GLOBAL STRATEGY FOR THE CONSERVATION AND USE OF *VIGNA*

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Global Strategy for the Conservation and Use of *Vigna*

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COVER

Bambara groundnuts. Photo: Sacha de Boer/Oxfam Novib

DISCLAIMER

This report aims to provide a framework for the efficient and effective *ex situ* conservation of globally important collections of *Vigna* crops and their wild relatives. The Crop Trust considers this document to be an important framework for guiding the allocation of its resources. However, the Crop Trust does not take responsibility for the relevance, accuracy or completeness of the information in this document and does not commit to funding any of the priorities identified. This strategy document (dated 31 March 2023) is expected to continue to evolve and will be updated as and when circumstances change, or new information becomes available.

NOTE ABOUT THE ESTIMATED NUMBERS OF ACCESSIONS PRESENTED IN THE STRATEGY

The numbers of accessions presented in the text and tables of this strategy are the best estimates the authors were able to make at the time of writing based on the data available and the methods used. Such estimates can differ depending on the sources of data and their completeness, the time of the analyses, and the assumptions made in carrying out the analyses.

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緑豆

Vigna radiata (L.) R.Wilczek. Source: *Japanese agriculture in the early 19th century* (17930-1804)

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Vigna unguiculata Sesquipedalis Group, Kariyavattam, Trivandrum. Photo: Vinayaraj/Wikimedia Commons


Various varieties of *Vigna unguiculata*.
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EXECUTIVE SUMMARY

The genus *Vigna* includes species cultivated mainly in tropical and subtropical climates and belongs to the order Fabales and the family Fabaceae (which comprises nearly 20,000 species). More than 100 wild species are reported under the genus *Vigna*, and at present 10 domesticated species are cultivated as a vegetable or grain legume crop for human consumption. Among these cultivated *Vigna* species, mungbean (*Vigna radiata* (L.) Wilczek), urdbean (*Vigna mungo* (L.) Hepper), adzuki bean (*Vigna angularis* (Willd.) Ohwi & Ohashi), moth bean (*Vigna aconitifolia* (Jacq.) Maréchal), rice bean (*Vigna umbellata* (Thunb.) Ohwi & Ohashi), minni payaru (*Vigna stipulacea* Kuntze), creole bean (*Vigna reflexo-pilosa* Hayata) and tuber cowpea (*Vigna vexillata* (L.) A. Rich.) are mainly cultivated in Asia, whereas cowpea (*Vigna unguiculata* (L.) Walp) and Bambara groundnut (*Vigna subterranea* (L.) Verdc.) are predominantly cultivated in Africa. The *Vigna* germplasm collections maintained in different genebanks across the world harbor novel genetic resources for research and crop improvement. We evaluated the current conservation and use of *Vigna* genetic resources with the aim to develop a strategy document for future reference. First, we searched two of the global databases, i.e., Genesys and the Food and Agriculture Organization World Information and Early Warning System (FAO-WIEWS), to evaluate the existing *Vigna ex situ* collections. As a result, we found 129,903 *Vigna* accessions in global genebanks, wherein *V. unguiculata* has the largest number of accessions (46,767).

A survey on *Vigna* was sent to 30 collection holders identified from the databases. The collection holders were asked to complete an online survey on the status and challenges of their collections. We received responses from 21 genebanks, which were all included in our analyses. Most of the genebanks that responded are governmental bodies (76%), while the others are non-governmental organizations (NGOs) (19%) and non-departmental government bodies (5%). On the basis of the results of the survey, we recognize that there are numerous challenges associated with the sustainability of the conservation and use of *Vigna* crop diversity.

The overall objective of the proposed strategy is to outline a plan for the effective conservation of the diversity of *Vigna* crops and their wild relatives. This global strategy suggests several key aims for the years to come:

1. Further develop and expand the prevailing worldwide collaborations with the aim to conserve a global *Vigna* collection and make information available across different genebanks with an emphasis on harmonizing and maintaining all collections under one platform.
2. Promote regeneration and safety duplication of collections through collaboration with research and breeding institutes.
3. Genebanks and other institutes (such as universities and research institutes) should work closely on germplasm characterization, and add these data to global databases to identify collection gaps and reduce duplicate holdings.
4. Preserve endangered crop wild relative species, providing support for, and emphasizing the importance of, successful pre-breeding; and encourage the use of crop species belonging to different gene pools that have been neglected in the past.
5. Work towards developing a strong common international platform that assists small genebanks by providing technical and financial support for germplasm conservation.
6. Strengthen *in situ* conservation of *Vigna* genetic resources, particularly *Vigna* crop wild relatives, and connect this with *ex situ* conservation activities.

Photo: WorldVeg

ABOUT THIS STRATEGY

The initiative to prepare the global strategy for the conservation ad use of *Vigna* (GSCV) was led by the World Vegetable Center (WorldVeg), in association with a number of other participating institutes/genebanks. The Global Crop Diversity Trust (The Crop Trust) facilitated the development of this document, which was funded by the German Federal Ministry of Food and Agriculture (BMEL). The outcome of this work in the form of GSCV will be available in open-access form to researchers and people working on conservation and use of plant genetic resources worldwide.

A total of 30 *Vigna* genebanks worldwide were identified through database searches. All the genebanks were asked to complete an online survey on the status and challenges of their collection. We received responses from 21 genebanks, and included all of this input in further analyses. Sixteen (76%) of the genebanks that responded are governmental organizations, four (19%) are NGOs and one (5%) is a non-departmental government body. We identified several challenges related to the sustainability of the conservation and use of *Vigna* genetic resources. Shortages of funds and staff were seen as major threats in many countries. The present document is based on:

- A review on relevant scientific literature;
- Searches of publicly available databases (Genesys and FAO-WIEWS); and
- Data collected through a survey of genebanks around the world with *ex situ Vigna* collections.

Meetings and email communications with specialists were conducted as part of the strategy's compilation phase. Therefore, the present strategy for *Vigna* conservation should be viewed as a compilation of expert perspectives from a diversity of stakeholders involved in the conservation and utilization of *Vigna* genetic resources.

The strategy document is divided into four main chapters:

- Chapter 1. Background information based on recent literature review;
- Chapter 2. Analyses on the current *ex situ* collections based on FAO-WIEWS and Genesys;
- Chapter 3. Results from the recent survey of genebanks on conservation and use; and
- Chapter 4. Recommendations.

Cowpea growing on riverbank in the Peruvian Amazon where it is known as chiclayo. Photo: Michael Major

1 OVERVIEW OF THE GENUS *VIGNA*

1.1 Taxonomy and domestication

The genus *Vigna* is a member of the Fabaceae family and is native to the tropical and subtropical regions of both the Old and New Worlds (Maxted et al. 2004; Tomooka et al. 2002; Tomooka et al. 2009). *Vigna* species are predominantly self-pollinating, often before the flower opens. Even so, pollination by bumblebees and other insects increases fruit set by enhancing self-pollination, as well as by stimulating cross-pollination. The insect-mediated increase in pollination ranges from 1% to 10% depending on the climate, cultivar and the insects present (Vaz et al. 1998). The growth habit of *Vigna* species varies from erect/semi-erect bushes to prostrate/trailing plants with profuse vegetative growth. Although most *Vigna* species used for commercial crop production are annuals, the genus contains many perennial species. *Vigna* species display considerable variation in flower color, stem pigmentation, and the size and colour of pods and seeds. These morphological characters are used as descriptors to gather morphological data that are useful for identification. The genus *Vigna* has more than 100 wild species (Schrire et al. 2005) and 10 domesticated (crop) species, and is one of the agriculturally important taxa worldwide. About 80% of the species are diploid ($2n = 2x = 22$), a few are aneuploids ($2n = 2x = 18$, 20 or 24) and *Vigna reflexo-pilosa* is the only known amphidiploid ($2n = 4x = 44$) (Parida et al. 1990; Yang et al. 2014). At present, five subgenera are recognized in the genus *Vigna, viz*., *Ceratotropis, Haydonia, Lasiospron, Plectrotropis* and *Vigna (*Takahashi et al. 2016). All the domesticated food crop species are in only three subgenera; *Ceratotropis, Plectrotropis* and *Vigna*.

The subgenus *Ceratotropis*, also known as Asian *Vigna*, is an agronomically important taxonomic group from which seven crops have been domesticated: mungbean (*Vigna radiata* (L.) Wilczek), urdbean (*Vigna mungo* (L.) Hepper), adzuki bean (*Vigna angularis* (Willd.) Ohwi & Ohashi), moth bean (*Vigna aconitifolia* (Jacq.) Maréchal), rice bean (*Vigna umbellata* (Thunb.) Ohwi & Ohashi), minni payaru (*Vigna stipulacea* Kuntze) and creole bean (*V. reflexo-pilosa* Hayata). Asian *Vigna* include a broad spectrum of species at various stages of domestication and with different plant parts used by humans (seeds, sprouts, leaves, green pods and swollen roots). *V. stipulacea*, *Vigna luteola* and *Vigna marina* are useful forage species. Some agronomic characteristics have extreme forms in Asian *Vigna*: for example, yardlong bean (*Vigna unguiculata* subsp. *unguiculata* cv.-gr. sesquipedalis) has the longest pod among domesticated legumes; and mungbean (*V. radiata*), urdbean (*V. mungo*), and moth bean (*V. aconitifolia*) have some of the smallest seeds among domesticated grain legumes that are used for their seeds (Tomooka et al. 2014).

The subgenus *Plectrotropis* consists of two sections with seven species (four species in section *Plectrotropis* and three species in section *Pseudoliebrechtsia*) (Maréchal et al. 1978). Importantly, the subgenus *Plectrotropis* consists of a lesser known but potentially important food legume, 'tuber cowpea' (*Vigna vexillata* (L.) A. Rich.) (Karuniawan et al. 2006). The fully domesticated form of this crop is cultivated in Bali and Timor, Indonesia.

The subgenus *Vigna* consists of two domesticated species: cowpea (*V. unguiculata* (L.) Walp) and Bambara groundnut (*Vigna subterranea* (L.) Verdc.). Maréchal et al. (1978) described 36 species in six sections (two species in section *Catiang*, two in *Comosae*, one in *Liebrechtsia*, two in *Macrodontae*, nine in *Reticulatae* and 20 in *Vigna*), among which cowpea is grouped under *Catiang* and Bambara groundnut is grouped under section *Vigna*. The taxonomy of *Vigna* has changed over time and is complex. The classification of the important domesticated crop species and corresponding primary, secondary and tertiary genepools is presented in Table 1.1. The taxonomic classification is adopted from Takahashi et al. (2016) and van Zonneveld et al. (2021). This classification excludes several wild *Vigna* species that are reported to be genetically remote or incompatible.

Table 1.1 Taxonomic classification of relevant food species in the genus *Vigna* (adapted from Takahashi et al. (2016) and van Zonneveld et al. (2020).

Sub Genus	Section	Species
Ceratotropis	*Ceratotropis*	*V. radiata* (Mungbean)
		V. radiata subsp. *sublobata*
		V. mungo (Blackgram)
		V. mungo var. *silvestris*
	Aconitifoliae	*V. trilobata*
		V. aconitifolia (Moth bean)
	Angulares	*V. angularis* (Azuki bean)
		V. angularis var. *nipponensis*
		V. umbellata (Rice bean)
		V. umbellata var. *gracilis*
		V. reflexo-pilosa (Creole bean)
		V. reflexo-pilosa subsp. *glabra* (Creole bean)
Plectrotropis	*Plectrotropis*	*V. vexillata* (Tuber Cowpea)
		V. vexillata var. *angustifolia*
		V. vexillata var. *macrosperma*
		V. vexillata var. *youngiana*
		V. vexillata (L.) A. Rich. var. *davyi* (Bolus) B. J. Pienaar
Vigna	*Catiang*	*V. unguiculata* (L.) *Walp.* subsp. *unguiculata* var. *unguiculata* (Cowpea)
		V. unguiculata subsp. *sesquipedalis* (Yardlong bean)
		V. unguiculata Unguiculata Group
		V. unguiculata Biflora Group
		V. unguiculata Sesquipedalis Group
		V. unguiculata subsp. *dekindtiana sensu Verdc.*
		V. unguiculata subsp. *cylindrica*
		V. unguiculata subsp. *mensensis*
		V. unguiculata (L.) *Walp.* subsp. *pubescens* (R. Wilczek) Pasquet
		V. unguiculata subsp. *tenuis*
		V. unguiculata var. *spontanea*
		V. unguiculata (L.) *Walp.* subsp. *stenophylla* (Harv.) Maréchal et al.
	Vigna	*V. subterranea* (Bambara groundnut)
		V. subterranea var. *spontanea*
		V. marina
		V. luteola

Apart from the three crop-containing subgenera, *Lasiospron* is another subgenus that has been explored recently (Delgado-Salinas et al. 2022). *Lasiospron* species have an amphi-Atlantic distribution and are morphologically distinct from all other *Vigna* species. All the *Lasiospron* species have deeply emarginate standards, wing petals embracing the keel, all with a left-hand curvature (as viewed face-on), and fruits becoming resupinate by the torsion of the pedicels. *Lasiospron* is monophyletic and comprises six species: *Vigna diffusa* (Scott Elliott) A. Delgado & Verdc., *Vigna juruana* (Harms) Verdc., *Vigna lasiocarpa* (Mart. ex Benth.) Verdc., *Vigna longifolia* (Benth.) Verdc., *Vigna schottii* (Benth.) A. Delgado & Verdc. and *Vigna trichocarpa* (C. Wright) A. Delgado. Other *Vigna* subgenera include *Haydonia*, *Sigmoidotropis* and *Macrorhyncha* (Maxted et al. 2004). These subgenera include wild *Vigna* species that are not included in the identified genepools. Additional important wild relatives in Africa include the endangered endemic *Vigna ramanniana* Rossbach and *Vigna mendesii* Torre (Catarino et al. 2021). However, it is not clear to which genepools these two latter species belong.

1.2 Cultivation of *Vigna* species

Globally, domesticated *Vigna* species (crops) are cultivated across more than 25 million hectares of land annually, among which cowpea has the largest cultivation area, 14.5 million hectares, with a total annual grain production of 6.2 million metric tons (Kebede et al. 2020). Mungbean has the second largest cultivation area with over 7.3 million hectares (Nair et al. 2020), whereas urdbean is cultivated over 5 million hectares. Other domesticated species, such as adzuki bean, creole bean, rice bean, moth bean and yardlong bean, are mostly cultivated in Asia. Bambara groundnut and tuber cowpea are predominantly cultivated in Africa.

Some of the cultivated *Vigna* species can be cultivated under harsh environmental conditions, such as high temperature and low rainfall, and in low-fertility soils. Numerous edible products produced from these cultivated species contribute to the continuity of food supply for subsistence farmers during the cropping season, and dried seeds are easily preserved and transported for cooking and food preparation later on. On the other hand, several *Vigna* species, such as cowpea and mungbean offer several fresh products including, tender shoot tips, leaves of plants at seedling stage, immature pods, and microgreens.

Some other popular products made from *Vigna* are: the transparent noodles made from mungbean starch that are common in China, and the mungbean paste that is used as an ingredient in the preparation of sweets in some parts of Asia. In East Asia Adzuki bean is culturally important because it is mixed with glutinous rice (red rice) on celebratory days (Lumpkin and McClary 1994). Rice bean (*V. umbellata*) is a rich source of protein for poor people living in the hills of Southeast Asia. In addition to human food, livestock feed can be produced from the plant residues (Nair et al. 2021. Furthermore, *Vigna* food products have many good nutritional qualities, and they are a welcome addition to diets heavy on grains, tubers, and roots. Cowpea contains approximately 22–30% crude protein in seeds and leaves on a dry weight basis (Bressani 1985; Nielsen et al. 1997), while its highly digestible haulms contain 13–17% crude protein and have a low fiber content (Tarawali et al. 1997). Thus, cowpea is an important grain and fodder crop (Fatokun et al. 1992; Samireddypalle et al. 2017). Mungbean contains 22–28% crude protein and 4–17% crude fiber (Mubarak 2005; Longvah et al. 2017; Sharanagat et al. 2019). These legumes are also good sources of micronutrients such as iron, zinc and vitamins.

