jarvis, A., L. Guarino, D. Williams, K. Williams, I. Vargas, and G. Hyman. 2002. Spatial analysis of wild peanut distributions and the implications for plant genetic resource conservation. *Plant Genetic Resources Newsletter* 131: 28–34.
- Jarvis, A., M.E. Ferguson, D.E. Williams, L. Guarino, P. Jones, H.T. Stalker, J.F.M. Valls, R.N. Pittman, C.E. Simpson, and P. Bramel. 2003. Biogeography of wild *Arachis*: assessing conservation status and setting future priorities. *Crop Science* 43(3): 1100–1108.

- Jarvis, D.I., and T. Hodgkin (eds.). 1998. Strengthening the scientific basis of *in situ* conservation of agricultural biodiversity on-farm. Options for data collecting and analysis. Proc., Workshop to Develop Tools and Procedures for *In Situ* Conservation On-Farm, 25–29 August 1997. Int. Plant Genetic Resources Inst., Rome, Italy.
- Jarvis, D.I., L. Myer, H. Klemick, L. Guarino, M. Smale, A.H.D. Brown, M. Sadiki, B. Sthapit and T. Hodgkin. 2000. A Training Guide for *In Situ* Conservation On-farm. Version 1. International Plant Genetic Resources Institute, Rome, Italy.
- Jeremy, L., J.L. Jelliffe, B.E. Bravo-Ureta, C.M. Deom, and D.K. Okello. 2018. Adoption of High-Yielding Groundnut Varieties: The Sustainability of a Farmer-Led Multiplication-Dissemination Program in Eastern Uganda. *Sustainability* 10: 1597.
- Jiang, H.F., and N.X. Duan. 1998. Utilization of groundnut germplasm resources in breeding programme. *Crop Genetic Resources* 2: 24–25.
- Jiang, H., and X.P. Ren. 2006. Genetic diversity of peanut resource on morphological characters and seed chemical components in China. *Chin. J. Oil Crop Sci.* 28: 421–426.
- Jiang, H.F., and N.X. Duan. 2006. Descriptors and Data Standard for Peanut (*Arachis* spp.). China Agricultural Press, Beijing. ISBN: 7–109-10911–9 (in Chinese).
- Jiang, H.F., X.P. Ren, B.S. Liao, J.Q. Huang, Y. Lei, B.Y. Chen, B.Z. Guo, C.C. Holbrook, and H.D. Upadhyaya. 2008. Peanut core collection established in China and compared with ICRISAT mini core collection. *Acta Agron. Sin.* 34: 25–30.
- Jiang, H.F., X. Ren, X. Zhang, J. Huang, Y. Lei, L. Yan, B. Liao, H.D. Upadhyaya, and C.C. Holbrook. 2010a. Comparison of genetic diversity based on SSR markers between peanut mini core collections from China and ICRISAT. *Acta Agron. Sin.* 36(7): 1084–1091.
- Jiang, H.F., X.P. Ren, X.J. Zhang, J.Q. Huang, S.Y. Wang, Y. Lei, L.Y. Yan, and B.S. Liao. 2010b. Genetic diversity of peanut mini core collection detected by SSR markers. *Chin. J. Oil Crop Science* 32: 472–478.
- Jiang, H., L. Huang, X. Ren, Y. Chen, X. Zhou, Y. Xia, J. Huang, Y. Lei, L. Yan, L. Wan, and B. Liao. 2014. Diversity characterization and association analysis of agronomic traits in a Chinese peanut (*Arachis hypogaea* L.) mini-core collection. *Journal of Integrated Plant Biology* 56: 159–169.
- Khoury, C.K., S. Brush, D.E. Costich, H.A. Curry, S. de Haan, J.M.M. Engels, L. Guarino, S. Hoban, K.L. Mercer, A.J. Miller, G.P. Nabhan, H.R. Perales, C. Richards, C. Riggins, and I. Thormann. 2021. Crop genetic erosion: understanding and responding to loss of crop diversity. *New Phytologist* (2021).
- Khoury, C.K., S. Sotelo, D. Amariles, L. Guarino, and A. Toledo. 2021. A global indicator of the importance of cultivated plants, and interdependence with regard to their genetic resources worldwide. Forthcoming.
- Kochert, G., T. Halward, W.D. Branch, and C.E. Simpson. 1991. RFLP variability in peanut (*Arachis hypogaea* L.) cultivars and wild species. *Theoretical and Applied Genetics* 81: 565–570.
- Kochert, G., H. T. Stalker, M. Gimenes, L. Galgaro, C. R. Lopes, and K. Moore. 1996. RFLP and cytological evidence on the origin and evolution of allotetraploid domesticated peanut, *Arachis hypogaea* (Leguminosae). *American Journal of Botany* 83: 1282–1291.
- Konate, M., J. Sanou, A. Miningou, D.K. Okello, H. Desmae, J. Pasupuleti and R.H. Mumm. 2020. Past, present and future perspectives on groundnut breeding in Burkina Faso. *Agronomy* 2020, 10(5): 704.
- Krapovickas, A. 1995. El origen y dispersión de las variedades del maní. *Academia Nacional de Agronomía y Veterinaria* 49(12): 18–26.
- Krapovickas, A. 1998. *Arachis hypogaea* var. *hirsuta* y las relaciones transoceánicas precolombinas. *Anal. Acad. Nac. Cs. Ex. Fís. y Nat., Buenos Aires* 50: 211–216.
- Krapovickas, A. 2010. Las ilustraciones de la “Historia General y Natural de las Indias, Islas y Tierraferme del mar Océano de Gonzalo Fernández de Oviedo y Valdéz”. *Bonplandia* 19(1): 91–96.
- Krapovickas, A. and W.C. Gregory. 1994. Taxonomía del género *Arachis* (Leguminosae). *Bonplandia* 8(1–4): 1–186. ISSN 0524–0476.
- Krapovickas, A. and W.C. Gregory. 2007. Taxonomy of the genus *Arachis* (Leguminosae). Translated by D.E. Williams and C.E. Simpson. *Bonplandia* 16 (Supl.): 1–205. ISSN 0524–0476.
- Krapovickas, A. and R.O. Vanni. 2009. El maní de Lullaillaco. *Bonplandia* 18 (1): 51–55. ISSN: 0524–0476.
- Krapovickas, A., R.O. Vanni, J.R. Pietrarelli, D.E. Williams and C.E. Simpson. 2009. Las razas de maní de Bolivia. *Bonplandia* 18(2): 95–189.
- Krapovickas, A., R.O. Vanni, J.R. Pietrarelli and C.E. Simpson. 2013. Las razas de maní de Perú. *Bonplandia* 22(1): 19–90.
- Krapovickas, A., R.O. Vanni, J.R. Pietrarelli, D.E. Williams and C.E. Simpson. 2021. Las razas de maní de Ecuador. *Bonplandia* 30(2): 203–278.
- Kumari, V., M.V.C. Gowda, V. Tasiwal, M.K. Pandey, R.S. Bhat, N. Mallikarjuna, H.D. Upadhyaya, and R.K. Varshney. 2014. Diversification of primary gene pool through introgression of resistance to foliar diseases from synthetic amphidiploids to cultivated groundnut (*Arachis hypogaea* L.). *The Crop Journal*.
- Lavia, G.I. A.M. Ortiz, and A. Fernández. 2009. Karyotypic studies in wild germplasm of *Arachis* species (Leguminosae). *Genetic Resources and Crop Evolution* 56: 755–764.
- Lavia, G.I. 2001. Chromosomal characterization of germplasm of wild species of *Arachis* L. belonging