1.3 Phenotypic diversity analysis

Morphological traits such as seed color, size and shape, the number of seeds per pod, days to flowering and 100-seed weight are useful for grouping accessions within similar species. Some of these attributes can be highly variable within crop species in the genus *Vigna*, such as the average number of pods per plant and leaf length in mungbean (Mwangi et al. 2021). The characterization of *Vigna* species in terms of different morphological traits revealed significant variation in particular characteristics among groups of species. For example, members of the *mungo-radiata* group have epigeal germination and sessile first and second leaves; members of the *angularis-umbellata* group have hypogeal germination and petiolate first and second leaves; and members of the *aconitifolia-trilobata* group have epigeal germination and petiolate first and second leaves (Bisht et al. 2005). The flower color of species in the subgenus *Ceratotropis* ranges from yellow to purple/violet, while those of *Vigna vexillata* and *Vigna pilosa* in two other subgenera are pale lilac (Bisht et al. 2005). The evaluation of hundreds of accessions of *V. radiata* (822) and *V. mungo* (164) from the N. I. Vavilov All-Russian Institute of Plant Genetic Resources (VIR) collection (originating from 54 countries) revealed historical shifts before and after the Green Revolution (before 1920 into the 21st century) in three of the most important traits for breeding, i.e., maturity period, seed productivity per plant, and 100-seed weight. It was observed that the Indian landraces of *V. radiata* were characterized by an erect bush form, small pods and predominantly dark seeds, and were more phenotypically diverse compared with landraces in other regions. This suggests that morphological traits of varieties and landraces differ according to the geographic origin and distribution (Burlyaeva et al. 2019).

1.4 Genetic diversity

Determining the genetic diversity within germplasm at the molecular level would greatly benefit crop improvement programs, since it would reveal the extent and nature of genetic variation within and among species. This information could then be considered to select diverse parents of the same species or to identify the most closely related parents for interspecific crossing, to increase heterosis, and to introgress only the desirable genes from more diverse backgrounds into elite germplasm (Henry, 1997). Among different genetic markers available for diversity analysis, random amplified polymorphic DNA markers (RAPD) have been widely used to study patterns of diversity in several legume species, including mungbean (Kaga et al. 1996; Santalla et al. 1998), adzuki bean (Yee et al. 1999), urdbean (Kaga et al. 1996) and cowpea (Mignouna et al. 1998). In addition, sequence-tagged microsatellite site markers (STMS) have been used to analyze mungbean (Yu et al. 1999), cowpea (Li et al. 2001), chickpea (Choumane et al. 2000) and field pea (Ford et al. 2002); and simple sequence repeat (SSR) markers have been used to analyze genetic differentiation in *Vigna* species (Dikshit et al. 2007; Wang et al. 2017; Mwangi et al. 2021). The genetic diversity and population structure of *V. unguiculata* have been analyzed on the basis of single nucleotide polymorphisms (SNPs) (Zuluaga et al. 2021; Huynh et al. 2013; Xiong et al. 2016).

The process of crop breeding has been accelerated by the use of modern genomic technologies. Next-generation sequencing (NGS) has provided whole genome sequences for several *Vigna* crop species and wild relatives. A significant landmark in genomic research on *Vigna* was reached in 2014, when the complete genome sequences of VC1973A, a *V. radiata* cultivar, its polyploid relative *V. reflexo-pilosa* var. *glabra* (accession V1160), and its wild relative *V. radiata* var. *sublobata* (accession TC1966) were obtained by *de novo* sequencing. *De novo* assembly of RNA-sequencing data derived from 22 accessions of 18 *Vigna* species was also completed. Together, these data facilitated advances in omics research on the subgenus *Ceratotropis* and provided insights into the evolution of *Vigna* species (Kang et al. 2014). The mungbean genome was sequenced on the Illumina HiSeq 2000 and GSFLX+ platforms, and analyses of the data revealed 22,427 high-confidence protein-coding genes and 160 *Vigna* gene clusters that will facilitate genomic research and accelerate molecular breeding. A near-complete reference genome sequence developed for mungbean using long PacBio reads serves as a reference genome sequence for *Vigna* species and continues to facilitate genome-assisted improvement in mungbean breeding programs. Construction of an ultra-high-resolution linkage map for mungbean using re-sequencing data identified several quantitative trait loci (QTLs) and the underlying candidate genes affecting synchronous pod maturity (SPM). That study also identified two flowering genes, *E3* (phytochrome A) and *J* (early flowering 3), as candidate genes for QTLs in mungbean through homologous searches against soybean (Ha et al. 2021).

A draft genome sequence of urdbean developed by hybrid genome assembly of Illumina reads and third-generation Oxford Nanopore sequencing technology identified 42,115 genes with a mean coding sequence length of 1131 bp. A total of 1,659 protein sequences (encoded by 3.9% of the total genes) were found to contain domains related to R-gene (Resistance gene) domains (Jegadeesan et al. 2021).

In East Asia, adzuki bean is an economically important grain legume because of its nutritional properties, and it is widely used in desserts. A complete reference genome sequence and resequencing data for two separate wild adzuki beans, *V. angularis* var. *angularis* and *Vigna nepalensis*, proved to be a useful source of genetic markers. Analyses of these data revealed loci under various levels of selection pressure and potential candidate genes for a number of agriculturally important attributes (Kang et al. 2015).

Beach cowpea (*V. marina*), a close relative of cultivated *Vigna* species such as adzuki bean (*V. angularis*), cowpea (*V. unguiculata*), mungbean (*V. radiata*) and urdbean (*V. mungo*), is tolerant to salt stress. Hence, it is a potential source of salt-tolerance genes for the development of new salt-tolerant lines of cultivated *Vigna* species. A draft genome sequence of beach cowpea was generated using high-throughput next-generation sequencing. Analyses of these data revealed 50,670 genes with mean coding sequence length of 1042 bp (Singh et al. 2019). Phylogenetic analyses revealed the highest sequence similarity with *V. angularis*, followed by *V. radiata*. In-depth comparisons between the new beach cowpea sequence and already published draft genomes of mungbean and adzuki bean will shed light on the mechanisms underlying salt and drought tolerance in *Vigna* species.

1.5 *Vigna* gene pool and genes related to biotic and abiotic stress resilience

The proper identification and characterization of accessions contributes to the existing gene pool in terms of new genetic resources that can be used for the improvement of specific crop species. It is particularly important to characterize those accessions in genebanks that remain unidentified. Considering this, Takahashi et al. (2016) identified and grouped several new collections within existing *Vigna* taxa based on morphological analyses and estimated phylogenetic relationships on the basis of DNA sequences of nuclear rDNA-ITS and chloroplast atpB-rbcL spacer regions (Appendix 1). Crop wild relatives are another valuable resource to introduce features into crop varieties to enable them to withstand, escape, or avoid abiotic stresses and to resist pests and diseases. In this way, new varieties can be developed to sustain legume production under climate change (Dwivedi et al. 2016; Sharma et al. 2013). Crop wild relatives have been underutilized by breeders in developing varieties because of the lack of information on traits of economic importance in these wild species, linkage drag of undesirable traits, and crossing barriers (Prohens et al. 2017). For these reasons, genetic improvement of legume crops has lagged behind that of cereal crops (Foyer et al. 2016). Exploiting the diversity of legume crops and identifying conservation needs in legume crop gene pools will be made easier with a better understanding of how traits are distributed among and within legume gene pools. Studies found that crops' wild cousins can adapt to hot, dry, or humid growing environments without relying on one particular characteristic (Khoury et al. 2015; Khoury et al. 2019).

One study explored in detail the distribution of traits related to abiotic stress resilience across four *Vigna* gene pools on the basis of a comprehensive eco-geographic analysis of heat and drought stress (van Zonneveld et al. 2020). This approach was used because of the large number of traits related to abiotic and biotic stress resilience. The study recognized a number of gene pools. Gene pool A comprises Asian *Vigna* taxa in the subgenus *Ceratotropis*, including *V. radiata* (mungbean), *V. mungo* (urdbean), *V. angularis* (adzuki bean), *V. umbellata* (rice bean), *V. reflexo-pilosa* var. *glabra* (creole bean) and *V. aconitifolia* (moth bean) (Figure 1.1). *Vigna trilobata* (jungle bean) and *Vigna trinervia* (tooapee) are two other wild taxa that are also regionally used and grown in Southeast Asia (Aitawade et al. 2012; Tomooka et al. 2011). Taxa from the subgenus *Plectotropis*, which includes domesticated *V. vexillata* (tuber cowpea) and its wild relatives, make up gene pool B. Domesticated *V. vexillata* comes in two different varieties; the pea type was domesticated in Africa, and the tuber type was first cultivated in Asia (Garba and Pasquet 1998).

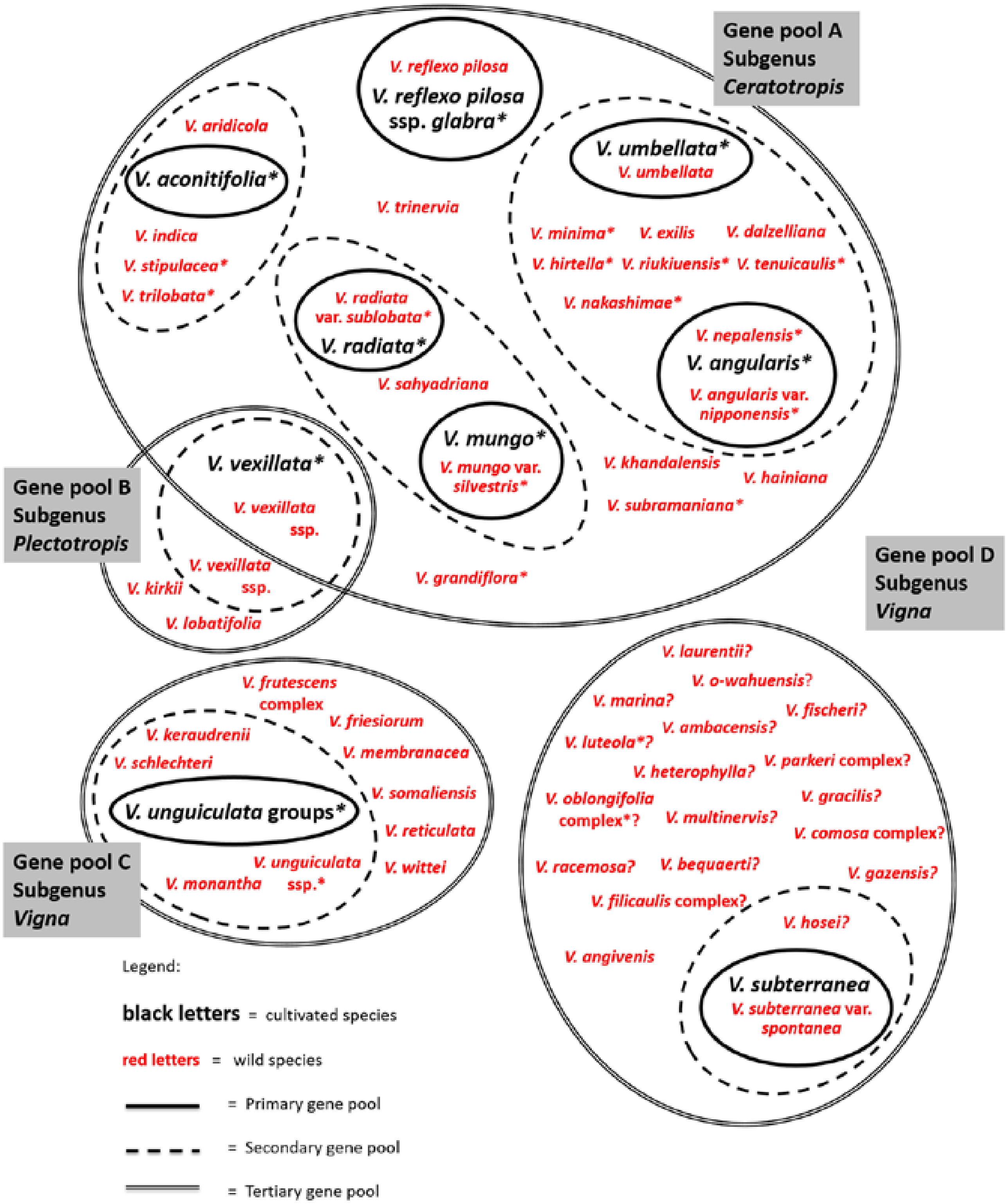
Taxa in the subgenus *Vigna* sections *Catiang*, *Macrodontae* and *Reticulatae* make up gene pool C. The *V. unguiculata* Sesquipedalis Group (yardlong bean) and the *V. unguiculata* Unguiculata Group (grain and vegetable cowpea) are the domesticated taxa in gene pool C. The domesticated species *V. subterranea* (Bambara groundnut) and other taxa in section *Vigna* of the subgenus *Vigna* are included in gene pool D. It is believed that *V. subterranea* was domesticated in West Africa (Somta et al. 2011). For local consumption, farmers raise a number of wild species from this gene pool, including *V. marina* and *V. luteola* (Tomooka et al. 2014; Maxted et al. 2004). Numerous species in this genus, such as *V. luteola*, *Vigna hosei*, and *Vigna parkeri*, are cultivated extensively as forages in the tropics (Maxted et al. 2004).

1.6 Role of the *Vigna* germplasm in biotic stress resilience

The identification and introgression of traits responsible for resistance or tolerance to biotic and abiotic stresses has a huge impact on the successful cultivation of crop species. The genus *Vigna* is a diverse group with more than 100 species, and as such it provides ample opportunity to dissect traits of interest and transfer them into breeding materials or cultivated *Vigna* species. Genetic mapping of *Vigna* wild relatives identified more sources of resistance to pest and diseases than to abiotic stresses (van Zonneveld et al. 2020), suggesting that *Vigna* taxa have more readily acquired traits related to biotic stress than to abiotic stress. The authors found that sources of abiotic stress resilience were present in <30% of screened taxa whereas >75% of the *Vigna* taxa screened had attributes related to pest and disease resistance. Resistance to bruchids (*Callosobruchus* spp.) was found in 18 out of 24 taxa (75%), while resistance to Yellow Mosaic Disease (YMD) was detected in all taxa in gene pool A of *V. radiata* and other Asian *Vigna* crops, and in gene pool C of the *V. unguiculata* Unguiculata Group and the *V. unguiculata* Sesquipedalis Group. Significantly less research has been conducted on resistance to other pests and diseases. Resistance to pod borer, whitefly, stem borer and thrips species has been reported only among germplasm of *V. radiata* and *V. mungo* in gene pool A (van Zonneveld et al. 2020). There are no reports of resistance to powdery mildew, bacterial blight or leaf spot in gene pool A. However, resistances to bacterial blight, thrips species and legume pod borer were detected in gene pool C, in germplasm from the primary gene pool of *V. unguiculata* Unguiculata Group and *V. unguiculata* Sesquipedalis Group. There have been no reports of anthracnose resistance. While some studies have evaluated resistance to bruchids and cowpea mottle virus, few have evaluated resistance to biotic stresses in members of gene pools B and D.

1.7 Role of the *Vigna* germplasm in abiotic stress resilience

A collection of 15 domesticated and 54 wild accessions originating from highly humid to arid regions was evaluated under terminal and non-terminal drought stresses (Iseki et al. 2018). The relative shoot biomass was higher in 19 non-terminal drought-tolerant wild accessions than in domesticated accessions. Compared



* = Tested in intercrossing experiments. Other species are positioned on the basis of genetic proximity.
? = Species belong to the same taxonomic section of the cultigen but their position in the genepool is uncertain because of limited information on crossing compatibility and genetic proximity.