- to sections *Trierectoides*, *Erectoides* and *Procumbentes*. *Caryologia* 54: 115–119. Edit. Università degli studi di Firenze. ISSN 0080/7114.
- Lavia, G.I., A. Fernández, C. Simpson, and G. Seijo. 2001. Meiotic analysis in wild diploid *Arachis* species. *Cytologia* 66: 293–298. Edit. Japan Mendel Society. ISSN 0011/4545.
- Leal-Bertioli, S.C.M., S.P. Santos, K.M. Dantas, P.W. Inglis, and S. Nielsen et al. 2015. *Arachis batizocoi*: a study of its relationship to cultivated peanut (*A. hypogaea* L.) and its potential for introgression of wild genes into the peanut crop using induced allo-tetraploids. *Ann. Bot. (Lond.)* 115: 237–249.
- Leal-Bertioli, S.C.M., M.C. Moretzsohn, S.P. Santos, A.C.M. Brasileiro, P.M. Guimarães, D.J. Bertioli, and A.C.G. Araujo. 2017. Phenotypic effects of allotetraploidization of wild *Arachis* and their implications for peanut domestication. *American Journal of Botany* 104(3): 379–388
- Levinson, C., Y. Chu, X. Luo, H.T. Stalker, D. Gao, C.C. Holbrook, and P. Ozias-Akins. 2021. Morphological and reproductive characterization of nascent allo-tetraploids cross-compatible with cultivated peanut (*Arachis hypogaea* L.). *Genetic Resources and Crop Evolution*.
- Liao, B.S. 2014. Peanut breeding. Pages 61–78 *In*: Nalini, M. and R.K. Varshney (eds.), *Genetic, Genomics and Breeding of Peanuts*. CRC Press Taylor and Francis Group, Boca Raton, London, New York.
- Linnaeus, C. 1753. *Species Plantarum*. L. Salvius, Stockholm. v.2: 741.
- Loko, Y.L.E., D. Montcho, M. Zandjanakou-Tachin, A. Orobiyi, J. Toffa, E. Hounmakou, D. Gavoedo, and A. Dansi. 2020. Farmers' management of peanut (*Arachis hypogaea* L.) diversity, their varietal preference traits and uses in Southern and Central Benin. Published in the online *Journal of Crop Science and Biotechnology*.
- Mallikarjuna, N., S. Senthilvel, and D. Hoisington. 2010. Development of new sources of tetraploid *Arachis* to broaden the genetic base of cultivated groundnut (*Arachis hypogaea* L.). *Genetic Resources and Crop Evolution*.
- Massa, A.N., M. Bressano, J.H. Soave, M.I. Buteler, G. Seijo, V.S. Sobolev, V.A. Orner, C. Oddino, S.J. Soave, P.C. Faustinelli, F.J. de Blas, M.C. Lamb, and R.S. Arias. 2021. Genotyping tools and resources to assess peanut germplasm: smut-resistant landraces as a case study. *PeerJ* 9: e10581.
- Michelotto, M.D., I.J. de Godoy, M.Z. Pirotta, J.F. dos Santos, E.L. Finoto, and A. Pereira Fávero. 2017. Resistance to thrips (*Enneothrips flavens*) in wild and amphidiploid *Arachis* species. *PLoS ONE* 12(5): e0176811.
- Milla S.R., T.G. Isleib and H.T. Stalker. 2005. Taxonomic relationships among *Arachis* sect. *Arachis* species as revealed by AFLP markers. *Genome* 48: 1–11.
- Moretzsohn, M.C., M.S. Hopkins, S.E. Mitchell, S. Kresovich, J.F.M. Valls, and M.E. Ferreira. 2004. Genetic diversity of peanut (*Arachis hypogaea* L.) and its wild relatives based on the analysis of hyper-variable regions of the genome. *BMC Plant Biology* 4:11.
- Nascimento E.F.M.B., S.C.M. Leal-Bertioli, D.J. Bertioli, C. Chavarro, F.O. Freitas, M.C. Moretzsohn, P.M. Guimarães, J.F.M. Valls, and A.C.G. Araujo. 2020. Brazilian Kayabi Indian accessions of peanut, *Arachis hypogaea* (Fabales, Fabaceae): origin, diversity and evolution. *Genetics and Molecular Biology* 43(4): e20190418.
- Ojiewo, C.O., J. Pasupuleti, P. Bhatnagar-Mathur, M.K. Pandey, H. Desmae, P. Okori, ... and R.K. Varshney. 2020. Advances in Crop Improvement and Delivery. Research for Nutritional Quality and Health Benefits of Groundnut (*Arachis hypogaea* L.). *Front. Plant Sci.* 11: 29.
- Otyama P.I., R. Kulkarni, K. Chamberlin, P. Ozias-Akins, Y. Chu, L.M. Lincoln, G.E. MacDonald, N.L. Anglin, S. Dash, D.J. Bertioli, D. Fernández-Baca, M.A. Graham, S.B. Cannon, and E.K.S. Cannon. 2020. Genotypic Characterization of the U.S. Peanut Core Collection, G3 Genes|Genomes|Genetics, Volume 10, Issue 11, 1 November 2020, Pages 4013–4026.
- Ortiz, A.M., M.C. Silvestri, and G.I. Lavia. 2013. Karyotypic studies in wild species of *Arachis* (Leguminosae) belonging to sections *Erectoides*, *Procumbentes* and *Rhizomatosae*. *Bol. Soc. Argent. Bot.* 48: 295–300.
- Pandey, M.K., E. Monyo, P. Ozias-Akins, X. Liang, P. Guimarães, S.N. Nigam, H.D. Upadhyaya, P. Janila, X. Zhang, B. Guo, D.R. Cook, D.J. Bertioli, R. Michellmore, and R.K. Varshney. 2012. Advances in *Arachis* genomics for peanut improvement. *Biotechnology Advances* 30: 639–651.
- Piperno D.R., and D.M. Pearsall. 1998. The origins of agriculture in the Lowland Neotropics. Academic Press, New York.
- Pittman, R.N. 1995. United States Peanut Descriptors. United States Department of Agriculture, ARS-132. ISSN: 1052–5386. 16 pp.
- Pasupuleti, J., S.N. Nigam, M.K. Pandey, P. Nagesh and R.K. Varshney. 2013. Groundnut improvement: use of genetic and genomic tools. *Frontiers in Plant Science* 4: 23.
- Rago, A.M., L.I. Cazón, J.A. Paredes, J.P. Edwards Molina, E.C. Conforto, E.M. Bisonard, and C. Oddino. 2017. Peanut smut: From an emerging disease to an actual threat to Argentine peanut production. *Plant Disease* 101(3): 400–408.
- Rao, V.R.M., and T. Hodgkin. 2002. Genetic diversity and conservation and utilization of plant genetic resources. *Plant Cell Tissue Organ Cult.* 68: 1–19.
- Robledo, G, G.I. Lavia, and G. Seijo. 2009. Species relations among wild *Arachis* species with the A genome as revealed by FISH mapping of rDNA loci

- and heterochromatin detection. *Theoretical and Applied Genetics* 118: 1295–1307.
- Robledo, G., G.I. Lavia, and G. Seijo. 2010. Genome re-assignment of *Arachis trinitensis* (Sect. *Arachis*, Leguminosae) and its implications for the genetic origin of cultivated peanut. *Genetics and Molecular Biology* 33: 714–718
- Robledo, G., and G. Seijo. 2010. Species relationships among the wild B genome of *Arachis* species (section *Arachis*) based on FISH mapping of rDNA loci and heterochromatin detection: a new proposal for genome arrangement. *Theoretical and Applied Genetics* 121: 1033–1046.
- Sanchez-Dominguez, S., and D.E. Williams. 1993. Results of a recent plant exploration in Mexico to collect the *hirsuta* peanut. *Proc. Amer. Peanut Res. Ed. Soc.* 25: 35 (abstract).
- Santana, S.H., and J.F.M. Valls. 2015. *Arachis veigae* (Fabaceae), the most dispersed wild species of the genus, and yet taxonomically overlooked. *Bonplandia* 24(2): 139–150.
- Seijo, G., G.L. Lavia, A. Fernández, A. Krapovickas, D. Ducasse, and E.A. Moscone. 2004. Physical mapping of the 5S and 18S-25S rRNA genes by FISH as evidence that *Arachis duranensis* and *A. ipaensis* are the wild diploid progenitors of *A. hypogaea* (Leguminosae). *American Journal of Botany* 91: 1294–1303.
- Seijo, G.J., G.I. Lavia, A. Fernández, A. Krapovickas, D. Ducasse, D.J. Bertoli, and E.A. Moscone. 2007. Genomic relationships between the cultivated peanut (*Arachis hypogaea* – Leguminosae) and its close relatives revealed by double GISH. *American Journal of Botany* 94: 1963–1971.
- Seijo, G.J., M. Atahuachi, C.E. Simpson, and A. Krapovickas. 2021. *Arachis inflata*: A new B genome species of *Arachis* (Fabaceae). *Bonplandia* 30(2): 169–174.
- Silvestri, M.C., A.M. Ortiz, G. Robledo, J.F.M. Valls, and G.I. Lavia. 2017. Genomic characterisation of *Arachis porphyrocalyx* (Valls & C.E. Simpson, 2005) (Leguminosae): multiple origin of *Arachis* species with  $x = 9$ . *Comparative Cytogenetics* 11: 29–43.
- Simpson, C.E., S.C. Nelson, J.L. Starr, K.E. Woodard, and O.D. Smith. 1993. Registration of TxAG-6 and TxAG-7 peanut germplasm lines. *Crop Science* 33: 1418.
- Simpson, C.E. 2001. Use of wild *Arachis* species: Introgression of genes into *A. hypogaea* L. *Peanut Science* 28: 114–116.
- Simpson, C.E., A. Krapovickas, and J.F.M. Valls. 2001. History of *Arachis* including evidence of *A. hypogaea* L. progenitors. *Peanut Science* 28: 78–80.
- Simpson, C.E., and M.J. Faries. 2001. Advances in the characterization of diversity in section *Arachis*: Archeological evidence, crossing results and their relationship in understanding the origin of *Arachis hypogaea* L. Pp. 103–104 *In: Abstracts of III SIRGEALC – Simpósio de Recursos Genéticos para a América Latina e Caribe*. Instituto Agronômico do Paraná, Londrina.
- Simpson, C.E., and J.L. Starr. 2001. Registration of ‘COAN’ peanut. *Crop Science* 41: 918.
- Simpson, C.E., J.L. Starr, J.T. Church, M.D. Burow, and A.H. Paterson. 2003. Registration of ‘Nema-Tam’ peanut. *Crop Science* 43: 1561.
- Singh, A.K., and J.P. Moss. 1982. Utilization of wild relatives in genetic improvement of *Arachis hypogaea* L. Part 2. Chromosome complements of species of section *Arachis*. *Theoretical and Applied Genetics* 61: 305–314.
- Singh, A.K., and S.N. Nigam. 2016. *Arachis* Gene Pools and Genetic Improvement in Groundnut. *In: Gene Pool Diversity and Crop Improvement*, Springer.
- Smartt, J., W. Gregory, and M.P. Gregory. 1978. The genomes of *Arachis hypogaea*. 1. Cytogenetic studies of putative genome donors. *Euphytica* 27: 665–675.
- Smartt, J. (Ed.). 1994. *The Groundnut Crop. A Scientific Basis for Improvement*. Chapman & Hall, UK.
- Smith, C.E. 1967. Plant Remains. Pages 220–255 *In: DS Byers* (Ed.), *The Prehistory of the Tehuacan Valley*, Vol. 1, Environment and Subsistence. University of Texas Press, Austin.
- Stalker, H.T. 1991. A new species in section *Arachis* of peanuts with a D genome. *American Journal of Botany* 78: 630–637.
- Stalker, H.T. 2017. Utilizing wild species for peanut improvement. *Crop Science* 57:1102–1120
- Stalker, H.T., and C.E. Simpson. 1995. Germplasm resources in *Arachis*. Pages 14–53 *In: Pattee, H.E.* and H.T. Stalker (Eds.), *Advances in Peanut Science*. American Peanut Research and Education Society, Stillwater, OK.
- Stalker, H.T., J.F.M. Valls, R.N. Pittman, C.E. Simpson and P. Bramel-Cox. 2002. Catalog of *Arachis* Germplasm Collection. Patancheru: ICRISAT.
- Stalker, H.T., S.P. Tallury, P. Ozias-Akins, D. Bertoli, and S.C. Leal-Bertoli. 2013. The value of diploid peanut relatives for breeding and genomics. *Peanut Science* 40: 70–88.
- Stalker, H.T., S.P. Tallury, G.R. Seijo, and S.C. Leal-Bertoli. 2016. Biology, speciation, and utilization of peanut species. Chapter 2, pages 27–66 *In: Stalker, H.T.* and R.F. Wilson (eds.), *Peanuts: Genetics, Processing and Utilization*. Academic Press and AOCS Press. ISBN: 9781630670382.
- Sun, D.R. 1998. *Breeding of Groundnut*. China Agricultural Press, Beijing. (in Chinese). ISBN:7–109-05154–4/5.3261.
- Talawar, S. 2004. *Peanut in India: History, Production, and Utilization*. Peanut in Local and Global Food Systems Series Report No. 5. Department of Anthropology, University of Georgia. 33 pp.