Figure 1.1 *Vigna* gene pool (Source: van Zonneveld et al. 2020).

with the accessions showing non-terminal drought tolerance, those showing tolerance to terminal drought stress showed greater variations under drought stress conditions, and there were significant differences between the non-terminal drought-tolerant and terminal drought-tolerant groups. This suggested that different tolerance mechanisms function under non-terminal and terminal drought conditions. Furthermore, the wild species *V. trilobata* (which grows in seasonally hot climates) and *V. vexillata* (which grows in seasonally dry climates) were highly tolerant to dehydration and salinity. *Vigna aridicola* occurs in permanently hot climate conditions and tolerates high levels of dehydration. *V. unguiculata* Sesquipedalis Group grows in seasonally hot climate conditions and is tolerant to high levels of salinity. High levels of salinity tolerance were also detected in the domesticated species *V. unguiculata* and *V. vexillata*, and the wild species *V. luteola*, *V. marina*, *Vigna nakashimae*, *Vigna riukiuensis*, and *V. vexillata* var. *macrosperma*.

1.8 Comparison between the global conservation strategy for *Vigna* and the global strategy for cowpea

A global strategy for the conservation of cowpea genetic resources and its wild relatives, with an emphasis on Africa, was developed in 2010. That project was led by the International Institute of Tropical Agriculture (IITA), commissioned by the Global Crop Diversity Trust. In total, 36,383 accessions of cowpea and 23,013 accessions of other *Vigna* species were found in genebanks. Among the different genebanks surveyed, most were in Africa. Because that strategy was mainly developed with an African perspective, the collection of accessions might have been biased towards particular species, ecogeographic conditions and adaptive characters or traits. Therefore, the new, more comprehensive strategy for the global conservation of *Vigna* has been developed through a survey of all genebanks around the world, taking into account some of the shortcomings of the previous strategy focused on cowpea.

The present survey for the global *Vigna* conservation strategy reports a total of 96,161 accessions across different species under the genus *Vigna,* including domesticated crop species like mungbean, cowpea and urdbean. Compared with the previous cowpea global conservation strategy, the present survey reports a total of 39,878 accessions of *V. unguiculata,* consisting of 33,015 accessions of cultivated cowpea and 6,863 accessions of the *V. unguiculata* subsp. *unguiculata* Unguiculata Group, as well as 1387 accessions of *V. unguiculata* subsp. *sesquipedalis.* Species-level data for *Vigna* accessions available from online platforms such as the FAO-WIEWS and Genesys were included in these analyses. The results of these analyses were used to identify collection gaps, and hence to formulate the future strategy for the conservation of *Vigna* species.

One risk associated with the collection and conservation of genetic resources of any crop species is unintended duplication within and among collections. The identification of duplicates is important, because excessive duplication increases the management costs of genebanks. However, each accession should ideally be safety-duplicated in the Svalbard Global Seed Vault (SGSV) and another genebank following international standards of genebank conservation. Hence, the survey also sought to obtain specific information about unique collections of each crop species at individual genebanks.

Core and mini-core collections are useful in enhancing the use of genetic resources, because they represent the genetic variability of the entire germplasm collection efficiently in a relatively small number of accessions and can thus be more economically used in evaluation programs. Information on core, mini-core and trait-specific subsets of a few crops collated in the present survey will be useful for the further development of collections of other *Vigna* species.

Genetic erosion is an important concern in conservation and requires an appropriate management strategy. The recent survey sought to obtain comprehensive information on the percentage of accessions of different *Vigna* species lost and regenerated during the past 10 years. The survey also reports on the mandate of the genebanks in terms of the conditions of conservation (long-, medium- or short-term storage), and how they promote the use of their collections. The strategy was also developed on the basis of responses to questions about the processes involved in germplasm collection and conservation in genebanks, such as seed processing, seed health testing, availability of regeneration facilities, and the types and levels of data management. The survey also provides information on the phenotyping of *Vigna* crop species in terms of their biotic and abiotic stress resistance, as well as genotyping.

Cowpea varieties on display at IITA genebank. Photo: IITA

2 OVERVIEW OF *VIGNA EX SITU* CONSERVATION

2.1 Review of *Vigna ex situ* collections

Genetic resources from cultivated *Vigna* are secured outside their natural habitat in genebanks around the world. Some genebanks and botanical gardens also maintain collections of wild relatives outside their natural habitat, but such genetic resources are often under-represented in *ex situ* repositories (Castañeda-Álvarez et al. 2016).

A review of the literature on *ex situ* collections of *Vigna* highlighted that in 2017, 96 institutions conserved 89,288 accessions of the targeted *Vigna* taxa (van Zonneveld et al. 2020). It was reported that 53,756 (>60%) accessions were maintained in eight genebanks. As safety duplication, about 31,500 accessions belonging to 25 taxa were stored at the SGSV as of 2018. A more recent search (June 2022) in Genesys and FAO-WIEWS (see section 2.2) found 129,903 *Vigna* accessions in genebanks globally and on the SGSV web portal indicated that 40,622 accessions of *Vigna* belonging to 64 species and 142 taxa, deposited by 29 institutes, are stored at the SGSV.

Among the domesticated taxa, IITA conserves the largest collections of *Vigna unguiculata* (cowpea) and *Vigna subterranea* (Bambara groundnut). World Veg conserves the largest collection of *Vigna radiata* (mungbean) and *Vigna angularis* (adzuki bean). The Indian Bureau of Plant Genetic Resources (NBPGR) maintains the largest collections of *Vigna mungo* (urdbean), *Vigna umbellata* (rice bean), and *Vigna aconitifolia* (moth bean). CIAT holds the largest collection of *Vigna vexillata* (tuber cowpea). The Genetic Resources Center of the Japanese Agriculture and Food Science Organization holds the largest collection of *V. reflexo-pilosa* (creole bean). The Australian Grains Genebank and IITA maintain important collections of African wild *Vigna,* while the Japanese Agriculture and Food Science Organization and NBPGR hold important collections of wild Asian *Vigna*. Meise Botanic Garden (formerly the National Botanic Garden of Belgium) holds the most diverse *Vigna* collection (in terms of the number of taxa) but has only a limited number of accessions per taxon.

2.2 Present status of *ex situ* collections

The information in the following overview was obtained in June 2022 from two global genebank databases, Genesys and FAO-WIEWS. The data were extracted using the following procedure:

1. Data for the genus *Vigna* were downloaded from both the Genesys and FAO-WIEWS databases.
2. The data from the two databases were merged into a single dataset, and the number of accessions was counted. If the same accession was recorded in both databases, the accession was counted only once.
3. The data was then collated for the analysis as a data sheet including the genebank name, its acronym, FAO-designated genebank code, type of institution and the total number of *Vigna* accessions in each genebank.
4. Another summary data sheet was prepared, using the same dataset (point 1 and 2 above), with the total number of accessions for each crop species across all genebanks.

Based on analyses of the data retrieved from Genesys and FAO-WIEWS, we identified a total of 133 genebank collections across 87 countries holding *Vigna* accessions (Appendix 2). A total of 129,903 accessions were found globally. This number included all the domesticated crop species and their wild relatives. The species with the largest number of stored accessions was *V. unguiculata* (46,767 accessions), followed by *V. radiata* var. *radiata* (19,838 accessions) and *V. radiata* (17,761 accessions) (Table 2.1). 27 genebanks conserved more than 500 accessions of the genus *Vigna* (Figure 2.1). The institute storing the largest number of *Vigna* accessions was the World Vegetable Center (22,491 accessions); the International Institute of Tropical Agriculture (IITA , 20,088 accessions); the NBPGR, India (13,964 accessions); the Plant Genetic Resources Conservation Unit (PGRCU), University of Georgia USDA-ARS, USA (13,060 accessions); and the National Agricultural and Food Research Organization (NARO), Japan (12,038 accessions). These five ex situ collections includes 63% of all the *Vigna* accessions recorded in Genesys and FAO-WIEWS.

Of all the genebanks involved in conserving *Vigna* collections, 83% are government institutes; 3% are CGIAR institutes; 3% are in the parastatal sector; 2% are in the private sector; 2% are regional institutes; 2% are NGOs, 2% are international organizations; and the remaining 5% are other types of institutes (Figure 2.2). These genebanks conserve *Vigna* accessions in long-term, medium-term or short-term storage, or a combination. Based on the information published on WIEWS (2022) About 38% of the global *Vigna* collection is under medium-term conservation, 60% is under long-term conservation and 28% is under short-term conservation. Another 8% consists of living plants in botanical gardens (Figure 2.3).

2.3 Germplasm collection gap analysis

Taxonomic and geographic gaps in *Vigna* collections in genebanks were identified using a two-step procedure, based on 28,313 georeferenced presence records for 84 of the 88 *Vigna* taxa (van Zonneveld et al.

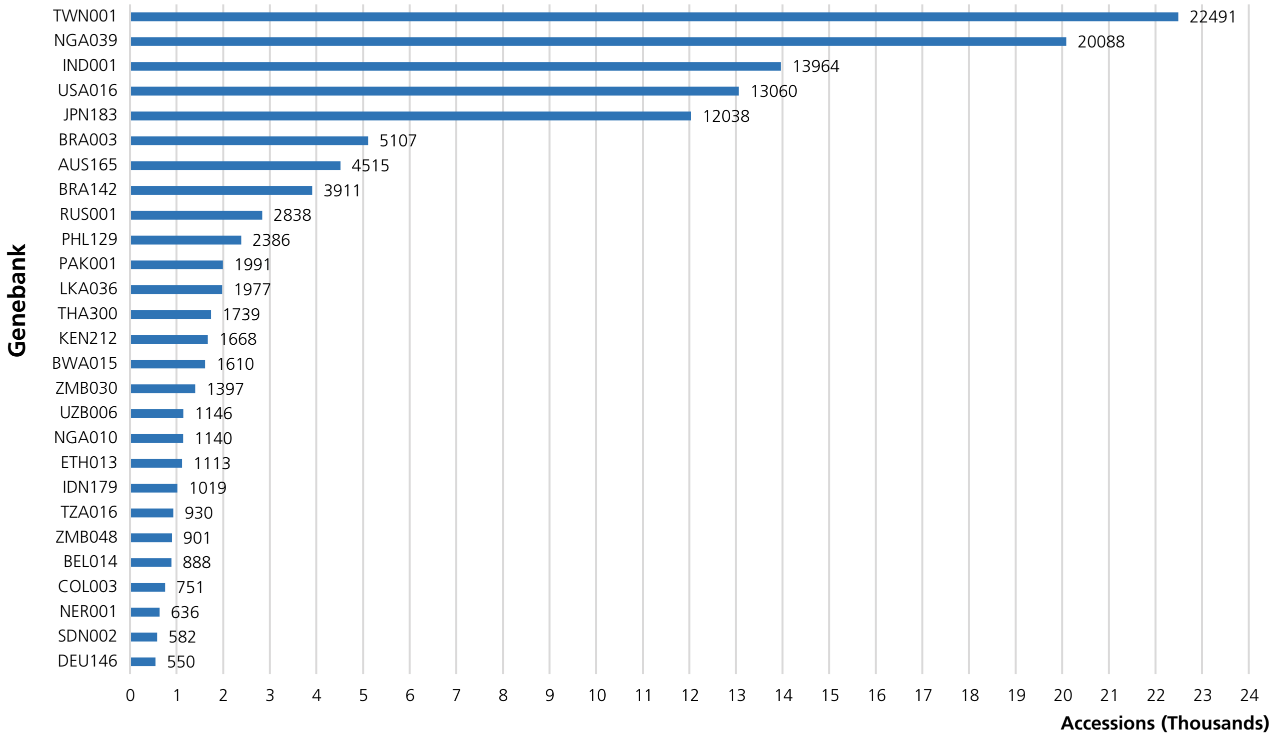


Figure 2.1 Genebanks worldwide with largest *Vigna* collections (source: Genesys and WIEWS, 2022).
Note: Names of genebanks with FAO codes in this figure can be accessed at FAO-WIEWS webpage.

Table 2.1 Total number of existing accessions for respective crop species in the genus *Vigna* (Source: Genesys and WIEWS, 2022)

Crop species	Total number of accessions
Vigna unguiculata (L.) Walp.	46,767
Vigna radiata var. *radiata*	19,838
Vigna radiata (L.) R. Wilczek	17,761
Vigna unguiculata subsp. *unguiculata* cv.-gr. *Unguiculata*	7,299
Vigna angularis (Willd.) Ohwi & H. Ohashi	6,420
Vigna mungo (L.) Hepper	5,940
Vigna subterranea (L.) Verdc.	4,975
Vigna umbellata (Thunb.) Ohwi & H. Ohashi	4,288
Vigna unguiculata subsp. *unguiculata*	3,244
Vigna unguiculata subsp. *unguiculata* cv.-gr. *Sesquipedalis*	1,950
Vigna aconitifolia (Jacq.) Marechal	1,933
Vigna vexillata (L.) A. Rich.	1,617
Vigna sp.	1,305
Vigna trilobata (L.) Verdc.	451
Vigna luteola (Jacq.) Benth.	404
Vigna radiata var. *sublobata* (Roxb.) Verdc.	321
Vigna mungo var. *mungo*	315
Vigna marina (Burm.) Merr.	307
Vigna racemosa (G. Don) Hutch. & Dalziel	297
Vigna mungo var. *silvestris* Lukoki et al.	268
Vigna minima (Roxb.) Ohwi & H. Ohashi	255
Vigna ambacensis Welw. ex Baker	230
Vigna reticulata Hook. f.	225
Vigna oblongifolia A. Rich.	223
Vigna unguiculata subsp. *unguiculata* var. *spontanea*	189
Vigna unguiculata subsp. *unguiculata* cv.-gr. *Biflora*	185
Vigna trinervia (B. Heyne ex Wight & Arn.) Tateishi & Maxted	169
Vigna riukiuensis (Ohwi) Ohwi & H. Ohashi	163
Vigna vexillata var. *angustifolia* (Schumach.) Baker	148
Vigna unguiculata subsp. *dekindtiana* (Harms) Verdc.	141
Vigna nakashimae (Ohwi) Ohwi & H. Ohashi	136
Vigna hirtella Ridl.	130
Vigna reflexopilosa Hayata	121
Vigna lanceolata Benth.	111
Vigna tenuicaulis N. Tomooka & Maxted	104
Vigna vexillata var. *vexillata*	97
Vigna lasiocarpa (Mart. ex Benth.) Verdc.	95
Vigna stipulacea Kuntze	84
Vigna parkeri Baker	77
Vigna hosei (Craib) Backer	71
Vigna membranacea A. Rich.	65
Vigna oblongifolia var. *oblongifolia*	61
Vigna gracilis (Guill. & Perr.) Hook. f.	56
Vigna unguiculata subsp. *baoulensis* (A. Chev.) Pasquet	55
Vigna dalzelliana (Kuntze) Verdc.	50
Vigna nigritia Hook. f.	44
Vigna exilis Tateishi & Maxted	42
Vigna grandiflora (Prain) Tateishi & Maxted	42
Vigna frutescens A. Rich.	39
Vigna oblongifolia var. *parviflora* (Welw. ex Baker) Verdc.	36
Vigna schimperi Baker	36
Vigna heterophylla A. Rich.	35