- Tallury, S.P. 2020. Peanut Vulnerability Report. Unpublished report to the Peanut Crop Germplasm Committee. USDA-ARS-NPGS, 10 June 2020. 88 pp.
- Tallury S.P., K.W. Hilu, S.R. Milla, S.A. Friend, M. Alsaghir, H.T. Stalker, and D. Quandt. 2005. Genomic affinities in *Arachis* section *Arachis* (Fabaceae): molecular and cytogenetic evidence. *Theoretical and Applied Genetics* 111: 1229–1237.
- Tossim, H.A., J.R. Nguepjob, C. Diatta, A. Sambou, M. Seye, D. Sane, J.F. Rami, and D. Fonckea. 2020. Assessment of 16 peanut (*Arachis hypogaea* L.) CSSLs derived from an interspecific cross for yield and yield component traits: QTL validation. *Agronomy* 2020, 10, 583.
- Upadhyaya, H.D., P.J. Bramel, R. Ortiz, and S. Singh. 2002. Developing a mini core of peanut for utilization of genetic resources. *Crop Science* 42: 2150–2156.
- Upadhyaya, H.D., R. Ortiz, P.J. Bramel, and S. Singh. 2003. Development of groundnut core collection using taxonomical, geographical and morphological descriptors. *Genetic Resources and Crop Evolution* 50: 139–148.
- Valls, J.F.M. 2015. *Arachis* in Lista de Espécies da Flora do Brasil. Jardim Botânico do Rio de Janeiro. Available online. Accessed 15 February 2021.
- Valls, J.F.M., V. Ramanatha Rao, C.E. Simpson, and A. Krapovickas. 1985. Current status of collection and conservation of South American groundnut germplasm with emphasis on wild species of *Arachis*. Pp. 15–35 *In*: Moss, J.P. (Ed.), *Proc. Intern. Workshop on Cytogenetics of Arachis*. Oct. 31–Nov. 2, 1983. ICRIASAT, Patancheru, Andhra Pradesh, India.
- Valls, J.F.M. and C.E. Simpson. 2005. New species of *Arachis* (Leguminosae) from Brazil, Paraguay and Bolivia. *Bonplandia* 14(1–2): 35–63.
- Valls, J.F.M., L.C. Costa and A.R. Custodio. 2013. A novel trifoliolate species of *Arachis* (Fabaceae) and further comments on the taxonomic section *Triecretoides*. *Bonplandia* 22(1): 91–97.
- Van Treuren, R., J.M.M. Engels, R. Hoekstra and T.J. van Hintum. 2009. Optimization of the composition of crop collections for *ex situ* conservation. *Plant Genetic Resources* 7(2): 185–193.
- Varshney, R. K., et al. 2009. High level of natural variation in a groundnut (*Arachis hypogaea* L.) germplasm collection assayed by selected informative SSR markers. *Plant Breeding* 128.5: 486–494.
- Vincent, H., J. Wiersema, S. Kell, H. Fielder, S. Dobbie, N.P. Castañeda-Álvarez, L. Guarino, R. Eastwood, B. León, N. Maxted. 2013. A prioritized crop wild relative inventory to help underpin global food security. *Biological Conservation* 167:265–275.
- VMABCC-BIOVERSITY. 2009. *Red Book of Crop Wild Relatives in Bolivia*. Editores Plural. La Paz. 340 pp.
- Waldron, R.A. 1919. The Peanut (*Arachis hypogaea*) – Its History, Histology, Physiology, and Utility. Penn. Univ. Bot. Lab. Contrib. 4: 301–338.
- Wang, M.L., S. Sukumaran, N.A. Barkley, Z. Chen, C.Y. Chen, B. Guo, R.N. Pittman, H.T. Stalker, C.C. Holbrook, G.A. Pederson, and J. Yu. 2011. Population structure and marker–trait association analysis of the US peanut (*Arachis hypogaea* L.) mini-core collection. *Theoretical and Applied Genetics* 123.8: 1307–1317.
- Wang, Hui, K. Pawan, H. Bingyan, Y. Mei, K. Ramesh, Z. Weijian, K. Harris-Shultz, K.M. Moore, A.K. Culbreath, X. Zhang, R.K. Varshney, L. Xie, and B. Guo. 2016. Analysis of genetic diversity and population structure of peanut cultivars and breeding lines from China, India and the US using simple sequence repeat markers. *Journal of Integrative Plant Biology* 58(5): 452–465.
- Wann, D.Q., A. Falco, M. Cavigliasso and C. Cassano. 2020. Phenotypic variation of peanut smut (*Thecaphora frezii*) Incidence and severity in the U.S. Peanut Mini-Core Collection. *Peanut Science* 47: 46–53.
- WIEWS. 2021. World Information and Early Warning System on Plant Genetic Resources for Food and Agriculture. FAO.
- Williams, D.E. 1989. Exploration of Amazonian Bolivia yields rare peanut landraces. *Diversity* 5(4): 12–13.
- Williams, D.E. 1991. Peanuts and peanut farmers of the Rio Beni: traditional crop genetic resource management in the Bolivian Amazon. PhD dissertation, City University of New York. University Microfilms International, number 9207138. 170 pp.
- Williams, D.E. 1992. Aboriginal farming system provides clues to groundnut evolution. Pages 11–17 *In*: B. Pickersgill and J.M. Lock (eds.), *Advances in Legume Systematics: Legumes of Economic Importance*. Royal Botanic Gardens, Kew, England.
- Williams, D.E. 2001. New directions for collecting and conserving peanut genetic diversity. *Peanut Science* 28: 136–141.
- Williams, D.E. 2004. Columbian exchange: The role of analogue crops in the adoption and dissemination of exotic cultigens. Pages 292–296 *In*: *Encyclopedia of Plant and Crop Science*, Marcel Dekker, Inc.
- Williams, K.A. and D.E. Williams. 2001. Evolving political issues affecting international exchange of *Arachis* genetic resources. *Peanut Science* 28:132–135.
- Yao, G. 2004. Peanut Production and Utilization in the People's Republic of China. *Peanut in Local and Global Food Systems Series Report No. 4*.
- Zheng, Z., et al. 2018. Genetic Diversity, Population Structure, and Botanical Variety of 320 Global Peanut Accessions Revealed Through Tuneable Genotyping-by-Sequencing. *Scientific Reports* 8.1: 14500.



Arachis diversity on display at ICRISAT. Photo: Shawn Landersz

# 7 ACRONYMS

<b>ABS</b>	Access and Benefit Sharing
<b>CAAS</b>	Chinese Academy of Agricultural Sciences
<b>CBD</b>	Convention on Biological Diversity (UN)
<b>CENARGEN</b>	Embrapa Recursos Genéticos e Biotecnología (EMBRAPA)
<b>CGIAR</b>	Consultative Group on International Agricultural Research
<b>CIAT</b>	Centro Internacional de Agricultura Tropical (CGIAR)
<b>CWR</b>	Crop Wild Relatives
<b>DSI</b>	Digital Sequence Information on Genetic Resources
<b>EMBRAPA</b>	Empresa Brasileira de Pesquisa Agropecuária (Brazil)
<b>FAN</b>	Fundación Amigos de la Naturaleza (Bolivia)
<b>FAO</b>	Food and Agriculture Organization of the United Nations
<b>FIGS</b>	Focused Identification of Germplasm Strategy
<b>GRIN-Global</b>	Germplasm Resources Information Network-Global (USDA)
<b>IBONE</b>	Instituto de Botánica del Nordeste (Argentina)
<b>IAG</b>	International Advisory Group (Global Peanut Conservation Strategy)
<b>ICAR</b>	Indian Council of Agricultural Research
<b>ICRISAT</b>	International Crops Research Institute for the Semi-Arid Tropics (CGIAR)
<b>INTA</b>	Instituto Nacional de Tecnología Agropecuaria (Argentina)
<b>IPGI</b>	International Peanut Genome Initiative
<b>ISRA</b>	Senegalese Institute of Agricultural Research
<b>ITPGRFA</b>	International Treaty on Plant Genetic Resources for Food and Agriculture (FAO)
<b>IUCN</b>	International Union for the Conservation of Nature
<b>MLS</b>	Multi-Lateral System of Access and Benefit Sharing (ITPGRFA)
<b>MTA</b>	Material Transfer Agreement
<b>NBPGR</b>	National Bureau of Plant Genetic Resources (ICAR)
<b>NCSU</b>	North Carolina State University (USA)
<b>NGO</b>	Non-Governmental Organization
<b>PGRFA</b>	Plant Genetic Resources for Food and Agriculture
<b>OCRI</b>	Oilseed Crops Research Institute (CAAS)
<b>SADC-SPGRC</b>	Southern African Development Community, Plant Genetic Resources Centre (Zambia)
<b>SARDI</b>	South Australian Research and Development Institute
<b>SGSV</b>	Svalbard Global Seed Vault
<b>SMTA</b>	Standard Material Transfer Agreement (ITPGRFA)
<b>SPC-PAPGREN</b>	Secretariat of the Pacific Community, Pacific Plant Genetic Resources Network (Fiji)
<b>SSR</b>	Single Sequence Repeats, a microsatellite marker
<b>TAMU</b>	Texas A&M University (USA)
<b>USDA</b>	United States Department of Agriculture
<b>UGA</b>	University of Georgia (USA)
<b>VMABCC</b>	Vice-Ministry for the Environment and Biodiversity and Climate Change (Bolivia)
<b>WIEWS</b>	World Information and Early Warning System on Plant Genetic Resources (FAO)



Special facility for wild *Arachis* at ICRISAT. Photo: Shawn Landersz

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## Annex 2. Peanut Online Survey Questionnaire

–A Global Strategy for the Conservation of Peanut Diversity (*Arachis* spp.)