Crop species	Total number of accessions
Vigna unguiculata subsp. *pubescens* (R. Wilczek) Pasquet	34
Vigna wittei Baker f.	33
Vigna unguiculata subsp. *tenuis* (E. Mey.) Marechal et al.	32
Vigna aridicola N. Tomooka & Maxted	31
Vigna reflexopilosa subsp. *glabra* (Roxb.) N. Tomooka & Maxted	25
Vigna vexillata var. *tsusimensis* Matsum.	25
Vigna multinervis Hutch. & Dalziel	24
Vigna decipiens Harv.	22
Vigna longifolia (Benth.) Verdc.	21
Vigna venusta (Piper) Marechal et al.	21
Vigna vexillata var. *macrosperma* Marechal et al.	20
Vigna membranacea subsp. *hapalantha* (Harms) Verdc. Verdc. (Harms)	17
Vigna unguiculata subsp. *alba* (G. Don) Pasquet	17
Vigna nepalensis Tateishi & Maxted	16
Vigna unguiculata subsp. *stenophylla* (Harv.) Marechal et al.	15
Vigna kirkii (Baker) J. B. Gillett	14
Vigna membranacea subsp. *caesia* (Chiov.) Verdc.	14
Vigna bourneae Gamble	13
Vigna friesiorum Harms	13
Vigna membranacea subsp. *membranacea*	13
Vigna angularis var. *angularis*	12
Vigna comosa Baker	11
Vigna hookeri Verdc.	11
Vigna radicans Welw. ex Baker	11
Vigna umbellata var. *umbellata*	11
Vigna monophylla Taub.	10
Vigna parvifolia Planch. ex Baker	10
Vigna vexillata var. *ovata* (E. Mey.) B. J. Pienaar	10
Vigna angularis var. *nipponensis* (Ohwi) Ohwi & H. Ohashi	9
Vigna frutescens var. *frutescens* A. Rich.	9
Vigna subramaniana (Babu ex Raizada) Raizada	9
Vigna vexillata var. *davyi* (Bolus) B. J. Pienaar	9
Vigna filicaulis Hepper	8
Vigna filicaulis var. *filicaulis*	8
Vigna angivensis Baker	7
Vigna laurentii De Wild.	7
Vigna parkeri subsp. *maranguensis* (Taub.) Verdc.	7
Vigna sp.	7
Vigna venulosa Baker	7
Vigna lobatifolia Baker	6
Vigna schlechteri Harms	6
Vigna membranacea subsp. *macrodon* (Robyns & Boutique) Verdc. Verdc. (Robyns & Boutique)	5
Vigna platyloba Hiern	5
Vigna unguiculata subsp. *letouzeyi* Pasquet	5
Vigna frutescens subsp. *incana* (Taub.) Verdc.	4
Vigna hosei var. *pubescens*	4
Vigna hybr.	4
Vigna triphylla (R. Wilczek) Verdc.	4
Vigna unguiculata subsp. *pawekiae* Pasquet	4
Vigna filicaulis var. *pseudovenulosa* Marechal et al.	3
Vigna juruana (Harms) Verdc. Verdc. (Harms)	3
Vigna khandalensis (Santapau) Sundararagh. & Wadhwa	3

Crop species	Total number of accessions
Vigna pilosa (J. G. Klein ex Willd.) Baker	3
Vigna truxillensis (Kunth) N. Zamora	3
Vigna verticillata	3
Vigna comosa var. *comosa*	2
Vigna dolomitica R.Wilczek	2
Vigna fischeri Harms	2
Vigna hainiana Babu, Gopin. & S.K.Sharma	2
Vigna o-wahuensis Vogel	2
Vigna sahyadriana Aitawade, Bhat, K.V. & S.R.Yadav	2
Vigna indica Â T. M. Dixit et al.	1
Vigna kokii B.J.Pienaar	1
Vigna lobata Endl. ex Miq.	1
Vigna mudenia B.J.Pienaar	1
Vigna nyangensis R.Mithen	1
Vigna phoenix Brummitt	1
Vigna praecox Verdc.	1
Vigna reflexopilosa subsp. *reflexopilosa* Hayata	1
Vigna schottii (Benth.) A. Delgado & Verdc.	1
Vigna unguiculata subsp. *burundiensis* Pasquet	1
Vigna unguiculata subsp. *unguiculata* cv.-gr. Textilis	1
Vigna vexillata var. *youngiana* F. M. Bailey	1

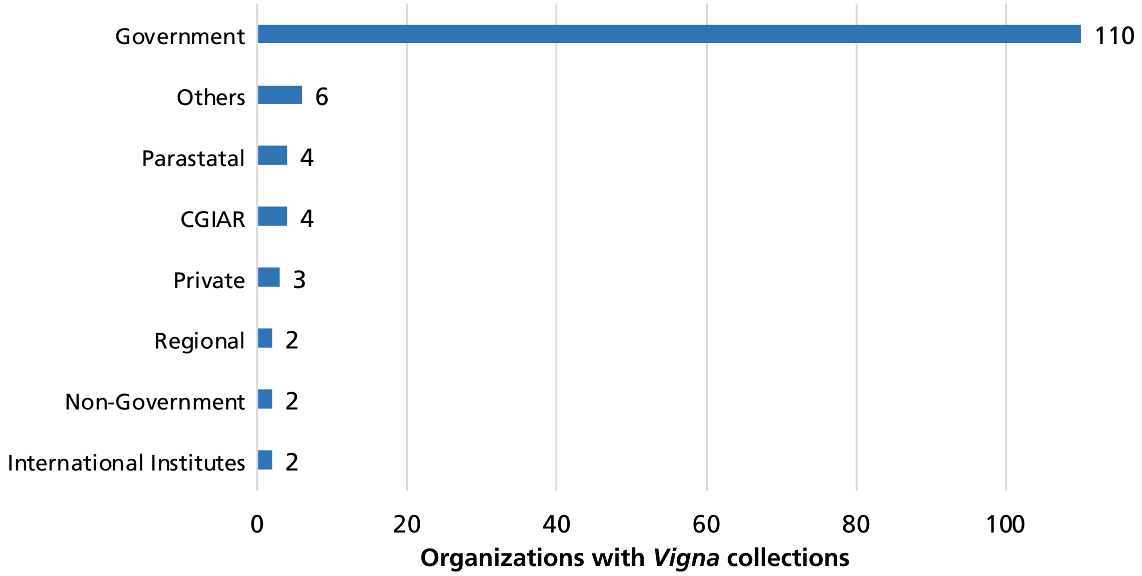


Figure 2.2 Types of organizations with *Vigna* collections (Source: Genesys and WIEWS, 2022).

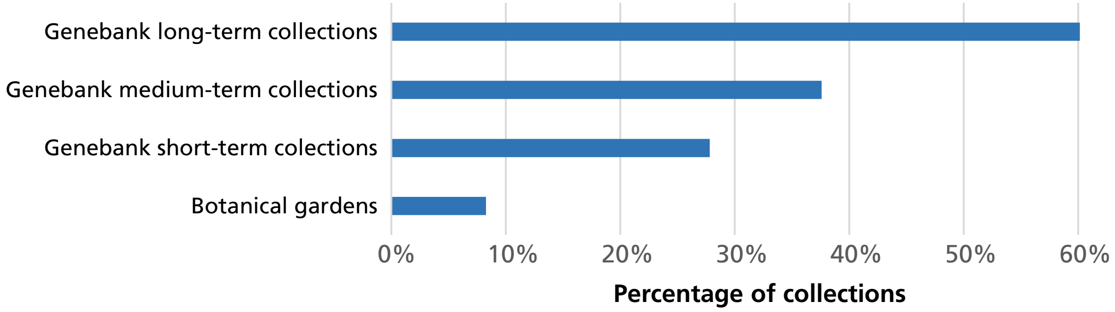


Figure 2.3 Percentage of the total 126 *Vigna* collections that is under long-term, medium-term and short-conservation in genebanks worldwide (Source: Genesys and FAO-WIEWS, 2022).

2020). First, by comparing sampled taxonomic richness reported in genebanks and living collections with sampled taxonomic richness reported by herbaria, taxa and countries underrepresented in *ex situ* collections were identified. Second, using ecological niche modelling with MaxEnt, a widely used algorithm to detect areas where climate conditions are suitable for plant species, geographic regions where taxa were expected to occur but had not previously been reported were identified (Elith et al. 2011).

As a result of the gap analysis, two Asian and four African *Vigna* species that were not represented in any of the genebanks reporting to FAO-WIEWS were identified: *Vigna sahyadriana*, *Vigna indica*, *Vigna keraudrenii* (endangered according to IUCN red list 2013), *Vigna monantha* (endangered according to IUCN red list 2016), *Vigna somaliensis* and *Vigna gazensis*. In addition, *Vigna bosseri* (endangered according to IUCN red list 2019), *Vigna mendesii* and *Vigna ramanniana* (Catarino et al., 2021) require urgent collecting because these species are not represented in genebanks. In addition, genebanks maintain fewer than 10 accessions for nine other Asian *Vigna* and seven other African *Vigna* species (Appendix 3). Thailand, India, Sri Lanka and Myanmar have been identified as priority countries for germplasm collection to obtain materials of 22 poorly conserved Asian taxa (Appendix 4). Priority countries for collection in Africa include Madagascar, the Democratic Republic of the Congo (DRC), South Africa, Benin, Burundi, Somalia, Namibia and Tanzania. Catarino et al. (2021) identified Angola as another country for collection. A total of 27 accessions of the endemic and critically endangered *Vigna o-wahuensis* have been collected by the Hawaiian Rare Plant Program and stored at the Lyon arboretum (Pers. Comm, Marian M. Chau, Lyon Arboretum, 2018). Taiwan, Northeast Australia, and India are geographical gaps in Asia and the Pacific. These regions have high taxonomic richness of *Vigna* as reported by herbaria but low coverage in genebanks and living collections (Appendix 5). When the reported overall taxonomic richness was compared with the modelled taxonomic richness, the current analysis revealed gaps in West Cambodia, Central Thailand, South Vietnam and coastal India. Burundi, Benin and Uganda are geographical gaps in Africa with high reported taxonomic richness but low coverage in genebank collections. Furthermore, the modelled richness analysis revealed that the East DR Congo has a significant collection gap.

Two case studies were performed to understand in more detail the collection gaps for cowpea and Bambara groundnut. The number of accessions in individual genebanks and their country of origin were obtained from Genesys and FAO-WIEWS. The results of the gap analysis for cowpea and Bambara groundnut are presented in the following sections.

2.3.1 Gap analysis for cowpea

A case study was conducted to identify gaps in cowpea collections with respect to the country of origin (Table 2.2 and Figure 2.4 and 2.5A, B), or groups of countries, across genebanks. The groups and the countries included in this analysis are based on the *Vigna* diversity tree. The *Vigna* diversity tree includes a stratification of the cowpea gene pool in hierarchical groups, based on expert opinion and information from the literature. The largest numbers of landrace accessions (3,613 accessions) were from Nigeria. Other regions/countries of origin of large numbers of conserved landraces (>1000 accessions) were east central Africa (2,775 accessions), India (2,433 accessions), Botswana (1,784 accessions), parts of Asia (1,588 accessions) and Niger (1,268 accessions). Other geographic regions were the origin of fewer than 1000 stored landrace accessions (2 to 992 accessions). Not a single landrace accession was reported from South Sudan, Cape Verde, Gambia, Saint Helena. In addition, 3,356 accessions in different genebanks had no information on the country of origin. This suggests that there is an urgent need of collecting from the regions where not a single accession is reported, and further it is also important to give specific importance to the regions where relatively few accessions were reported.

2.3.2 Gap analysis for Bambara groundnut

A similar case study was performed for Bambara groundnut. The *Vigna* diversity tree was used to identify groups/countries to include in the analysis. The results of the analysis with number of accessions for each group/country of origin are shown in Table 2.3, in Choropleth maps in the Supplementary material, and a brief overview by region is given below.

Western Africa: we found a small number of accessions (<50) collected from Côte d›Ivoire (1), Guinea (17), and Senegal (29). We did not find any accessions collected from Guinea-Bissau, Sierra Leone and Benin.

Southern and Eastern Africa: we found a small number of accessions collected from Mozambique (1), Uganda (9), Burundi (15), and Madagascar (16). We did not find any accessions collected in South Sudan in our dataset. Although it is possible that accessions collected before 2011, in the area currently corresponding to South Sudan, are still recorded in the passport data as originating from Sudan.

Central Africa: we found a small number of accessions collected from the Central African Republic (1), Angola (16), Democratic Republic of the Congo (25). We did not find any accessions collected from Congo, and Chad.

Table 2.2 Total number of cowpea accessions conserved in genebanks sorted by country of origin. A) Accessions reported as landraces. B) Accessions recorded as either landrace or as unknown biological status (Data source: Genesys and FAO-WIEWS 2022). *Following UNSD definition (UNSD 2022).

Country Origin	Total accessions conserved in genebanks	
	A. Accessions reported as landraces	B. Accessions recorded as either landrace or or as as unknown biological status
NGA	3,613	7,775
Unknown origin	3,356	3,466
IND	2,433	3,190
Other East and Middle African countries* (IOT, BDI, COM, DJI, ATF, MUS, MYT, REU, SYC, SOM, ZMB, ZWE, CMR, CAF, TCD, COG, GNQ, GAB, STP)	2,775	2,917
BWA	1,784	2,156
NER	1,268	1,861
others Asian countries* (BRN, KHM, IDN, LAO, MYS, MMR, PHL, SGP, THA, TLS, VNM, AFG, BGD, BTN, IRN, MDV, NPL, PAK, LKA)	1,588	1,828
Europe	968	1,153
TZA	992	1,021
Latin America* (AIA, ATG, ABW, BHS, BRB, BES, VGB, CYM, CUB, CUW, DMA, DOM, GRD, GLP, HTI, JAM, MTQ, MSR, PRI, BLM, KNA, LCA, MAF, VCT, SXM, TTO, TCA, VIR, BLZ, CRI, SLV, GTM, HND, MEX, NIC, PAN, ARG, BOL, BVT, BRA, CHL, COL, ECU, FLK, GUF, GUY, PRY, PER, SGS, SUR, URY, VEN)	487	708
Central West Asia* (KAZ, KGZ, TJK, TKM, UZB, ARM, AZE, BHR, CYP, GEO, IRQ, ISR, JOR, KWT, LBN, OMN, QAT, SUA, PSE, SYR, TUR, ARE, YEM)	593	670
MWI	666	668
KEN	386	568
North America* (BMU, CAN, GRL, SPM, USA)	156	508
GHA	466	478
SEN	297	410
MLI	403	406
BEN	340	340
SDN	252	256
AGO	205	205
BFA	200	205
UGA	126	139
TGO	109	137
CIV	133	133
NAM	131	131
ZAF	94	130
GIN	93	93
ETH	77	84
SWZ	70	70
Oceania* (AUS, CXR, CCK, HMD, NZL, NFK, FJI, NCL, PNG, SLB, VUT, GUM, KIR, MHL, FSM, NRU, MNP, PLW, UMI, ASM, COK, PYF, NIU, PCN, WSM, TKL, TOM, TUV, WLF)	46	65
East Asia* (CHN, PRK, JPN, MNG, KOR)	51	60
COD	23	53
LSO	41	41
MDG	36	39
ERI	38	38
MOZ	24	31
LBR	9	9
SLE	9	9
MRT	5	5
GMB	4	4
RWA	2	2
CPV	0	0
GNB	0	0
SHN	0	0
SSD	0	0

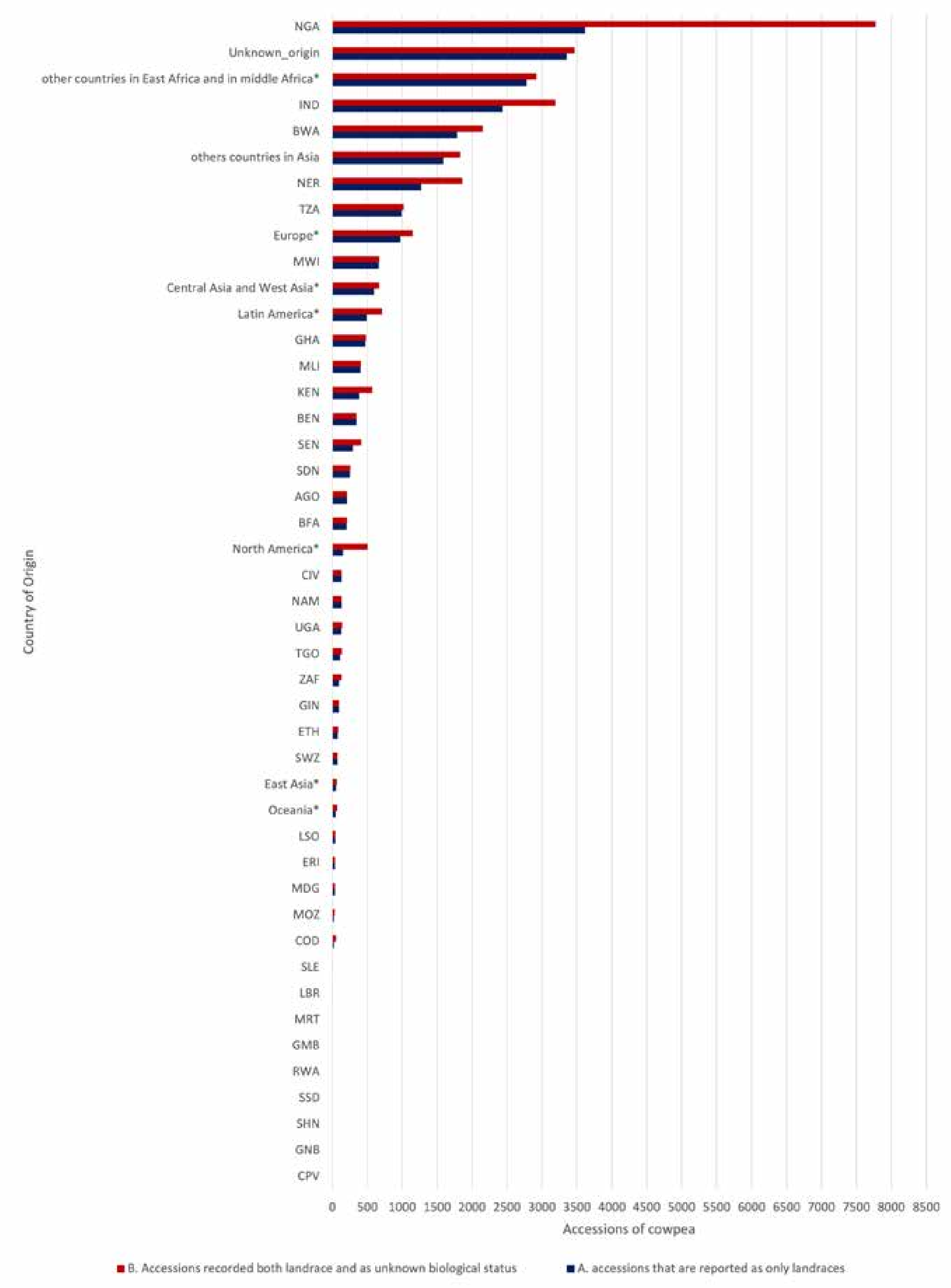


Figure 2.4 Total accessions of cowpea conserved in genebanks sorted by country of origin. A) Accessions reported as landraces. B) Accessions recorded as either landrace or as unknown biological status (source: Genesys and FAO-WIEWS, 2022). *World regions following UNSD definition (UNSD 2022).

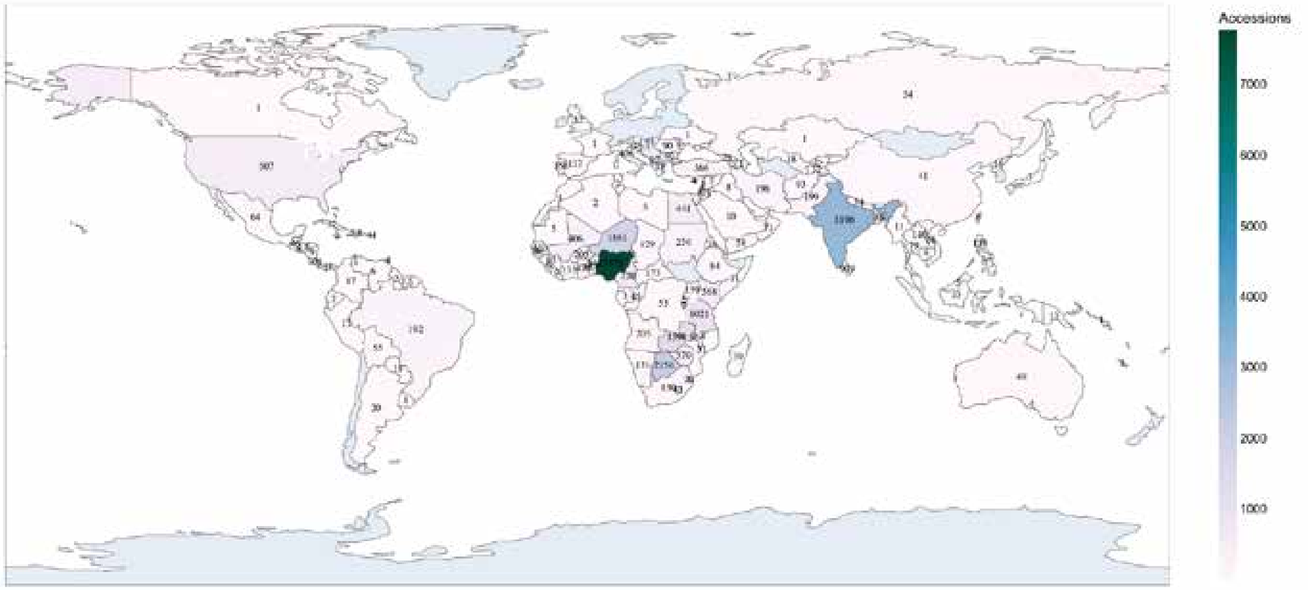


Figure 2.5 A. Origin cowpea landraces and material of unknown biological types conserved *ex situ* (data from Genesys and FAO-WIEWS 2022). Interactive map available in the supplementary material.

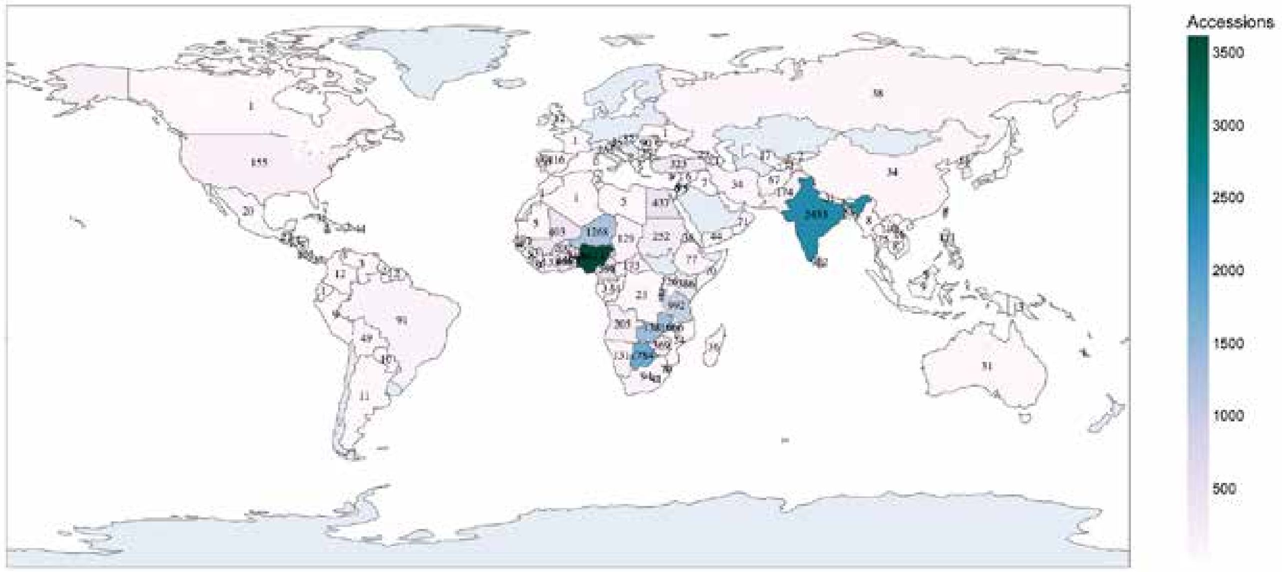


Figure 2.5 B. Origin of cowpea landraces conserved *ex situ* (data from Genesys and FAO-WIEWS 2022). Interactive map available in the supplementary material.

Vigna mungo. Photo: Sanjay Acharya/Wikimedia Commons

Table 2.3 Total number of bambara nut accessions conserved in genebanks sorted by country of origin A) Accessions reported as landraces. B) Accessions recorded as either landrace or as unknown biological status (Data source: Genesys and FAO-WIEWS 2022).

Country of origin	Total accession conserved in genebanks	
	A. Accessions reported as landraces	B. Accessions recorded as either landraces or as unknown biological status
BWA	567	570
ZMB	372	488
Unknown origin	96	392
NGA	237	375
TZA	266	286
ZAF and SWZ	220	264
NER	229	229
ZWE	157	185
GHA	102	172
MWI	142	151
NAM	106	112
CMR	102	108
SDN	84	84
MLI	59	69
BFA	0	53
KEN	27	29
SEN and GMB	0	29
COD	0	25
TGO	25	25
GIN	0	17
MDG	0	16
AGO	0	16
BDI	0	15
UGA	7	9
MOZ	0	1
CAF	0	1
CIF	0	1
SSD	0	0
Other countries in Eastern Africa (SOM, ERI, DJI, RWA)	0	0
Other countries in Southern_Africa (LSO)	0	0
TCD	0	0
COG	0	0
Other countries in Central Africa (GNQ, GAB, STP)	0	0
BEN	0	0
GNB	0	0
Other countries in West Africa (CPV, LBR, MRT, SHN)	0	0
Vigna subterranea var. *spontanea* (wild Bambara nut)	108	108


Mung beans evaluation in India. Photo: WorldVeg

3 INTERPRETATION OF THE 2021–2022 SURVEY RESULTS ON GLOBAL *VIGNA* CONSERVATION

3.1 General information about the survey

The 2021-2022 survey on global *Vigna* conservation was conducted through an online platform and was sent to 30 different *Vigna* genebanks worldwide. Twenty-one genebanks completed the survey (details are provided in Table 3.1). Among the genebanks that responded, most are government organizations (16), four are NGOs, and one is a non-departmental government body. Among the 21 respondents, the oldest *Vigna* collection center was VIR, Russia, which was established in 1910, and the newest was the Australian Pastures Genebank, SARDI, which was established in 2014. Of the 21 genebanks, 40% reported that they conserve their *Vigna* collection under a national conservation strategy or policy (question 1.5 of the survey in Appendix 6). The Australian Grains Genebank reported that it operates under the International Treaty for Plant Genetic Resources for Food and Agriculture (ITPGRFA) and the Australian National Research Development and Extension Program.
The germplasm collection at the Centre National de Recherche Agronomique (CNRA), Côte d'Ivoire, reported that it operates under the CNRA strategic plan. ILRI (Ethiopia) and IITA (Nigeria) are CGIAR centres, which collections operate under Article 15 of the ITPGRFA.

3.2 Composition of *Vigna* collection

3.2.1 Mandate crops and genebank objectives

The survey results showed that mandate crops and objectives vary among genebanks (Table 3.2.). Genebanks usually had additional objectives for *Vigna* collections; for example, long-term conservation of *Vigna* accessions for public organizations (18 of the 21 respondents); to provide working collections for public breeding programs (16 of the 21 respondents) and research institutes; and to provide working collections for private breeding programs (nine of the 21 respondents). Some genebanks, e.g., WorldVeg, maintain promising germplasm of *Vigna* crops to distribute for direct cultivation by farmers and schools (Figure 3.1).

Table 3.1 Genebanks participating in the survey and their details.

S. No	Name of organization	Country	FAO Code	Institute type	Name of respondent
1	Australian Pastures Genebank, South Australian Research and Development Institute (SARDI)	Australia	AUS167	Government	Alan Humphries
2	Australian Grains Genebank	Australia	AUS165	Governmental	Sally Norton
3	Bangladesh Agricultural Research Institute (BARI)	Bangladesh	BGD003	(Governmental, Autonomous body)	Md. Mubarak Ali
4	Meise Botanic Garden	Belgium	BEL014	Governmental	Filip Vandelook
5	Institut de l'Environnement et de Recherches Agricoles (INERA)	Burkina Faso	BFA057	Governmental	Batieno Benoit Joseph
6	Alliance of Bioversity International & CIAT	Colombia	COL003	International	Juan José González
7	Centre National de Recherche Agronomique (CNRA)	Côte d'Ivoire	CAF010	Governmental	Coulibaly Noupé Diakaria
8	Ethiopian Biodiversity Institute	Ethiopia	ETH085	Governmental	Webeshet Teshome
9	International Livestock Research Institute (ILRI)	Ethiopia	ETH098	International	Alice Muchugi
10	ICAR-National Bureau of Plant Genetic Resources	India	IND556	Governmental	Padmavati G Gore
11	National Agriculture and Food Research Organization (NARO)	Japan	JPN183	Governmental	Yu Takahashi
12	National Agriculture Genetic Resources Center	Nepal	NPL069	Governmental	Mukunda Bhattarai
13	International Institute of Tropical Agriculture (IITA)	Nigeria	NGA039	International	Michael Abberton
14	National Centre for Genetic Resources and Biotechnology (NACGRAB)	Nigeria	NGA010	Governmental	Sunday E. Aladele
15	National Plant Genetic Resources Laboratory, Institute of Plant Breeding, University of the Philippines Los Baños	Philippines	PHL018	Governmental	Hidelisa D. de Chavez
16	Federal Research Centre N.I. Vavilov All-Russian Institute of Plant Genetic Resources (VIR)	Russia	RUS001	Governmental	Burlyaeva M.O.
17	Plant Genetic Resources Centre	Sri Lanka	LKA141	Governmental	D.G.C. Jeewani
18	World Vegetable Center	Taiwan	TWN001	International	Jessica Ching-huan Chang
19	Royal Botanic Gardens, Kew – Millennium Seed Bank	UK	GBR004	Non-departmental government body	Chris Cockel
20	USDA-ARS, Plant Genetic Resources Conservation Unit (PGRCU)	US	USA016	Government	Shyam Tallury
21	Plant Resources Center	Vietnam	VNM049	Governmental	Vu Dang Toan

Vigna umbellata. Photo: Samuel Wong/Wikimedia Commons

Table 3.2 Mandate crops at the 21 institutes participating in the survey.