### SURVEY QUESTIONNAIRE

(final draft – 08 July 2020)

#### INTRODUCTION

Since 2007, the Global Crop Diversity Trust (Crop Trust) has been supporting the development of an ongoing series of crop-specific global strategies to promote and facilitate the more efficient and effective conservation of the diversity of those crops, particularly in *ex situ* collections. 26 crop strategies have been developed to date, and can be accessed at: <https://www.croptrust.org/our-work/supporting-crop-conservation/conservation-strategies/>

The Crop Trust has recently commissioned an independent external consultant (David Williams) to coordinate the development of a **Global Strategy for the Conservation of Peanut Diversity (*Arachis* spp.)**. The Strategy will identify key priority actions that must be taken to secure the full scope of peanut genetic diversity, including the resources and collaborations needed to ensure a rational and sustainable global conservation system.

The following survey has been designed to secure the inputs and advice of peanut specialists and collection managers. The survey will serve as a baseline assessment of the current conservation status of *Arachis* genetic resources, and is an essential element for the development of the Global Strategy.

We would like to invite you to become a partner in this global initiative by taking part in this survey of *Arachis* germplasm collections. Please take the time to fill out this detailed questionnaire about your collection, which should take approximately ninety minutes to complete. The survey is addressed either to the genebank curator or to the chief representative of the institution – kindly note that only one questionnaire per institution should be completed.

Your work is very important for the future conservation of peanut/groundnut genetic resources, and the Crop Trust is keen to have your active participation in the development of this Global Strategy. After the survey is completed, we may contact you again to get further feedback on the global conservation system and the recommended actions needed to facilitate its implementation for securing *Arachis* genetic resources worldwide. When the Global Strategy is completed later this year, we will be pleased to send you a copy of the final document, where your participation and inputs will be gratefully acknowledged.

Many thanks in advance for your valued contribution to this important initiative.

If you have any questions or concerns regarding this survey or the proposed Global Strategy, please do not hesitate to contact David Williams ([reddog.williams@gmail.com](mailto:reddog.williams@gmail.com)).

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#### CONTACT INFORMATION

##### 1. Organization holding/maintaining the *Arachis* collection

Name of Organization	
Address	
City/Town	
State/Province	
ZIP/Postal Code	
Country	
Website	

##### 2. Type of Organization

- International/multinational organization
- Governmental organization
- University
- Private organization
- NGO
- Other (please specify) \_\_\_\_\_

##### 3. Is the institution in charge of the *Arachis* collection the legal owner of the collection?

- Yes
- No

If NO, please indicate the owner (or "no owner identified")

\_\_\_\_\_

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##### 4. Curator in charge of the *Arachis* collection:

Name	
Job Title	
Address	
City/Town	
Telephone(s)	
Email	

##### 5. Name of respondent to this survey (if not as above)

Name	
Function/Job Title	
Email	
Telephone	
Date of response	

##### 6. Additional key contact person for the above germplasm collections (1)

Name	
Function/Job Title	
Email	

##### 7. Additional key contact person for the above germplasm collections (2)

Name	
Function/Job Title	
Email	

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#### THE *ARACHIS* COLLECTION

##### 8. Basic information about the *Arachis* collection

Year of establishment	
Total number of accessions (today)	
Total number of species (today)	
Total number of accessions currently available for distribution	

##### 9. What are the main objectives of your *Arachis* collection? (select all applicable)

- Long-term conservation
- Working collection/medium term conservation
- Breeding collection
- Reference collection
- Other (please specify) \_\_\_\_\_

##### 10. Please indicate the NUMBER OF ACCESSIONS, by type of germplasm

Landraces	
Obsolete improved varieties	
Advanced improved varieties	
Breeding/research materials	
Specialist Genetic Stocks	
Related wild species	
Unknown	
Other	

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**11. Please indicate the percentage (%) of accessions AVAILABLE FOR DISTRIBUTION, by type of germplasm**

Landraces	
Obsolete improved varieties	
Advanced improved varieties	
Breeding/research materials	
Specialist Genetic Stocks	
Related wild species	
Unknown	
Other	

**12. Please indicate the number of accessions of cultivated peanut (*A. hypogaea*), including those identified to subspecies and botanical variety.**

Genus – species – subspecies – botanical variety	Number of Accessions
<i>Arachis hypogaea</i> – (subspecies and botanical variety unknown)	
<i>Arachis hypogaea</i> subsp. <i>hypogaea</i> – (botanical variety unknown)	
<i>Arachis hypogaea</i> subsp. <i>hypogaea</i> var. <i>hypogaea</i>	
<i>Arachis hypogaea</i> subsp. <i>hypogaea</i> var. <i>hirsuta</i>	
<i>Arachis hypogaea</i> subsp. <i>fastigiata</i> – (botanical variety unknown)	
<i>Arachis hypogaea</i> subsp. <i>fastigiata</i> var. <i>fastigiata</i>	
<i>Arachis hypogaea</i> subsp. <i>fastigiata</i> var. <i>vulgaris</i>	
<i>Arachis hypogaea</i> subsp. <i>fastigiata</i> var. <i>peruviana</i>	
<i>Arachis hypogaea</i> subsp. <i>fastigiata</i> var. <i>aequatoriana</i>	

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**13. Please record each of the wild *Arachis* species in your collection, with the number of accessions conserved, and the percentage (%) of those accessions conserved by the different storage methods:**

NOTE: If accessions are conserved by more than one storage method, total percentages may exceed 100%

Species name	Number of Accessions	Seeds in Cold Storage (%)	Plants in Greenhouse/Screenhouse (%)	Plants in Field Plots (%)	In vitro Tissue Culture (%)
(example: <i>A. pinto</i> )					
-- add additional rows as needed --					
Total wild <i>Arachis</i> accessions →					

**14. To what extent do you consider the *Arachis* accessions in your collection to be unique, i.e., not duplicated elsewhere (excluding safety duplication)?**

Fully unique  
 Mostly unique  
 Partially unique  
 Fully duplicated elsewhere

**15. Origin of the germplasm accessions. Please indicate the percentage (%) of the total accessions that were:**

	Percentage (%)
Collected originally in your own country (national origin)	
Collected originally in your own region (regional origin)	
Introduced from another genebank or by a collecting mission abroad	
Other origin (e.g., university, private collection, etc.), please specify: _____	

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**16. Please describe any other aspects of your collection that you consider to be unique, of special importance, or of particular value (e.g., endemic wild species, heritage cultivars, indigenous landraces, ethnic identity, culinary uses, advanced genetic stocks, etc.)**

\_\_\_\_\_

**17. Please describe the main importance and future potential for use of your collection**

Current importance	
Future potential	

**EX SITU CONSERVATION and MANAGEMENT**

**18. Please indicate the proportion (%) of *Arachis* accessions maintained under the following storage conditions:**

(NOTE: If accessions are maintained under more than one storage condition, total of percentages may exceed 100%)

Short-term storage	
Medium-term storage	
Long-term storage	
Other	

**19. Please describe the storage facilities: Storage Facility (1)**

Type of facility	(e.g. warehouse, cold chamber, freezer, N tank, greenhouse, field collection)
Conservation method	(e.g. seed, <i>in vitro</i> culture, cryopreservation, whole plants, DNA)
Temperature (°C)	
Relative humidity	
Packing material	
Other	

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**20. Please describe the storage facilities: Storage Facility (2)**

Type of facility	(e.g. warehouse, cold chamber, freezer, N tank, greenhouse, field collection)
Conservation method	(e.g. seed, <i>in vitro</i> culture, cryopreservation, whole plants, DNA)
Temperature (°C)	
Relative humidity	
Packing material	

**21. Please describe the storage facilities: Storage Facility (3)**

Type of facility	(e.g. warehouse, cold chamber, freezer, N tank, greenhouse, field collection)
Conservation method	(e.g. seed, <i>in vitro</i> culture, cryopreservation, whole plants, DNA)
Temperature (°C)	
Relative humidity	
Packing material	

**22. What proportion (%) of the *Arachis* accessions have agro-morphological (phenotypic) characterization data available? \_\_\_\_\_%**

**23. Indicate the descriptors used for agro-morphological characterization:**

IBPGR/IPGRI crop-specific descriptors  
 FAO/Bioversity Multi-Crop Passport Descriptors (MCPD)  
 UPOV descriptors  
 USDA descriptors  
 Institute-specific descriptors  
 Other (please specify) \_\_\_\_\_

**24. What is the proportion (%) of *Arachis* accessions that have molecular or genotypic characterization data available? \_\_\_\_\_%**

**25. Has your *Arachis* collection been at least partially evaluated for biotic stresses?**

Yes  
 No  
 Don't know

If YES, for what proportion of the collection? \_\_\_\_\_%

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26. Has your *Arachis* collection been at least partially evaluated for abiotic stresses?

- Yes
- No
- Don't know

If YES, for what proportion of the collection? \_\_\_\_\_%

### QUALITY MANAGEMENT

27. Have you established a genebank management system, or written procedures and protocols for:

Acquisition? (including collecting, introduction, and exchange)	<input type="checkbox"/> Yes <input type="checkbox"/> No
Regeneration?	<input type="checkbox"/> Yes <input type="checkbox"/> No
Characterization?	<input type="checkbox"/> Yes <input type="checkbox"/> No
Storage and maintenance?	<input type="checkbox"/> Yes <input type="checkbox"/> No
Documentation?	<input type="checkbox"/> Yes <input type="checkbox"/> No
Germplasm health? (phytosanitary)	<input type="checkbox"/> Yes <input type="checkbox"/> No
Distribution?	<input type="checkbox"/> Yes <input type="checkbox"/> No
Safety duplication?	<input type="checkbox"/> Yes <input type="checkbox"/> No
Other? (please specify):	

28. If you do have genebank procedures and protocols in place, are you able to provide the Crop Trust with this information (i.e., provide a written copy)?