Sr. No	Institute name	FAO Code	Mandate crops
1	Australian Grains Genebank	AUS165	Grain crops across temperate, sub-tropical and tropical either grown or could be grown in Australia (cereals, legumes, oilseeds and minor crops)
2	Australian Pastures Genebank, South Australian Research and Development Institute (SARDI)	AUS167	*
3	Meise Botanic Garden	BEL014	*
4	Institut de l'Environnement et de Recherches Agricoles (INERA)	BFA057	*
5	Bangladesh Agricultural Research Institute (BARI)	BGD003	Mungbean, blackgram, cowpea and rice bean
6	Centre National de Recherche Agronomique (CNRA)	CAF010	*Vigna unguiculata*
7	Alliance of Bioversity Intl. & CIAT	COL003	Beans, tropical forages and cassava
8	Ethiopian Bio Diversity Institute	ETH085	Not mentioned
9	International Livestock Research Institute (ILRI)	ETH098	Forage crops
10	Royal Botanic Gardens, Kew – Millennium Seed Bank	GBR088	*
11	ICAR-National Bureau of Plant Genetic Resources	IND556	Agricultural and horticultural crops
12	National Agriculture and Food Research Organization (NARO)	JPN183	*
13	Plant Genetic Resources Centre	LKA141	*
14	National Centre for Genetic Resources and Biotechnology (NACGRAB)	NGA010	All plant genetic resources
15	International Institute of Tropical Agriculture	NGA039	Banana and plantain, cassava, cowpea, maize, soybean and yam
16	National Agriculture Genetic Resources Center	NPL069	Agronomic and horticultural crops
17	National Plant Genetic Resources Laboratory, Institute of Plant Breeding, University of the Philippines Los Baños	PHL018	*
18	Federal Research Centre N.I. Vavilov All-Russian Institute of Plant Genetic Resources (VIR)	RUS001	No crops are officially recognized as mandate crops
19	World Vegetable Center	TWN001	*
20	USDA-ARS, Plant Genetic Resources Conservation Unit (PGRCU)	USA016	Sorghum, *Vigna* spp., peanut, warm season grasses, vegetable crops, other legumes and industrial crops
21	Plant Resources Center	VNM049	*

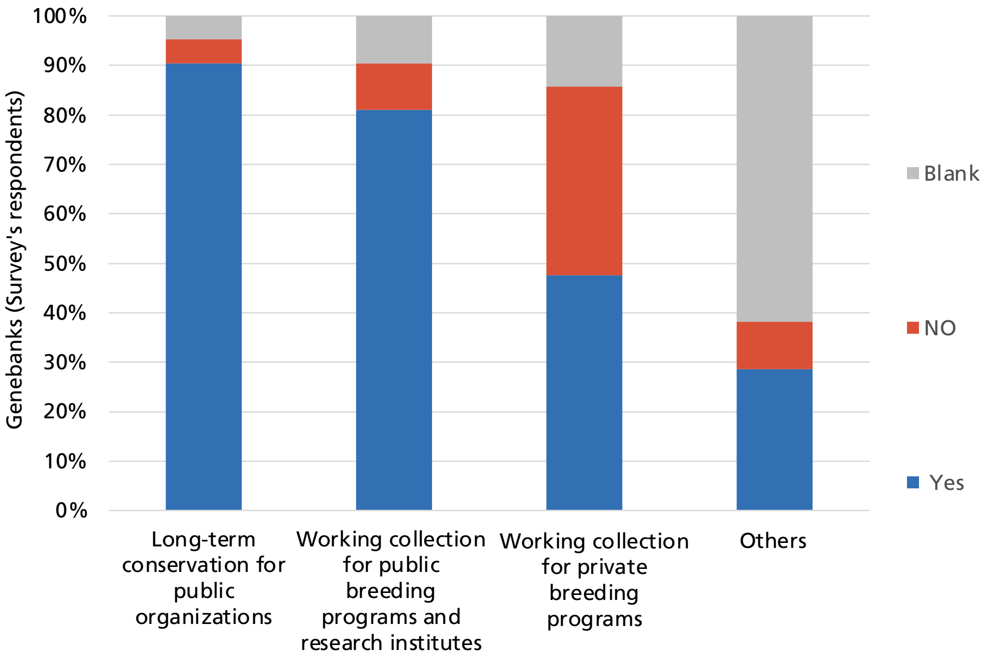


Figure 3.1 Main objectives of genebanks conserving *Vigna* accessions (n = 21, Survey 2021/2022)

3.2.2 *Vigna* accessions and crop species

A total of 96,161 *Vigna* accessions belonging to 34 taxa including wild relatives and landraces were reported across the 21 genebanks (Table 3.3). Although this number is slightly lower than that obtained in analyses of the Genesys and FAO-WIEWS databases (Chapter 2), the survey successfully targeted the major *Vigna* collections and collected comprehensive information from them. The largest collection of *Vigna* accessions was at the IITA (19,020 accessions), followed by WorldVeg, Taiwan (15,735 accessions), the NBPGR, India (14,505 accessions) and the USDA-ARS, USA (13,078 accessions). The other 17 genebanks each held collections of fewer than 10,000 *Vigna* accessions (Table 3.3).

The accessions shown in Table 3.4 are grouped under landraces or farmers' varieties collected within and outside the country, accessions of old cultivars and released varieties, advanced breeding lines and wild relatives. The species with the largest number of stored accessions was *V. unguiculata* subsp. *unguiculata* (33,015 accessions), followed by *V. radiata* (29,399 accessions). For landraces or farmers' varieties acquired outside the country, the species with the largest number of stored accessions was *V. radiata* (1,650 accessions), followed by *V. unguiculata* subsp. *unguiculata* (713 accessions). Similarly, the species with the largest number of accessions of landraces collected outside the country was *V. radiata* (14,313 accessions), followed by *V. unguiculata* subsp. *unguiculata* Unguiculata Group (4,744 accessions). The species with the largest number of accessions of old cultivars and released varieties was *V. unguiculata* subsp. *unguiculata* var. *unguiculata* (649 accessions) and that with the largest number of accessions of advanced breeding lines or genetic stocks was *V. radiata* (1,572 accessions). Among the wild relatives, *V. unguiculata* subsp. *unguiculata* var. *unguiculata* had the largest number of stored accessions (744 accessions). Among the genebank respondents, Meise Botanic Garden, Belgium had the largest number of wild species of *Vigna* (66 species).

Table 3.3 Total number of *Vigna* accessions conserved in each genebank.

Name of the organization	Country	Code	Total number of *Vigna* accessions across the taxa (Present status)
Australian Grains Genebank	Australia	AUS165	4,524
Australian Pastures Genebank, South Australian Research and Development Institute (SARDI)	Australia	AUS167	470
Meise Botanic Garden	Belgium	BEL014	1,802
Institut de l'Environnement et de Recherches Agricoles (INERA)	Burkina Faso	BFA057	417
Bangladesh Agricultural Research Institute (BARI)	Bangladesh	BGD003	254
Centre National de Recherche Agronomique (CNRA)	Côte d'Ivoire	CAF010	271
Alliance of Bioversity International & CIAT	Colombia	COL003	1,026
Ethiopian Biodiversity Institute	Ethiopia	ETH085	142
International Livestock Research Institute (ILRI)	Ethiopia	ETH098	1,113
Royal Botanic Gardens, Kew – Millennium Seed Bank, UK	UK	GBR004	307
ICAR-National Bureau of Plant Genetic Resources	India	IND556	14,505
National Agriculture and Food Research Organization (NARO)	Japan	JPN183	7,177
Plant Genetic Resources Centre	Sri Lanka	LKA141	2,109
National Centre for Genetic Resources and Biotechnology (NACGRAB)	Nigeria	NGA010	1,333
International Institute of Tropical Agriculture (IITA)	Nigeria	NGA039	19,020
National Agriculture Genetic Resources Center	Nepal	NPL069	186
National Plant Genetic Resources Laboratory, Institute of Plant Breeding, University of the Philippines Los Baños	Philippines	PHL018	5,422
Federal Research Centre N.I. Vavilov All-Russian Institute of Plant Genetic Resources (VIR)	Russia	RUS001	4,632
World Vegetable Center	Taiwan	TWN001	15,735
USDA-ARS, Plant Genetic Resources Conservation Unit (PGRCU)	USA	USA016	13,078
Plant Resources Center	Vietnam	VNM049	2,638
Total			**96,161**

Table 3.4 Total number of *Vigna* accessions for each specific crop species and each biological status

Sub Genus	Section	Species	TVA	LFWC	LFOC	ORV	ABGS	WR	Others
Ceratotropis	*Ceratotropis*	*V. radiata* (Mungbean)	29,399	1,650	14,313	181	1572	115	4,605
		V. radiata subsp. *sublobata*	474	2	27	0	12	219	4
		V. radiata var. *setulosa*	3	0	0	0	0	0	0
		V. mungo (Blackgram)	4,019	227	747	26	30	96	311
		V. mungo var. *silvestris*	281	4	1	0	0	9	250
	Aconitifoliae	*V. trilobata*	242	0	0	0	1	120	0
		V. aconitifolia (Moth bean)	1,771	2	115	6	31	5	52
	Angulares	*V. angularis* (Azuki bean)	5,979	227	1,917	15	68	3	1,065
		V. angularis var. *nipponensis*	16	0	1	0	0	2	1
		V. umbellata (Rice bean)	3,852	220	371	21	14	46	122
		V. umbellata var. *gracilis*	1	0	0	0	0	0	0
		V. reflexo-pilosa (Creole bean)	77	0	1	2	0	2	0
		V. reflexo-pilosa subsp. *glabra* (Creole bean)	1	0	0	0	0	0	1
Plectrotropis	*Plectrotropis*	*V. vexillata* (Tuber Cowpea)	1,805	5	77	3	0	614	15
		V. vexillata var. *angustifolia*	7	0	0	0	0	7	0
		V. vexillata var. *macrosperma*	1	0	0	0	0	1	0
		V. vexillata var. *youngiana*	2	0	0	0	0	1	1
		V. vexillata var. *davyi*	1	0	0	0	0	0	1
Vigna	*Catiang*	*V. unguiculata* subsp. *unguiculata* var. *unguiculata* (Cowpea)	33,015	713	4,518	649	621	744	1,593
		V. unguiculata subsp. *sesquipedalis* (yardlong bean)	1,387	384	10	2	41	0	90
		V. unguiculata Unguiculata Group	6,863	6	4,744	59	13	186	0
		V. unguiculata Biflora Group	16	0	0	0	0	0	0
		V. unguiculata Sesquipedalis Group	196	10	120	0	2	0	0
		V. unguiculata subsp. *dekindtiana*	183	0	46	0	0	48	43
		V. unguiculata subsp. *cylindrica*	14	0	8	0	0	0	0
		V. unguiculata subsp. *mensensis*	1	0	0	0	0	1	0
		V. unguiculata subsp. *pubescens*	17	6	0	0	0	1	9
		V. unguiculata subsp. *tenuis*	7	0	0	0	0	6	0
		V. unguiculata var. *spontanea*	344	2	0	0	0	0	0
		V. unguiculata subsp. *stenophylla*	5	0	0	0	0	0	5
	Vigna	*V. subterranea* (Bambara groundnut)	2,602	0	23	21	1	0	105
		V. subterranea var. *spontanea*	249	0	0	0	0	5	0
		V. marina	117	41	0	0	0	56	14
		V. luteola	70	2	1	0	1	53	13
Others			839	0	10	0	5	611	71

LFWC= Landraces or farmers' varieties collected within the country; LFOC= Landraces or farmers' varieties acquired from outside the country; ORV= Old cultivars and released varieties; ABGS= Advanced breeding lines or genetic stock; WR= Wild relative

3.2.3 Status of the *Vigna* collection over the past 10 years

To determine how many accessions may have been lost during conservation, the current collections (data collected through the survey) were compared with the collections 10 years ago. Among the genebank respondents, National Agriculture Genetic Resources Center, Nepal reported the loss of 312 accessions, Alliance of Bioversity International and CIAT reported the loss of 26 accessions and WorldVeg reported the loss of 399 accessions. Furthermore, Institut de l'Environnement et de Recherches Agricoles (Burkina Faso), National Centre for Genetic Resources and Biotechnology (Nigeria), The Plant Resources Center (Vietnam) and the USDA-ARS, Plant Genetic Resources Conservation Unit (USA) reported the loss of 152, 128, 47 and 29 accessions, respectively. Among 21 genebank respondents, only the National Agriculture Genetic Resources Center, Nepal (three species), and the Alliance of Bioversity International and CIAT (12 species) reported species-level information for the lost accessions.

The survey also intended to collect information on the number of lost accessions that have been replaced by re-collection or repatriation from other sources. None of the genebank respondents were able to provide information on re-collection and repatriation at the accession level. The following 10 genebanks were able to supply information about accessions collected in the past 10 years at the species level: National Agriculture Genetic Resources Center, Nepal (798 new accessions); WorldVeg (1,471 accessions); VIR, Russia (478 accessions); Australian Pastures Genebank, Australia (18 accessions); Australian Grains Genebank, Australia (seven accessions); Centre National de Recherche Agronomique, Cote d'Ivoire (15 accessions), Institut de l'Environnement et de Recherches Agricoles, Burkina Faso (16 accessions), International Institute of Tropical Agriculture, Nigeria (319 accessions), National Centre for Genetic Resources and Biotechnology, Nigeria (631 accessions) and the Plant Resources Center, Vietnam (500 accessions).

3.2.4 Collections of unique *Vigna* materials

The collections of unique materials in the genus *Vigna* require special conservation attention because the germplasm cannot be found elsewhere. Such unique collections may also have specific adaptive characters that can be used for breeding purposes. The survey gathered information on the extent to which the *Vigna* accessions conserved in individual genebanks differed from those in other collections; and which materials have not been duplicated extensively elsewhere within or outside the country (i.e., excluding safety duplication). On the basis of their responses, the genebanks were classified into three groups *viz*., those with unique accessions accounting for less than 50% of the collection, those with unique accessions accounting for more than 50% of the collection, and those with 100% unique accessions (Figure 3.2). Four genebank respondents reported 100% unique collections of *V. mungo*, and three genebanks reported 100% unique collections of *V. radiata, V. radiata* subsp. *sublobata*, *V. aconitifolia*, *V. angularis* and *V. umbellata*. Eight genebanks held collections with more than 50% unique materials of *V. unguiculata*, and six held collections with more than 50% unique materials of *V. radiata*. Six genebank respondents reported that their collections consisted of less than 50% unique materials of *V. radiata*, *V. mungo*, *V. umbellata* and *V. unguiculata.*

The survey also asked about the availability of passport information for the *Vigna* accessions in individual genebanks. Only nine out of 21 genebanks had passport data available for all *Vigna* accessions. Thirteen of the genebanks reported that the passport data for accessions were stored in a global standard format, but others used different formats. The reported passport descriptors include:

- FAO Multi-Crop Passport Descriptors (MCPD);
- WorldVeg descriptors for different *Vigna* species;
- International Board for Plant Genetic Resource (IBPGR), International Plant Genetic Resources Institute, Bioversity International descriptors; such as IBPGR/82/80 June 1983 (Descriptors for cowpea);
- EURISCO passport descriptors;
- GRIN-GLOBAL descriptors; and
- GLIS passport descriptors.

Eight of the 21 genebank respondents reported that they are involved in collaborations with other institutions for the collection of *Vigna* accessions at both national and international levels.

3.2.5 *Vigna* core, mini-core and trait-specific subsets

Table 3.5 summarizes information on the core, mini-core and trait-specific subsets available for important *Vigna* species. The USDA-ARS (USA) has distributed its cowpea core collection to 35 countries and its mungbean core collection to 25 countries. Similarly, WorldVeg, has shared its mungbean mini-core collection with 37 countries, and VIR, Russia, has shared its mungbean mini-core collection with WorldVeg. The Australian Grains Genebank has distributed a trait-specific (for example, Nested Association Mapping Population) mungbean collection to two countries and a core collection of adzuki bean within Australia. The Australian Pastures Genebank at SARDI reported that it has distributed a trait-specific subset of cowpea to two countries and *V. parkeri* to one country.

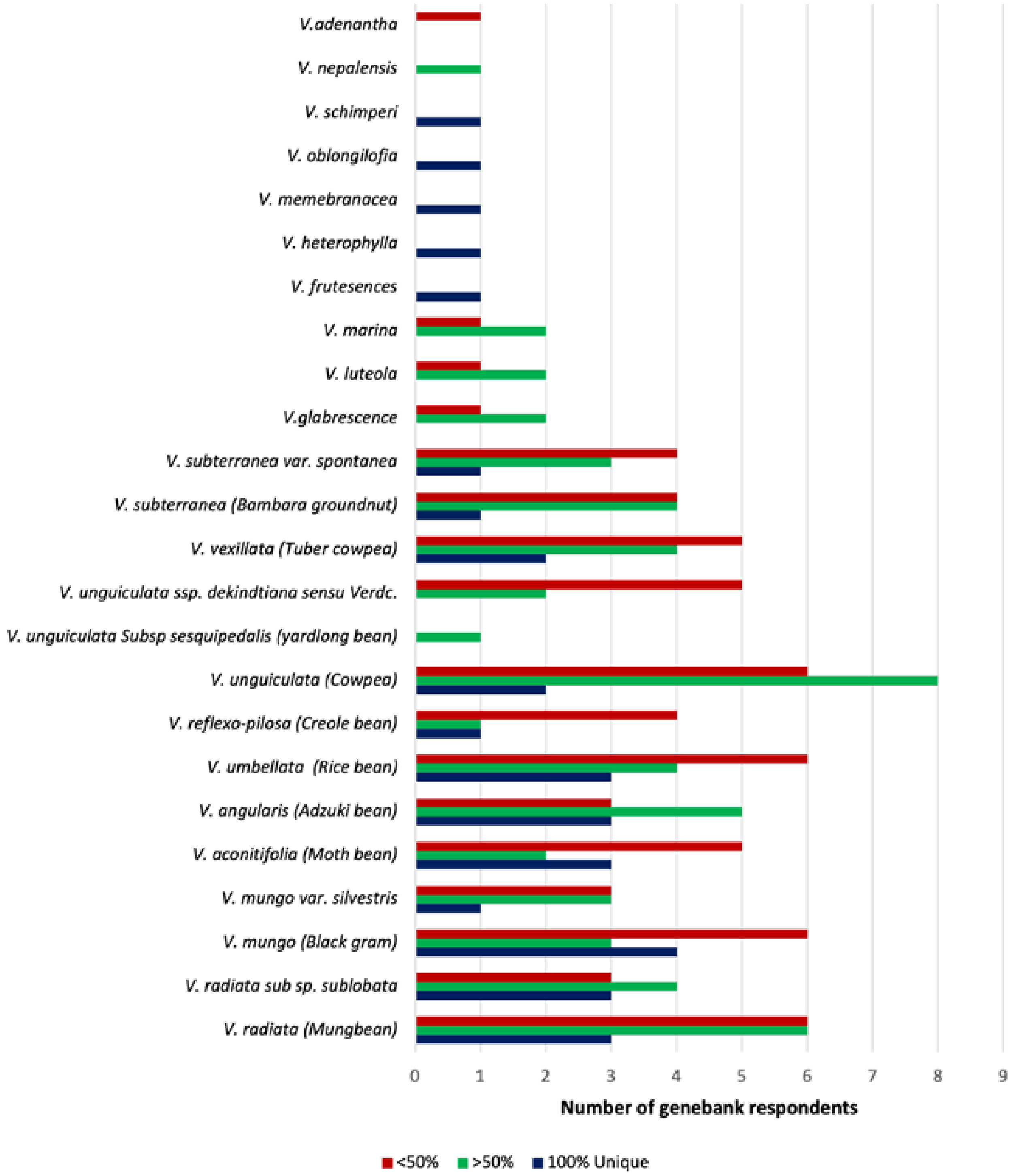


Figure 3.2. Number of genebank respondents conserving collections with <50%, >50%, and 100% unique collections of important *Vigna* species (n = 21, 2021–2022 Survey).

3.2.6 Major gaps in collections

It is important to identify possible taxonomic and ecogeographic gaps in the overall global collection and formulate a strategy to fully represent the extant diversity by optimizing the collection of accessions of different *Vigna* species around the world. Some collection gaps have been identified for cowpea and Bambara groundnut landraces (see Chapter 2). Other collection gaps for *Vigna* species in individual genebanks were also reported in the survey. For example, rare and endangered species were reported to be absent from the collection at the Meise Botanic Garden, Belgium. Some specific geographic regions such as the DR Congo and China are also not represented in the surveyed collections (China is likely to be well represented in China's genebanks, such as National Genebank of China at the Institute of Crop Science, Chinese Academy of Agricultural Sciences, but no data on collections located in China was available from open databases and from the survey). Furthermore, some genebanks reported that their collections only grow through exchange with other genebanks that have the same gaps. The regeneration and genomic characterization of *Vigna* collections would contribute to reveal gaps in collections, but the genebanks reported that these activities have a low priority, and this is a major concern. The unclear conservation status of *Vigna* wild relatives *in situ* is another major concern reported by a few of the genebank respondents.

3.2.6.1 Plans to fill the gaps

Some of the feedback with respect to the actions already taken, planned or sugggested to fill the collection gaps include analysis through collection maps and climate analog sites, and establishment of community seed banks. Several genebanks reported that they plan to initiate research collaborations and wild species sampling efforts with countries with high numbers of under-represented taxa. WorldVeg and its partners have already started to monitor wild *Vigna* populations in Madagascar, Benin, Tanzania and Eswatini with a focus on endemic species and those that are poorly conserved *ex situ* following van Zonneveld et al. (2020). The SADC crop wild relatives' network has established gene reserves including for *Vigna* wild relatives (Dulloo et al. 2021). This network will establish a basis for effective *in situ* conservation in sub-Saharan Africa that can be connected with other *ex situ* conservation and monitoring efforts.

3.3 Summary of *Vigna* conservation

3.3.1 Status of conservation efforts

Table 3.6 summarizes information on the status of *Vigna* conservation at the individual crop species level. These data were compiled from the responses of the 21 genebanks to questions about the total number of accessions available for species in different sections. The genebanks were asked about: the number of accessions under long-term storage and medium-term storage; the number of accessions whose baseline seed viability and seed health status have been evaluated; the baseline seed number of each accession; and the number of accessions that have been regenerated. The results showed that there were more accessions of domesticated crop species (cowpea, mungbean, urdbean, adzuki bean, moth bean and rice bean) than other (wild) species under long-term and medium-term storage. Cowpea had the largest number of accessions under long- and medium-term storage, followed by mungbean. Similarly, cowpea had the largest number of accessions tested for baseline seed viability and baseline seed health, and the largest number of regenerated accessions, followed by mungbean. However, mungbean had the largest number of accessions for which the baseline seed number was known.

Table 3.5 Total number of *Vigna* accessions available for important crop species in core and mini-core collections and trait-specific subsets.

Crop Species	Core collections
V. radiata (mungbean)	1,490 (TWN001)
	410 (USA016)
V. angularis (adzuki bean)	256 (AUS165)
V. unguiculata (cowpea)	2,062 (NGA039)
	720 (USA016)
Crop Species	**Mini core collections**
V. radiata (mungbean)	296 (TWN001)
	200 (VNM049)
	295 (RUS001)
	96 (JPN183)
V. acontifolia (moth bean)	90 (VNM049)
V. umbellata (rice bean)	50 (VNM049)
V. unguiculata (cowpea)	372 (NGA039)
V. angularis (adzuki bean)	80 (JPN183)
Crop Species	**Other trait-specific subsets, if any (trait)**
V. radiata (mungbean)	878 (RUS001)
	443 (AUS165)
V. unguiculata (cowpea)	323 (RUS001)
	210 (NGA039)
V. mungo (blackgram)	13 (RUS001)

Table 3.6 Conservation status of the most important *Vigna* species (2021–2022 Survey).

Sub Genus	Section	Species	SALS	SAMS	SABSV	SABSH	SABSN	SAR
Ceratotropis	*Ceratotropis*	*V. radiata* (Mungbean)	24474	14023	9611	3213	15594	19617
		V. radiata sub sp. *sublobata*	402	34	52	10	210	178
		V. radiata var. *setulosa*	3	0	0	0	0	0
		V. mungo (Black gram)	3602	973	1249	307	1057	1303
		V. mungo var. *silvestris*	171	150	150	0	155	156
	Aconitifoliae	*V. trilobata*	207	68	82	47	83	15
		V. aconitifolia (Moth bean)	1673	173	124	73	109	140
	Angulares	*V. angularis* (Azuki bean)	2159	1175	1388	409	1278	2001
		V. angularis var. *nipponensis*	16	0	2	1	3	3
		V. umbellata (Rice bean)	2841	667	573	100	466	637
		V. umbellata var. *gracilis*	1	0	0	0	0	0
		V. reflexo-pilosa (Creole bean)	4	2	0	1	4	4
		V. reflexo-pilosa ssp. *glabra* (Creole bean)	1	0	1	0	1	0
Plectrotropis	*Plectrotropis*	*V. vexillata* (Tuber Cowpea)	767	88	298	227	540	496
		V. vexillata var. *angustifolia*	7	0	1	0	7	6
		V. vexillata var. *macrosperma*	1	0	1	0	1	0
		V. vexillata var. *youngiana*	2	0	1	0	2	2
		V. vexillata (L.) A. Rich. var. *davyi* (Bolus) B. J. Pienaar	0	0	0	0	0	0
Vigna	*Catiang*	*V. unguiculata* (L.) Walp. subsp. *unguiculata* var. *unguiculata* (Cowpea)	24996	23069	20318	18088	3759	22471
		V. unguiculata subs. *Sesquipedalis* (Yardlong bean)	662	908	13	39	50	207
		V. unguiculata (L.) Walp. subsp. *unguiculata Unguiculata* Group (*V. unguiculata Unguiculata* Group)	607	6799	5856	0	5644	6227
		V. unguiculata (L.) Walp. subsp. *unguiculata Biflora* Group (*V. unguiculata Biflora* Group)	3	14	14	0	14	14
		V. unguiculata (L.) Walp. subsp. *unguiculata Sesquipedalis* Group (*V. unguiculata Sesquipedalis* Group)	85	192	191	0	182	194
		V. unguiculata ssp. *dekindtiana sensu* Verdc.	67	24	64	14	83	72
		V. unguiculata subsp. *cylindrica*	14	0	1	6	8	8
		V. unguiculata subsp. *mensensis*	1	0	0	1	1	1
		V. unguiculata (L.) Walp. subsp. *pubescens* (R. Wilczek) Pasquet	9	5	11	5	10	8
		V. unguiculata subsp. *tenuis*	6	0	0	1	6	6
		V. unguiculata var. *spontanea*	2	2	2	2	1	0
		V. unguiculata (L.) Walp. subsp. *stenophylla* (Harv.) Maréchal et al.	4	0	4	0	4	4
	Vigna	*V. subterranea* (Bambara groundnut)	104	222	231	42	74	69
		V. subterranea var. *spontanea*	3	344	225	0	3	103
		V. marina	52	18	24	21	44	16
		V. luteola	64	16	33	16	63	43
Others			1095	240	763	583	1020	795

SALS= Sum of accessions in long-term storage; SAMS= Sum of accessions in medium-term storage; SABSV=Sum of accessions with baseline seed viability; SABSH= Sum of accessions with baseline seed health status; SABSN=Sum of accessions with baseline seed number; SAR= Sum of accessions that have been regenerated.

3.3.2 Types of storage facilities available at genebanks

The genebanks were asked about the types of storage facilities used to conserve *Vigna* accessions. The results are summarized below.

3.3.2.1 Number of cold storage units

Eight of the genebanks reported that their genebanks were equipped with long-term cold-storage units for seeds, and most of them had at least two cold storage units (Table 3.7). Only two genebanks reported having individual freezers. One genebank reported that collections were stored in an air-conditioned room, and three genebanks reported that collections were stored in air-conditioned rooms equipped with dehumidifiers. Apart from these, eight genebanks reported that they were equipped with back-up generators. Among the 21 genebank respondents, only Royal Botanic Gardens, Kew – Millennium Seed Bank reported that they have cryopreserved *Vigna* accessions.[1] Their cryopreserved materials include *V. unguiculata* and *V. reticulata from* Mali, some accessions of *V. racemosa* from South Africa, accessions belonging to *V. radiata* var. *sublobata* and *Vigna angivensis* from Madagascar and a few other *Vigna* species from Botswana. The need for cryopreservation for *Vigna* needs to be explored as these seeds can normally be stored as orthodox seeds for long periods under 5 or minus 20 degrees Celsius after appropriate drying.

Eleven genebank respondents reported having at least one medium-term cold storage unit, four reported having at least two freezers, and two reported that they have air-conditioned rooms. Three genebank respondents reported using dehumidifiers and six reported that they have back-up generators.

Seven genebank respondents reported that they have short-term cold storage units. Of those, two reported having individual freezers and air-conditioned rooms, four reported having air-conditioned rooms with dehumidifiers, and three reported that they have back-up generators.

3.3.3 Types of packaging used at different genebanks

Figure 3.3 shows the types of packaging (sealed aluminum packs, sealed and vacuum-packed aluminum packs, air-tight plastic containers, air-tight glass container, non-airtight plastic/glass containers,

Table 3.7. Combinations of storage type among genebank respondents (n = 21, 2021-2022 Survey).

Storage type(s)	# of respondents (i.e. genebanks)
Only long term storage units or freezers	3
Only medium term storage units or freezers	2
Long and medium term storage units or freezers	5
medium and short term storage units or freezers	3
Long and short term storage units or freezers	2
Long, medium and short term storage units or freezers	2
Missing answer	4

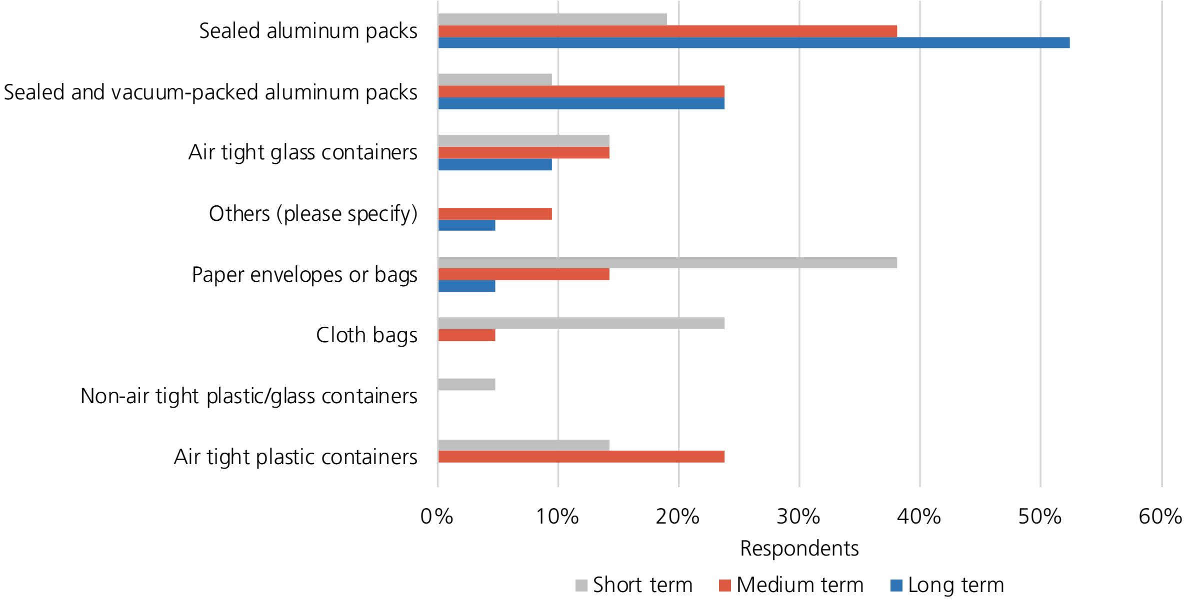


Figure 3.3 Number of genebank respondents (in percentage) using different types of packaging for long-term, medium-term and short-term storage (n = 21, 2021–2022 Survey)

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[1] A portion of a few seed accessions was cryopreserved in 2015 due to previous prioritization criteria (high conservation priority or CWR species).

paper envelopes or bags or cloth bags) used for long-term, medium-term, and short-term seed storage, as reported by the genebank respondents. The results of the survey indicate that sealed aluminum packs are used for long-term storage at 52% of the genebanks and for medium-term storage at 38% of the genebanks. However, for short-term storage, 38% of the genebanks use paper envelopes or bags.

3.3.4 Facilities to monitor storage units

The survey asked the genebanks about the control and monitoring of storage conditions, especially temperature and relative humidity, in long-term, medium-term and short-term conservation units (Figure 3.4).

Table 3.8 shows the range of temperatures and relative humidity reported by genebank respondents and Figure 3.4 shows the percentage of genebanks equipped with different monitoring facilities for their storage units (long-, medium-, and short-term).

3.3.5 Genebank facilities

Among 21 genebank respondents, 90% reported that they have separate work areas for seed processing (threshing, cleaning etc.) and clean seed handling. The majority (71%) of genebanks reported that they have separate work areas for seed packaging for storage and distribution with relative humidity control, and dedicated laboratory staff for seed viability testing (Figure 3.5). In addition, 57% of the genebanks reported having a low-temperature (20°C) seed-drying facility and a dedicated laboratory with trained staff for seed-health testing. Also, 86% of the genebanks reported that they have access to at least one field site in a key agro-ecological zone for regeneration and multiplication, and 67% reported that they have access to a field site or greenhouse/glasshouse near the genebank and to an irrigated field site for off-season regeneration and multiplication.