- Yes
- No
- Don't know

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29. Please describe your quality control activities

Activity	Frequency	Protocols / Methods
Germination testing		
Viability testing		
Health testing		
Other (please specify)		

30. Please indicate the proportion (%) of your *Arachis* collection that requires urgent regeneration (apart from the normal routine generation)

Wild species	
Landraces	
Obsolete improved varieties	
Modern improved varieties	
Breeding/research materials	
Unknown	
Other category (specify):	

31. Is the collection affected by diseases that can restrict the distribution of the germplasm?

- Yes, to a large extent
- Yes, to some extent
- No
- Don't know

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32. Please indicate the current and expected situation of your *Arachis* collection with respect to the following risk factors, where:

1 = high/good, 2 = adequate/moderate, 3 = not sufficient/bad, N/A = not applicable:

Risk Factors	Current Situation	Expected Situation in 2023
Funding for routine operations and maintenance		
Retention of trained staff		
Interest in PGR conservation by donors		
Genetic diversity in collections as needed by users/breeders		
Access to germplasm information (passport, characterization, evaluation)		
Active support and/or feedback from users		
Level of use by breeders		
Level of use by researchers		
Other risk factors (please specify):		

### SAFETY DUPLICATION

Safety duplication is defined as the storage of a duplicate/copy of an accession in another location for safety back-up as a protection against the loss of the original accession.

33. Are your collection's *Arachis* accessions safely duplicated in another genebank?

- Yes
- No
- Don't know

If YES please provide the information requested below.  
If NO, skip the following and Go to Next page.

34. If you answered YES to the previous question, please specify: (Safety Duplication 1)

Name of institute maintaining your safety duplicates	
Number of accessions	
Storage conditions (short-, medium-, or long-term)	

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Nature of the storage (e.g. black box, fully integrated into host collection, etc.)

35. If there is a second site for safety duplication, please specify: (Safety Duplication 2)

Name of institute maintaining your safety duplicates	
Number of accessions	
Storage conditions (short-, medium-, or long-term)	
Nature of the storage (e.g. black box, fully integrated into host collection, etc.)	

36. If there is a third site for safety duplication, please specify: (Safety Duplication 3)

Name of institute maintaining your safety duplicates	
Number of accessions	
Storage conditions (short-, medium-, or long-term)	
Nature of the storage (e.g. black box, fully integrated into host collection, etc.)	

37. Are there any constraints to duplicating the collection elsewhere outside your country?

- Yes
- No

If YES, please specify: \_\_\_\_\_

38. Are there *Arachis* accessions from other collections safety duplicated at your facilities?

- Yes
- No

If YES, please provide information on safety duplications at your genebank (below).  
If NO, Skip the following and Go to Next Section.

39. If accessions from other collections are safety duplicated at your genebank (1), please specify:

Name of holder of the original collection (1)	
Number of accessions	

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Storage conditions (Short-, medium-, long-term)	
Nature of the storage (e.g., black box; fully integrated into host collection; etc.)	

**40. If accessions from other collections are safety duplicated at your genebank (2), please specify:**

Name of holder of the original collection (2)	
Number of accessions	
Storage conditions (Short-, medium-, long-term)	
Nature of the storage (e.g., black box; fully integrated into host collection; etc.)	

**41. If accessions from other collections are safety duplicated at your genebank (3), please specify:**

Name of holder of the original collection (3)	
Number of accessions	
Storage conditions (Short-, medium-, long-term)	
Nature of the storage (e.g., black box; fully integrated into host collection; etc.)	

**IN SITU CONSERVATION**

*In situ* conservation refers to crop diversity that is preserved - either deliberately or fortuitously - in the native habitats where the material's special characteristics originally developed and continue to evolve. For wild *Arachis* species, *in situ* conservation takes place in natural populations occurring in protected areas or other relatively undisturbed ecosystems within the species' native range in South America. For cultivated peanut landraces, *in situ* conservation occurs on-farm, in traditional agroecosystems under the management of rural farmers whose ancestors have been selecting for preferred traits and attributes over generations. As material conserved *in situ* involves comparatively large populations that continue to actively evolve with their environment, the strategy is complementary to *ex situ* conservation methods.

**42. Ex situ-In situ linkages:** Please list and briefly describe any activities or programs that your genebank has been involved in that promote, enable, manage, or monitor the *in situ* (on-farm) conservation of peanut landraces. (e.g., community landrace registries; local seed systems; native seed fairs; restoration of ancestral varieties; participatory plant breeding, characterization & evaluation, etc.)

1.	
----	--

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2.	
3.	
4.	
5.	

**43. Please list the five most important obstacles you face in enabling, managing, or monitoring the *in situ* conservation of peanut landraces in your country. (e.g., lack of research interest, staffing, local partners, public awareness, policy constraints, etc.)**

1.	
2.	
3.	
4.	
5.	

**44. (ONLY for respondents in Argentina, Bolivia, Brazil, Paraguay and Uruguay): Please list the four most important obstacles you face to be able to more actively promote, manage, or monitor the *in situ* conservation status of wild *Arachis* populations in your country. (e.g., lack of staffing, local partners, public awareness, policy constraints, financial, etc.)**

1.	
2.	
3.	
4.	

**CONSERVATION RESEARCH ACTIONS, TARGETS, and CONSTRAINTS**

**45. Indicate the more important conservation research activities conducted by your genebank staff in the recent past, currently underway, or urgently needed. (e.g., collecting missions, core subsets, genotyping, safety duplication, etc.)**

	Activity	Status (past/underway/urgent)
1.		
2.		
3.		
4.		
5.		

**46. Briefly describe any past, recent, or planned germplasm collecting missions, the target area or region, the target taxa, and the number of samples collected or expected.**

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Year of mission	Target area or region	Target taxa	Number of samples collected or sought
(add rows as needed)			

**46. Please list the five most important constraints you face in the conservation and management of your *Arachis* collection. (e.g., financial, trained staff, research capacity, documentation, policy, infrastructure, etc.)**

1.	
2.	
3.	
4.	
5.	

**DOCUMENTATION and INFORMATION MANAGEMENT**

**47. Do you use a searchable electronic platform (database) for storing and retrieving accession-level data?**

Yes  
 No  
 Partly

If YES, what is the name of the software is used? \_\_\_\_\_

**48. The information database provides accession-level data about (check all that apply):**

Passport  
 Taxonomy  
 Characterization  
 Evaluation  
 Genotypes  
 Images  
 Storage conditions, germination, etc.  
 Distribution

**49. The accession-level information is (check all that apply):**

Public  
 Private  
 Available only upon request from the curator

**50. The accession-level information is publicly accessible through the internet?**

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Yes  
 No  
 Partly

If YES, please provide the web address: \_\_\_\_\_

**51. Please specify the proportion (%) of accessions with:**

Passport data: \_\_\_\_ %  
Geo-referenced data \_\_\_\_ %  
Characterization data: \_\_\_\_ %  
Evaluation data \_\_\_\_ %  
Storage conditions: \_\_\_\_ %  
Germination data \_\_\_\_ %

**52. Are data from your collection included in other, external databases?**

Yes  
 No  
 Partly

If YES or PARTLY, please indicate the database(s): \_\_\_\_\_

**ACCESS, DISTRIBUTION and USE of *Arachis* GENETIC RESOURCES**

**53. Do you distribute accessions from your collection?**

Yes  
 No  
If NO, why not? \_\_\_\_\_

**54. Accessions from the collection can be used by others outside the Institute subject to the terms and conditions of:**

The Nagoya Protocol for the CBD  
 The International Treaty on PGR for Food and Agriculture (ITPGRFA)  
 Freely distributed without any terms or conditions  
 Institutional MTA or other bi-lateral agreement

Could the agreement be shared if requested?

Yes  
 No

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55. Do you keep records of the germplasm distribution?

Yes  
 No

56. What kind of users within your country have received germplasm from you? (Please estimate the proportion (%) of total distribution over the past 5 years.)

	%
Breeding programs – public sector	
Breeding programs – private sector	
Academic researchers and students	
Other genebank curators	
Farmers and farmer organizations	
NGOs	
Other	

57. Of the materials distributed outside your country in the past 5 years, please indicate the proportion (%) of total number of accessions distributed to the following users:

	%
Breeding programs – public sector	
Breeding programs – private sector	
Academic researchers and students	
Other genebank curators	
Farmers and farmer organizations	
NGOs	
Other	

58. Are germplasm materials available in sufficient QUANTITY for distribution?

	Yes	No	Partially	Don't know
Seeds				
<i>In vitro</i> material				
Live plants				
Cryopreserved material				

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59. Are germplasm materials available in sufficient HEALTH for distribution?

	Yes	No	Partially	Don't know
Seeds				
<i>In vitro</i> material				
Live plants				
Cryopreserved material				

60. What proportion (%) of the collection is currently AVAILABLE for distribution...?

Nationally	
Regionally	
Internationally	

61. What is the total number of accessions that are typically distributed annually? (average of the last 3 years)

Nationally	
Regionally	
Internationally	

62. How do you expect your distributions to change over the next 3-5 years?

	Increasing	No change	Decreasing	Don't know
Nationally				
Regionally				
Internationally				

63. How do you inform potential users about the availability of accessions and their respective data in your collection?

64. If no material is being distributed outside your country, could you tell us why?

65. Do you have adequate procedures in place for:

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Phytosanitary certification?

Yes  
 No

Packaging?

Yes  
 No

Shipping?

Yes  
 No

Other? (please specify) \_\_\_\_\_

66. Do you set specific conditions on the AMOUNT OF SEEDS for distribution?

Yes  
 No

If YES, please specify: \_\_\_\_\_

67. What are the three (3) most important factors limiting the use of the materials maintained in your collection?

1. \_\_\_\_\_

2. \_\_\_\_\_

3. \_\_\_\_\_

68. Do you charge fees for the following services?

	Yes	No
The cost of accessions		
The cost of shipment		

If YES, please describe the fee policy and indicate the fee amount(s): \_\_\_\_\_

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69. Do you have any restrictions on who can receive materials?

Yes  
 No

If YES, please describe this restriction. \_\_\_\_\_

\_\_\_\_\_

\_\_\_\_\_

**GAPS and VULNERABILITY**

Gaps in a germplasm collection's diversity can be perceived or determined by genetic, taxonomic, ecogeographic analyses of the existing materials to determine what may be lacking, to make the collection more comprehensive and better serve the needs of germplasm users. Other specific traits, such as sources of heat, drought or disease resistance, may also serve as the basis for identifying gaps in a collection. Gaps are typically filled through targeted plant collecting missions, or through germplasm exchanges with other genebanks.

70. In general terms, in which of the following categories would you place your collection in terms of geographic representation? (check all that apply)

	Geographic coverage	Which countries?	Which regions?
Good national /multinational coverage?			
Good regional coverage			
Good hemispheric coverage			
Good global coverage			

71. What are the known or perceived gaps in your *Arachis* collection?

Type of Gap	Indicate the specific elements lacking in the collection
Genetic gaps	
Taxonomic gaps	
Ecogeographic gaps	
Other gaps	

72. How do you plan to fill these gaps, and when?

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Specific Gap	How the specific gaps will be filled	When
Genetic		
Taxonomic		
Ecogeographic		
Other		

73. What do you consider to be the 5 most important vulnerabilities or threats to your *Arachis* collection?

- 1.
- 2.
- 3.
- 4.
- 5.

### FUNDING

74. Does your organization provide most or all of the recurrent costs for maintaining the germplasm collection?

- Yes  
 No

75. How has the budget for conservation of the collection changed in the last 5 years?

- Stable  
 Increasing  
 Decreasing

If Decreasing, what are the sources of funds used to make up for the shortfall?

\_\_\_\_\_

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### NETWORKS and other COLLABORATIVE ACTIVITIES

This section focuses on any collaborations or partnerships you have with other genebanks, breeders (in the public or private sectors), research institutions, academia, farmers' organizations and/or NGOs in terms of peanut germplasm diversity, conservation and use. Please indicate your participation in any national, regional or global networks or initiatives that have current or potential significance for the establishment of a global system for peanut conservation and use.

76. Does your genebank collaborate with other genebanks and/or breeders in the public and/or private sector on aspects of peanut germplasm management (regeneration, characterization, preliminary evaluation), apart from safety duplication?

- Yes  
 No

If YES, please provide information on your collaboration(s) (below).

If NO, Skip the following and Go to Next Section.

#### 77. Information on Collaboration (1)

A. Name of institution: \_\_\_\_\_

Location: \_\_\_\_\_

Type (public or private) \_\_\_\_\_

B. Area of collaboration

- Regeneration  
 Characterization  
 Preliminary evaluation  
 Other

C. Type of collaboration

- National  
 Regional  
 International

D. Starting date: \_\_\_\_\_

Frequency of collaboration

- Constant  
 Frequent  
 Annually  
 Once every few years  
 Seldom

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#### 78. Information on Collaboration (2)

A. Name of institution: \_\_\_\_\_

Location: \_\_\_\_\_

Type (public or private) \_\_\_\_\_

B. Area of collaboration

- Regeneration  
 Characterization  
 Preliminary evaluation  
 Other

C. Type of collaboration

- National  
 Regional  
 International

D. Starting date: \_\_\_\_\_

Frequency of collaboration

- Constant  
 Frequent  
 Annually  
 Once every few years  
 Seldom

#### 79. Information on Collaboration (3)

A. Name of institution: \_\_\_\_\_

Location: \_\_\_\_\_

Type (public or private) \_\_\_\_\_

B. Area of collaboration

- Regeneration  
 Characterization  
 Preliminary evaluation  
 Other

C. Type of collaboration

- National  
 Regional  
 International

D. Starting date: \_\_\_\_\_

Frequency of collaboration

- Constant  
 Frequent  
 Annually  
 Once every few years  
 Seldom

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80. Do you collaborate in (a) network(s) of peanut/groundnut germplasm holders and/or users?

- Yes  
 No  
 Don't know

If YES, please provide information on your collaboration(s) (below).

If NO, Skip the following and Go to Next page.

#### 81. Information on Peanut/Groundnut Network (1)

A. Name of network

B. Reasons for participation

C. Network objectives

D. National, Regional, or Worldwide

#### 82. Information on Peanut/Groundnut Network (2)

A. Name of network

B. Reasons for participation

C. Network objectives

D. National, Regional, or Worldwide

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**FINAL CONSIDERATIONS**

83. Please add any other information, comments or recommendations you may have regarding your *Arachis* collection, this survey, and/or the Global Strategy for the Conservation of Peanut Diversity.

You have successfully completed the peanut survey questionnaire

Thank you very much!

If you have any questions about this survey or the global peanut strategy, please contact:

David E. Williams  
[reddog.williams@gmail.com](mailto:reddog.williams@gmail.com)

This supplementary document allows us to collect more detailed information than is possible within the online survey platform. Please be so kind as to fill this table out and upload it within the survey in question 13.

13. Please record each of the wild *Arachis* species in your collection, with the number of accessions conserved, and the percentage (%) of those accessions conserved by the different storage methods:

NOTE: If accessions are conserved by more than one storage method, total percentages may exceed 100%

Species name	Number of Accessions	Seeds in Cold Storage (%)	Plants in Greenhouse/Screenhouse (%)	Plants in Field Plots (%)	In vitro Tissue Culture (%)
(example: <i>A. pintoi</i> )					
-- add additional rows as needed --					
<b>Total wild <i>Arachis</i> accessions →</b>					

46. Briefly describe any past, recent, or planned germplasm collecting missions, the target area or region, the target taxa, and the number of samples collected or expected.

Year of mission	Target area or region	Target taxa	Number of samples collected or sought
(add rows as needed)			

### Annex 3. Organizations that responded to the online survey

INSTCODE	Name of Organization	Acronym	City/Town	State/Province	Country
ARG1211	Instituto Nacional de Tecnología Agropecuaria	INTA	Manfredi	Córdoba	Argentina
ARG1133	Instituto de Botánica del Nordeste (UNNE-CONICET)	IBONE	Corrientes	Corrientes	Argentina
AUS167	Australian Pastures Genebank (SARDI)	APG	Adelaide	South Australia	Australia
BENIN*	Ecole Nationale Supérieure des Biosciences et Biotechnologies Appliquées	ENSBBA	Dassa	Collines	Benin
BFA006	Institut d'Études et de Recherches Agricoles	INERA	Bobo-Dioulasso	Houet	Burkina Faso
BGR001	Institute of Plant Genetic Resources	IPGR	Sadovo	Plovdiv	Bulgaria
BOL316	Instituto Nacional de Innovación Agropecuaria y Forestal	INIAF	La Paz	Murillo	Bolivia
BRA002	Empresa Brasileira de Pesquisa Agropecuária	EMBRAPA	Brasília	Distrito Federal	Brazil
BRA006	Instituto Agronómico de Campinas	IAC	Campinas	São Paulo	Brazil
CHN003	Oil Crops Research Institute, Chinese Academy of Agricultural Sciences	OCRI-CAAS	Wuhan	Hubei	P. R. China
COL003	Centro Internacional de Agricultura Tropical	CIAT	Cali	Valle del Cauca	Colombia
ECU023	Departamento Nacional de Recursos Fitogenéticos (INIAP)	DENAREF	Quito	Pichincha	Ecuador
IND002	International Crop Research institute for the Semi-Arid Tropics	ICRISAT	Hyderabad	Telangana	India
PER773	Instituto Nacional de Innovación Agraria	INIA	Lima	Lima	Peru
PRT001	Banco Português de Germoplasma Vegetal (INIAV)	INIAV-BPGV	Braga	Norte	Portugal
PRY008	Centro de Investigación Capitán Miranda (IPTA)	IPTA-CICM	Capitán Miranda	Itapúa	Paraguay
PRY027	Facultad de Ciencias Agrarias, Universidad Nacional de Asunción	FCA-UNA	San Lorenzo	Central	Paraguay
PRY037	Centro de Investigación para la Agricultura Familiar (IPTA)	IPTA-CIAF	Choré	San Pedro	Paraguay
SDN002	Agricultural Plant Genetic Resources Conservation and Research Centre	ARC-APGRC	Wad Medani	Gezira	Sudan
SEN002	Centre National de la Recherche Agronomique (ISRA)	ISRA-CNRA	Bambey	Bambey	Senegal
SWZ015	Eswatini National Plant Genetic Resources Centre	NPGRC	Malkerns	Manzini	Eswatini
TWN001	The World Vegetable Center	AVRDC	Tainan	Taiwan	Taiwan
URY013	Facultad de Agronomía - Universidad de la Republica	UDELAR	Montevideo	Montevideo	Uruguay
USA016	USDA-ARS Plant Genetic Resources Conservation Unit	USDA	Griffin	Georgia	USA
USA317	North Carolina State University	NCSU	Raleigh	North Carolina	USA
USA520	Texas A&M AgriLife Research	TAMU	Stephenville	Texas	USA

\*Formal INSTCODE not yet assigned.

## Annex 4. Selected metrics for peanut (Genus *Arachis*) and soybean (as comparison)

This annex was written by Dr. Felix Frey, International Consultant, Global Crop Diversity Trust

Khoury et al. (2021) compiled a comprehensive 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 introduce five normalized reproducible indicators that provide an evidence base to prioritize actions with respect to conservation and use of crop genetic resources for food and agriculture. The indicators enclose metrics associated with the USE of a crop (Global importance), the INTERDEPENDENCE between countries with respect to genetic resources, the DEMAND of researchers for genetic resources, the SUPPLY of germplasm by gene banks and the SECURITY of germplasm conservation. The indicator results are visualized publicly available on an [interactive online website](#). To generate the five indicators, Khoury et al. 2021 collected a comprehensive dataset from multiple sources. In the following, we don't 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 numbers into context, we compare peanuts with soybeans. Both crops are globally important legumes. *Arachis* and *Arachis hypogaea* are the genus and species name of peanut, respectively, *Glycine* and *Glycine max* the genus and species name of soybean.

The metrics for "Global production", "Food supply" and "Quantity exported globally" from the indicator domain "Crop use" are annual average values drawn from FAOSTAT data (FAOSTAT 2019) between the years 2010–2014. The percentage of countries producing and consuming (being supplied with) the crop is calculated as the number of countries, where the respective crop is within the top 95% of most important crops divided by the number of countries which report respective numbers (can be different between metrics and crops). The global production of peanuts is at about 43 million tons annually, which is 17% of the global soybean production (about 261 M t). The quantity of food supply by peanuts, i.e. the average global consumption is with about 6 g/cap/day at about 45% of global soybean supply as food source (14 g/cap/day). Peanut food supply is thus relatively high, compared to its production, if related to soybean production and food supply. Considering low global production of peanut compared to soybeans, the percentage of countries producing peanuts is with 53% relatively high, where soybean is produced in only 44% of the worlds' countries. Peanuts are consumed in 97%

of all countries in the world, which is similar to the percentage of countries consuming soybean products (98%). Both, peanuts and soybeans are internationally traded crops. About 8% of total peanut production is being exported (3.6 M t annually). However, exports play a much larger role for soybean, putatively due to its global use as protein feed for livestock. About 66% of global soybean production are exported corresponds to a volume of 171.5 M t of soybeans.

The crop use metrics with respect to research were assessed by manual search on google scholar, searching for the respective genus or species in the titles of publications, including patents and citations, between the years 2009 and 2019 (Khoury et al. 2021). Google scholar search hits represent importance with respect to scientific interest in a crop. The *Arachis* genus is found in 5,410 publication titles, which is about one third of the amount of publication titles which include the soybean genus *Glycine*. Publication numbers including the species names *A. hypogaea* and *G. max* amount to 4,000 for the case of *A. hypogaea*, and to 9.460 for *Glycine max*. Peanut research receives thus about 33–50% of attention as compared to soybean research. If related to comparison of production, peanut research is, thus, overrepresented when compared to soybean research.

Khoury et al. (2021) defined interdependence as a measure for the degree of dependence of the global cultivation and use of a certain crop from germplasm present at the primary centers of diversity of the respective crop. Primary centers of diversity are not represented by countries, but by 23 agroecological zones (Khoury et al. 2016), as crop diversity does not follow national borders but rather climatic and agroecological boundaries. Interdependence is high in crops which originate from a small area and are cultivated and used globally. For production, interdependence is calculated by dividing a crops' production outside of the primary center of diversity by the global production. If all production would be outside the primary center of diversity, interdependence would be 100%. For food supply, interdependence is calculated by dividing the food supply by the world average. Food supply outside can be higher than inside of primary regions of diversity and thus also higher than the global mean. Therefore, interdependence with respect to food supply can be above 100%. The primary center of diversity of peanut is located in tropical South America. As most of peanuts are produced in Asia or Africa, interdependence of global production is with

99% comparably high. Although soybean originates from East Asia and a great part of soybeans are produced in the Americas, China produces still a big share of soybean. This is reflected in the relatively lower interdependence value of 90% of soybean production compared to peanut production. Interdependence of food supply of peanut per capita is, with 103% even higher than interdependence of production, meaning that a very small amount of peanuts is consumed in its primary center of diversity. By contrast interdependence of food supply for soybean is, with 85 % relatively lower, which is putatively due to the fact, that consumption of soybean as a food is high in East Asia, whereas soybean produced in the Americas is rather used as animal feed.

Demand for germplasm is defined by two metrics (Khoury et al. 2021). First, by the number of distributions of accessions by gene banks, as an annual average between 2014 and 2017 drawn from the Plant Treaty Information System. Second, by the number of varieties released during the five years between 2014 and 2018, obtained from the [International Union for the Protection of New Varieties of Plants \(UPOV\)](#). There is a relatively high use of peanut germplasm reflected by the 6,988 peanut accessions per year distributed by gene banks, which represents about one third of yearly distributions of soybean accessions (25,813). However, this is in contrast to a very low development of peanut cultivars. Only 488 varieties of peanuts were released during a five-year period, which represents only 3 % of soybean varieties released in the same time period (17,390 varieties).

Khoury et al. (2021) illustrated the supply of germplasm with the number of accessions available in ex situ collections around the world, with respect to the crop genus and the most important species of the respective crop. Furthermore, Khoury et al. (2021) assessed the number of accessions (again with respect to genus and species) which were available under the [multilateral system \(MLS\) of the Plant Treaty](#). This was done first, directly, as notation (in MLS / not in MLS) in the public online databases [Genesys](#), [FAO WIEWS](#) and [GBIF](#). Secondly, availability of accessions was assessed via the status of the country where the institution was located which held the respective germplasm collection. If the country was contracting partner of the Plant Treaty, the respective accession was regarded as available via the MLS. According to databases, global ex situ collections count a total of 56,332 accessions of *Arachis* including 53,973 accessions of the species *A. hypogaea*. These peanut collections account for about 57% of global soybean collections with 99,054 *Glycine* and 90,193 *G. max* accessions. None of the peanut accessions is available under the MLS, stated directly in respective databases, in contrast 16 % of soybean accessions, which are available directly under

MLS. Neither peanut nor soybean are listed in Annex I of the Plant Treaty. This is why none of the peanut and soybean accessions is available indirectly by matching institute countries with party status.

Security of germplasm conservation is represented here with two metrics, the safety duplication status at the Svalbard Global Seed Vault (SGSV) and the equality of global distribution with respect to several crop use metrics. The numbers of accessions safety duplicated with respect to genus and species were drawn from the [website of the SGSV](#) and divided by the total number of accessions stored in global ex situ collections (see paragraph above), resulting in the percentage of safety duplicated germplasm. To represent the equality of distribution across different agroecological 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 is the most commonly used inequality index (Gini index, 2008), foremostly known for the quantification of global income inequality. The 1-Gini index, presented here, ranges from 0 to 1, where 0 reflects very unequal distribution across world regions, 1 would represent a completely equal global distribution of the respective metric across the worlds' regions. It reflects the security of crop cultivation and use, where e.g. small indices of production and thus geographical restriction go hand in hand with a higher vulnerability of supply, e.g. in cases of natural disasters. Regarding plant genus and plant species, respectively, 23% and 24%, of both, peanut and soybean accessions are safety duplicated at SGSV. Equality of the distribution across the worlds' regions with respect to global production of peanut is, with 0.03, higher than equality of distribution of soybean production (0.01). This is in line with the higher percentage of countries in the world producing a significant amount of peanuts, compared to soybean, indicated previously. For equality of the distribution of food supply, there is a more consistent image. Food supply of peanut is about as equally distributed throughout the world with 0.17, compared to a value of 0.18 for soybean.

## Literature

- [FAOSTAT](#) (2019) Statistics for 2010–2014. Accessed 2019.
- [Gini Index](#). In: The Concise Encyclopedia of Statistics (2008) Springer, New York, NY.
- Khoury, C.K., Sotelo, S., Amariles, D., Guarino, L., and 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.M., Wiersema, J. H., Dempewolf, H., Sotelo S., Ramírez-Villegas, J., Castañeda-Álvarez, N. P., Fowler, C., Jarvis, A., Rieseberg, L. H., Struik, P. C. (2016). Origins of food crops connect countries worldwide. *Proceedings of the Royal Society B: Biological Sciences*, 283(1832), 20160792.

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

**Table 1** Selected metrics collected by Khoury et al. 2021 for peanuts and soybean, subdivided by indicator domain

Metric	Peanuts	Soybean	Peanuts / Soybean
<b>Crop use</b>			
Global production [tons]	43,188,302	261,275,656	17%
Food supply (Amount consumed) [g/capita/day]	6	14	45%
Percentage of countries producing crop *	53%	44%	121%
Percentage of countries consuming (being supplied with) crop *	97%	98%	99%
Quantity exported globally [t]	3,661,271	171,567,735	2%
Number of publications between 2009-2019, including patents and citations, searching title of publication (Google scholar search hits) for genus **	5,410	15,700	34%
Number of publications between 2009-2019, including patents and citations, searching title of publication (Google scholar search hits) for species ***	4,000	9,460	42%
<b>Interdependence</b>			
Interdependence of global production from germplasm from primary centers of diversity [0-1] ****	99%	90%	110%
Interdependence of global food supply from germplasm from primary centers of diversity [0-1] ****	103%	85%	122%
<b>Demand</b>			
Accessions distributed from gene banks (Annual average 2014-2017)	6,988	25,813	27%
Variety releases in 5 years (2014-2018)	488	17,390	3%
<b>Supply</b>			
Number of accessions in <i>ex situ</i> collections of genus **	56,332	99,054	57%
Number of accessions in <i>ex situ</i> collections of species ***	53,973	90,193	60%
Accessions of the genus ** available through Multilateral System (MLS) directly noted in databases [%]	0%	16%	
Accessions of the species *** available through Multilateral System (MLS) directly noted in databases [%]	0%	16%	
Accessions of the genus ** available through Multilateral System (MLS) indirectly by matching institute countries with party status [%]	0%	0%	
Accessions of the species *** available through Multilateral System (MLS) indirectly by matching institute countries with party status [%]	0%	0%	
<b>Security</b>			
Accessions of genus ** safety duplicated in Svalbard Global Seed Vault [%]	23%	23%	
Accessions of species *** safety duplicated in Svalbard Global Seed Vault [%]	24%	24%	
1-GINI index for equality of production across the world [0-1] *****	0.03	0.01	196%
1-GINI index for equality of food supply across the world [0-1] *****	0.17	0.18	93%

\* 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)

\*\* Peanuts: *Arachis*; Soybeans: *Glycine*

\*\*\* Peanuts: *Arachis hypogaea*; Soybeans: *Glycine max*

\*\*\*\* 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



## Annex 5. List of wild *Arachis* accessions at USA016

Taxon	Accessions
<i>Arachis appressipila</i>	5
<i>Arachis archeri</i>	3
<i>Arachis batizocoi</i>	14
<i>Arachis benensis</i>	4
<i>Arachis benthamii</i>	1
<i>Arachis burchellii</i>	4
<i>Arachis burkartii</i>	1
<i>Arachis cardenasii</i>	13
<i>Arachis chiquitana</i>	2
<i>Arachis correntina</i>	11
<i>Arachis cruziana</i>	2
<i>Arachis cryptopotamica</i>	2
<i>Arachis dardani</i>	7
<i>Arachis decora</i>	3
<i>Arachis diogoi</i>	5
<i>Arachis duranensis</i>	46
<i>Arachis glabrata</i>	43
<i>Arachis glabrata</i> var. <i>glabrata</i>	39
<i>Arachis glabrata</i> var. <i>hagenbeckii</i>	11
<i>Arachis glandulifera</i>	5
<i>Arachis gregoryi</i>	1
<i>Arachis guaranitica</i>	1
<i>Arachis helodes</i>	6
<i>Arachis hermannii</i>	4
<i>Arachis herzogii</i>	1
<i>Arachis hoehnei</i>	4
<i>Arachis hybr.</i>	50
<i>Arachis ipaensis</i>	1
<i>Arachis kempff-mercadoi</i>	5
<i>Arachis kretschmeri</i>	4
<i>Arachis kuhlmannii</i>	19
<i>Arachis lignosa</i>	1
<i>Arachis lutescens</i>	2

Taxon	Accessions
<i>Arachis macedoi</i>	2
<i>Arachis magna</i>	5
<i>Arachis major</i>	10
<i>Arachis matiensis</i>	9
<i>Arachis microsperma</i>	3
<i>Arachis monticola</i>	7
<i>Arachis nitida</i>	1
<i>Arachis palustris</i>	1
<i>Arachis paraguariensis</i>	12
<i>Arachis paraguariensis</i> subsp. <i>capibarensis</i>	2
<i>Arachis paraguariensis</i> subsp. <i>paraguariensis</i>	10
<i>Arachis pflugeae</i>	2
<i>Arachis pintoii</i>	26
<i>Arachis porphyrocalyx</i>	1
<i>Arachis praecox</i>	1
<i>Arachis pseudovillosa</i>	4
<i>Arachis pusilla</i>	11
<i>Arachis repens</i>	5
<i>Arachis retusa</i>	1
<i>Arachis rigonii</i>	2
<i>Arachis seridoensis</i>	1
<i>Arachis simpsonii</i>	6
<i>Arachis</i> spp.	42
<i>Arachis stenophylla</i>	2
<i>Arachis stenosperma</i>	22
<i>Arachis trinitensis</i>	1
<i>Arachis triseminata</i>	2
<i>Arachis valida</i>	4
<i>Arachis veigae</i>	30
<i>Arachis villosa</i>	9
<i>Arachis villosulicarpa</i>	4
<i>Arachis williamsii</i>	1
<b>Total</b>	<b>559</b>

## Annex 6. Historical *Arachis* collecting missions reported by USDA-ARS-PGRCU, Griffin, Georgia (USA016)

Year of Mission	Countries Visited	No. of Accessions	Cultivated <i>Arachis</i>	Wild <i>Arachis</i> species
1936	Argentina, Brazil, Mexico, Paraguay, Uruguay	97	<i>A. hypogaea</i>	<i>A. glabrata</i> , <i>A. glabrata</i> var. <i>hagenbeckii</i> , <i>A. marginata</i>
1947	Argentina, Bolivia	9	<i>A. hypogaea</i>	---
1959	Argentina, Bolivia, Brazil, Paraguay	39	<i>A. hypogaea</i>	<i>A. cardenasii</i> , <i>A. correntina</i> , <i>A. diogoi</i> , <i>A. duranensis</i> , <i>A. glabrata</i> var. <i>glabrata/hagenbeckii</i> , <i>A. hybrids</i> , <i>A. paraguariensis</i> subsp. <i>paraguariensis</i> , <i>A. pseudovillosa</i>
1961	Paraguay	2	---	<i>A. major</i> , <i>A. paraguariensis</i>
1967	Brazil	3	---	<i>A. dardani</i> , <i>A. pintoii</i> , <i>A. triseminata</i>
1968	Argentina, Brazil, Paraguay	80	<i>A. hypogaea</i>	<i>A. glabrata</i> var. <i>glabrata</i> , <i>A. major</i> , <i>A. pintoii</i> , <i>A. repens</i> , <i>A. spp.</i>
1976	Brazil	25	---	<i>A. appressipila</i> , <i>A. benthamii</i> , <i>A. cryptopotamica</i> , <i>A. diogoi</i> , <i>A. glabrata</i> var. <i>glabrata</i> , <i>A. helodes</i> , <i>A. hoehnei</i> , <i>A. kretschmeri</i> , <i>A. kuhlmannii</i> , <i>A. lutescens</i> , <i>A. matiensis</i> , <i>A. major</i> , <i>A. paraguariensis</i> subsp. <i>paraguariensis</i> , <i>A. spp.</i> , <i>A. subcoriacea</i> , <i>A. valida</i>
1977	Argentina, Bolivia, Brazil, Paraguay	215	<i>A. hypogaea</i> var. <i>fastigiata/hypogaea</i>	<i>A. archeri</i> , <i>A. batizocoi</i> , <i>A. correntina</i> , <i>A. diogoi</i> , <i>A. duranensis</i> , <i>A. glabrata</i> var. <i>glabrata/hagenbeckii</i> , <i>A. glandulifera</i> , <i>A. ipaensis</i> , <i>A. kempff-mercadoid</i> , <i>A. magna</i> , <i>A. major</i> , <i>A. matiensis</i> , <i>A. monticola</i> , <i>A. paraguariensis</i> subsp. <i>capibarensis/paraguariensis</i> , <i>A. pseudovillosa</i> , <i>A. stenophylla</i> , <i>A. valida</i>
1979	Bolivia	32	<i>A. hypogaea</i> var. <i>fastigiata/hypogaea</i>	<i>A. benensis</i> , <i>A. kempff-mercadoid</i>
1980	Argentina, Bolivia, Peru	176	<i>A. hypogaea</i> var. <i>hypogaea/fastigiata</i>	<i>A. cardenasii</i> , <i>A. chiquitana</i> , <i>A. correntina</i> , <i>A. cruziana</i> , <i>A. duranensis</i> , <i>A. herzogii</i> , <i>A. matiensis</i> , <i>A. simpsonii</i> , <i>A. spp.</i>
1981	Bolivia, Brazil, Peru	227	<i>A. hypogaea</i> var. <i>hypogaea/fastigiata</i>	<i>A. diogoi</i> , <i>A. glabrata</i> , <i>A. glabrata</i> var. <i>glabrata</i> , <i>A. gregoryi</i> , <i>A. helodes</i> , <i>A. kuhlmannii</i> , <i>A. lutescens</i> , <i>A. matiensis</i> , <i>A. praecox</i> , <i>A. spp.</i> , <i>A. tuberosa</i>
1982	Argentina, Brazil	16	<i>A. hypogaea</i> var. <i>fastigiata</i>	<i>A. pintoii</i> , <i>A. pusilla</i>
1983	Argentina, Bolivia, Brazil, Ecuador	274	<i>A. hypogaea</i> , <i>A. hypogaea</i> var. <i>aequatoriana/fastigiata/hypogaea</i>	<i>A. burkartii</i> , <i>A. duranensis</i> , <i>A. glabrata</i> , <i>A. stenosperma</i>
1984	Brazil	27	<i>A. hypogaea</i> , <i>A. hypogaea</i> var. <i>fastigiata/hypogaea</i>	---
1985	Brazil, Peru	61	<i>A. hypogaea</i> , <i>A. hypogaea</i> subsp. <i>fastigiata</i> , <i>A. hypogaea</i> var. <i>fastigiata/hirsuta/hypogaea</i>	---
1987	Brazil	4	<i>A. hypogaea</i> var. <i>fastigiata/peruviana</i>	---
1989	Bolivia	10	<i>A. hypogaea</i> var. <i>fastigiata/peruviana</i>	---
1990	Bolivia, Brazil	6	<i>A. hypogaea</i> var. <i>fastigiata/hypogaea/peruviana</i>	<i>A. trinitensis</i> , <i>A. williamsii</i>
1992	Bolivia, Brazil, Mexico	35	<i>A. hypogaea</i> var. <i>fastigiata/hirsuta/hypogaea</i>	---
1993	Mexico	11	<i>A. hypogaea</i> subsp. <i>hypogaea</i> , <i>A. hypogaea</i> var. <i>fastigiata</i>	---
1994	Bolivia	28	<i>A. hypogaea</i> var. <i>hypogaea</i>	<i>A. batizocoi</i> , <i>A. cardenasii</i> , <i>A. cruziana</i> , <i>A. duranensis</i> , <i>A. krapovickasii</i> , <i>A. spp.</i>
1995	Brazil, Ecuador	115	<i>A. hypogaea</i> , <i>A. hypogaea</i> subsp. <i>fastigiata/hypogaea</i> , <i>A. hypogaea</i> var. <i>aequatoriana/fastigiata/hirsuta/peruviana</i>	<i>A. helodes</i> , <i>A. matiensis</i> , <i>A. simpsonii</i> , <i>A. spp.</i>

Year of Mission	Countries Visited	No. of Accessions	Cultivated <i>Arachis</i>	Wild <i>Arachis</i> species
1996	Ecuador	100	<i>A. hypogaea</i> , <i>A. hypogaea</i> subsp. <i>fastigiata</i> , <i>A. hypogaea</i> var. <i>aequatoriana</i> / <i>fastigiata</i> / <i>hirsuta</i> / <i>hypogaea</i> / <i>peruviana</i>	---
1997	Guatemala	34	<i>A. hypogaea</i> var. <i>aequatoriana</i> / <i>fastigiata</i> / <i>hirsuta</i> / <i>hypogaea</i> / <i>peruviana</i> / <i>vulgaris</i>	---
1999	Guatemala	22	<i>A. hypogaea</i> var. <i>fastigiata</i> / <i>hirsuta</i> / <i>hypogaea</i> / <i>peruviana</i> / <i>vulgaris</i>	---
2002	Paraguay	86	<i>A. hypogaea</i> , <i>A. hypogaea</i> var. <i>fastigiata</i> / <i>hypogaea</i>	<i>A. batizocoi</i> , <i>A. correntina</i> , <i>A. duranensis</i> , <i>A. glabrata</i> , <i>A. microsperma</i> , <i>A. paraguariensis</i> , <i>A. pseudovillosa</i> , <i>A. spp.</i>
2003	Paraguay	28	<i>A. hypogaea</i>	<i>A. glabrata</i> , <i>A. paraguariensis</i> , <i>A. spp.</i>
2007	Paraguay	11	---	<i>A. glabrata</i> , <i>A. major</i> , <i>A. microsperma</i> , <i>A. nitida</i> , <i>A. paraguariensis</i> , <i>A. pflugeae</i>



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