3.3.6 Genebank status

The survey asked the genebanks about the average age of their buildings and how long the different facilities (storage, laboratory facilities, laboratory equipment, field equipment and generators) have been used (Figure 3.6). Of the respondents, 23% reported that most of their facilities were either in excellent or adequate working condition, while 22% reported that their facilities were inadequate. Lack of funds and/or budget, followed by lack of available space, particularly for the regeneration of (entire) collections, were reported to be the major constraints to the improvement of facilities at genebanks.

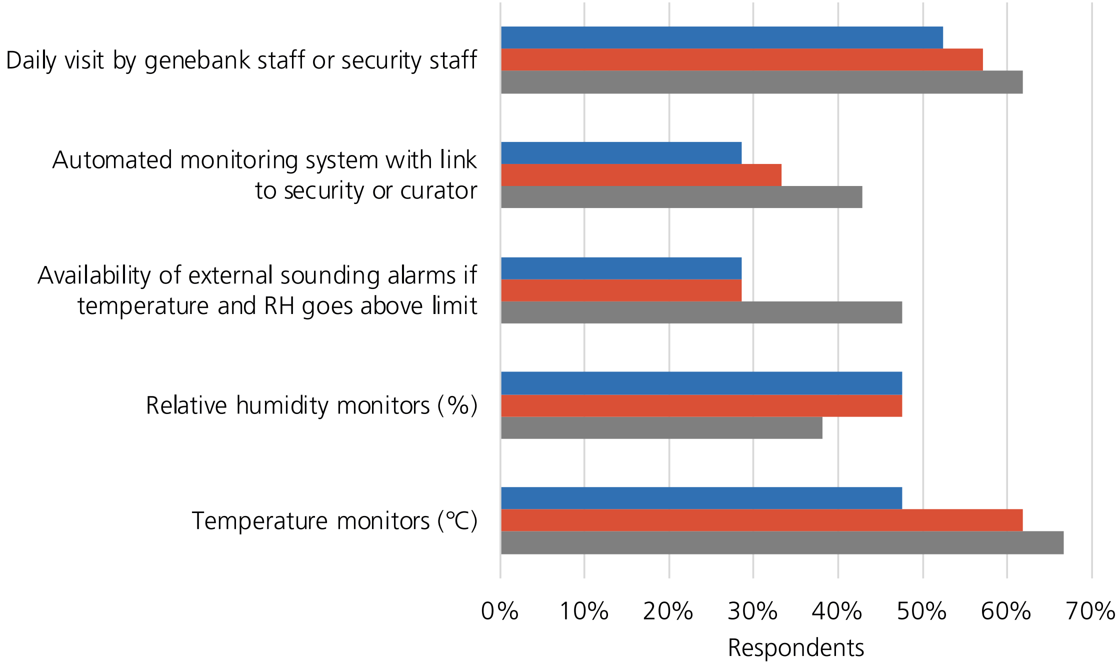


Figure 3.4 Number of genebanks using different types of monitoring for long-term, medium-term and short-term storage units (n =21, 2021-2022 Survey).

Table 3.8 Temperatures and relative humidity reported by genebank respondents (n = 21, 2021-2022 Survey).

	Long-term storage units	Medium-term storage units	Short-term storage units
Temperature ranges	-20 to -10 C	-1 to 10 C	4 to 20 C
Relative humidity ranges	12% to 15%	12% to 45%	15% to 45%

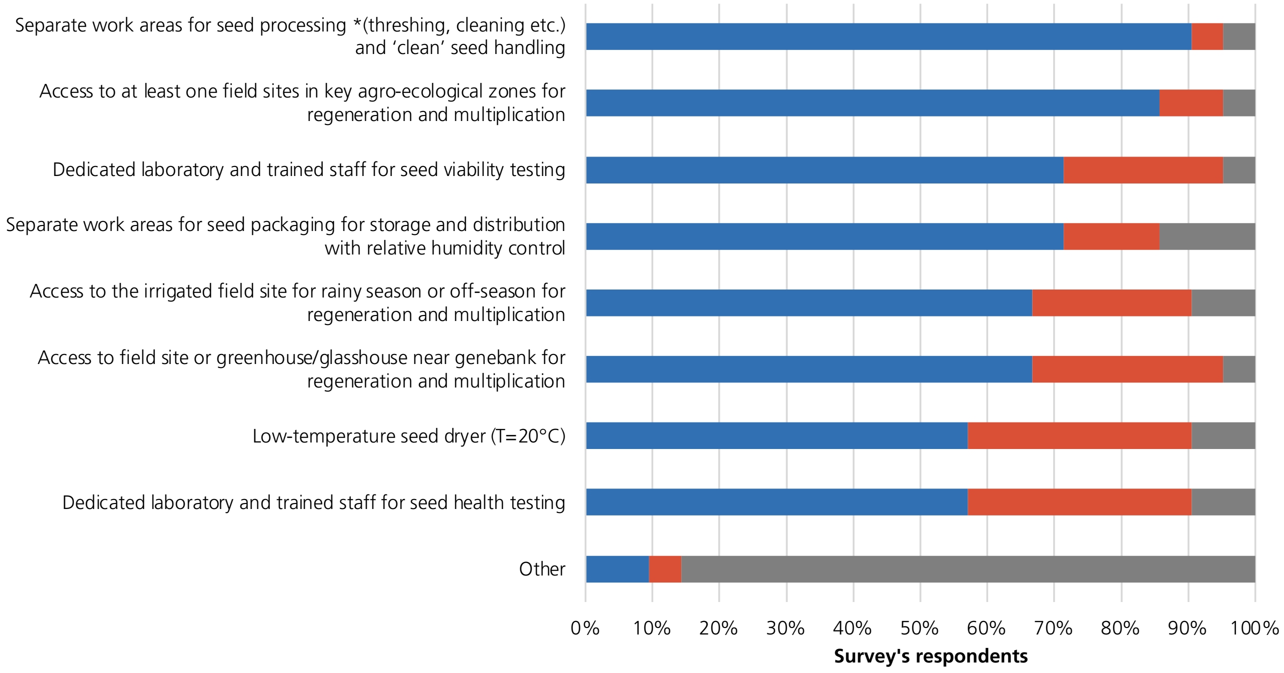


Figure 3.5 Percentage of genebank respondents with access to particular sites, facilities and equipment necessary to conserve *Vigna* (n = 21, 2021-2022 survey).

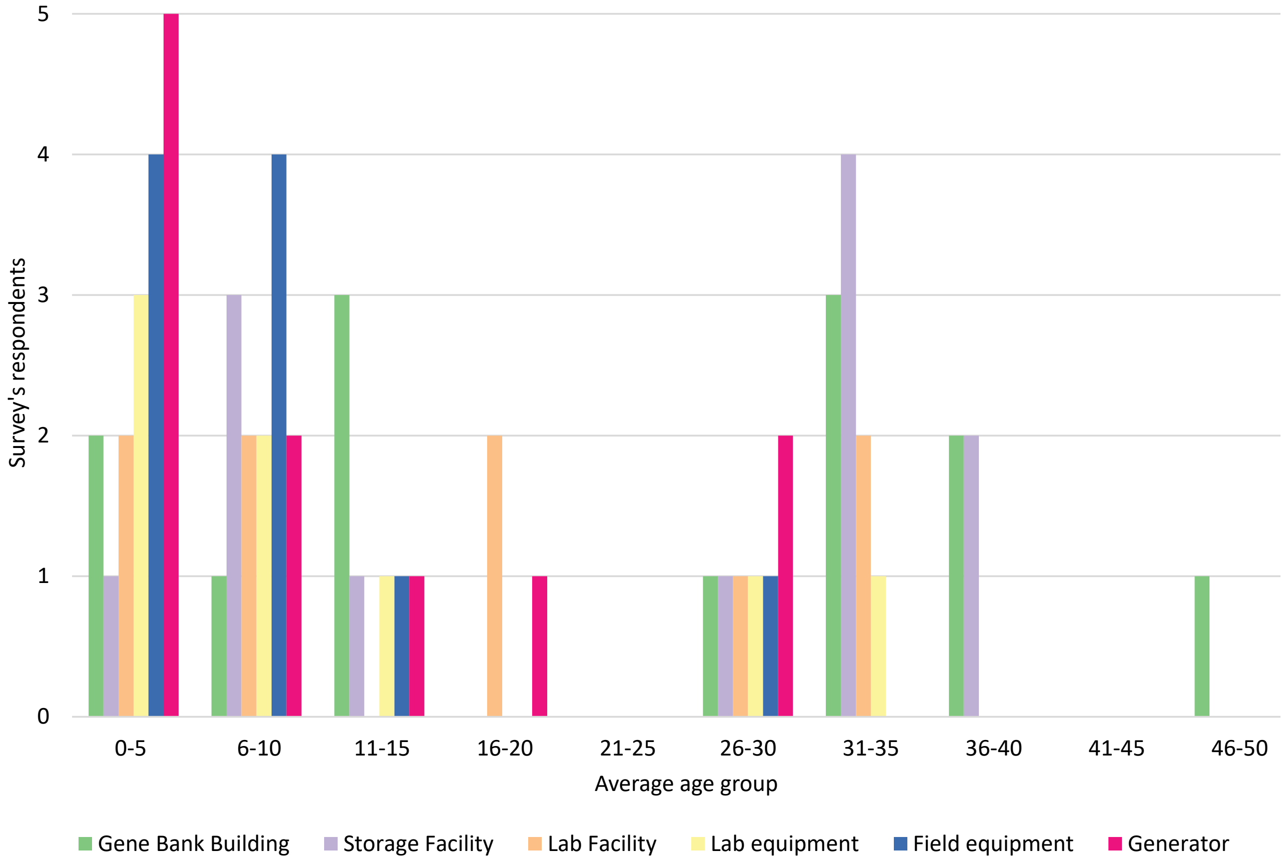


Figure 3.6 Key facilities and equipment at genebanks grouped according to years of use. All facilities and equipment are used for the procurement and conservation of *Vigna* accessions (n =21, 2021–2022 survey)

3.3.7 Alternate energy sources

Considering the long-term perspective of genebanks, it is advantageous to have an alternative energy source for uninterrupted operation on a daily basis. Fluctuation or loss of energy may affect seed viability. Of the 21 genebank respondents, only Meise Botanic Garden, Royal Botanic Gardens, Kew – Millennium Seed Bank, Alliance of Bioversity International & CIAT and IITA reported that they have an alternative energy source in the form of solar panels. However, the Australian Pastures Genebank reported that they plan to install solar panels in the near future.

Twelve of the 21 genebanks reported that they do not have alternative energy sources. Ten of the 21 genebanks reported that they have prioritized energy efficiency when procuring new and replacement facilities and equipment.

The genebanks that participated in the survey reported that they follow different standard operating protocols (SOPs) and procedures. Some of the procedures listed include those specified in:

- ENSCONET Manuals
- FAO Genebank Standards
- Vishnyakova et al. 2018
- ISTA protocols for germination
- WorldVeg SOP CONS-V1
- PGRCU Operations Handbook for Germplasm Maintenance,
- IBPGR

Figure 3.7 summarizes the responses to questions about ongoing research or resources and expertise for future research on *Vigna* conservation. The main responses included the following priorities:

- explore genetic diversity and/or phylogenetic relationships.
- improvement of procedures or protocols for conservation;

3.3.8 Major constraints to *Vigna* conservation

Some of the major constraints to *Vigna* conservation reported by the genebank respondents were as follows:

Biological constraints:

- regeneration of accessions with few stored seeds;
- genetic erosion;
- poor health and quality of seeds in short- and medium-term conservation;
- poor storability and dormancy of wild *Vigna* species;
- limited cultivation area;
- non-synchronous flowering;

Others:

- inability to acquire local/traditional knowledge about the uses of *Vigna* species;
- shortage of conservation staff;
- lack of information/knowledge about the diversity within collections;
- lack of gap analysis;
- lack of expertise to identify/characterize *Vigna* species;
- lack of characterization data.
- identification of duplicate accessions;
- inadequate room for long-term conservation;

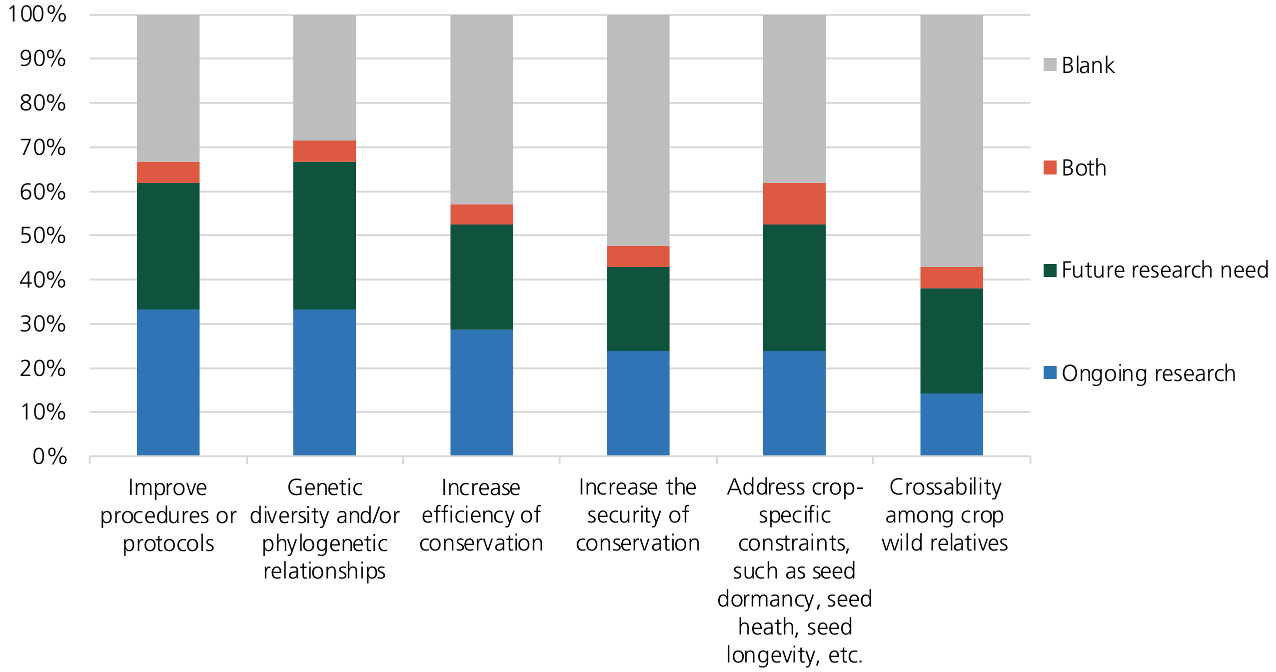


Figure 3.7 Number of genebank respondents with ongoing research or planned research on different aspects of *Vigna* conservation (n = 21, 2021-2022 survey).

3.4 Characterization and information management

3.4.1 Status of accession-level information for collections

Among the 21 genebanks that participated in the survey, 15 reported that characterization data are available for internal use, and 14 reported that these data are publicly available (Figure 3.8). Eleven genebanks reported that data are available in a paper catalog and can be accessed by contacting the curator. Thirteen genebanks reported that germplasm data are available on searchable online platforms that can be accessed from both within and outside the institute.

The survey asked the genebanks about the type of information they managed, whether the data were stored in a searchable database, which characterization data were available (e.g., data for a minimum number of traits), and whether each accession had georeference information (Table 3.9). According to the responses, 100% of the passport data are available for the accessions held at the Australian Grains Genebank (62 species), Alliance of Bioversity International & CIAT (eight species), VIR (eight species), WorldVeg (14 species) and USDA-ARS (all conserved *Vigna* species).

Once the accessions are held in collections by genebanks, useful information is generated for each accession. Such information includes passport data, taxonomic data, characterization data, genotype data, and images. Among the 21 genebank respondents, 16 reported that they have passport data for *Vigna* collections and 13 reported that they have taxonomic information (Figure 3.9). Ten genebanks reported that they have characterization data for accessions in their collections, and eight reported that they have images of their stored accessions.

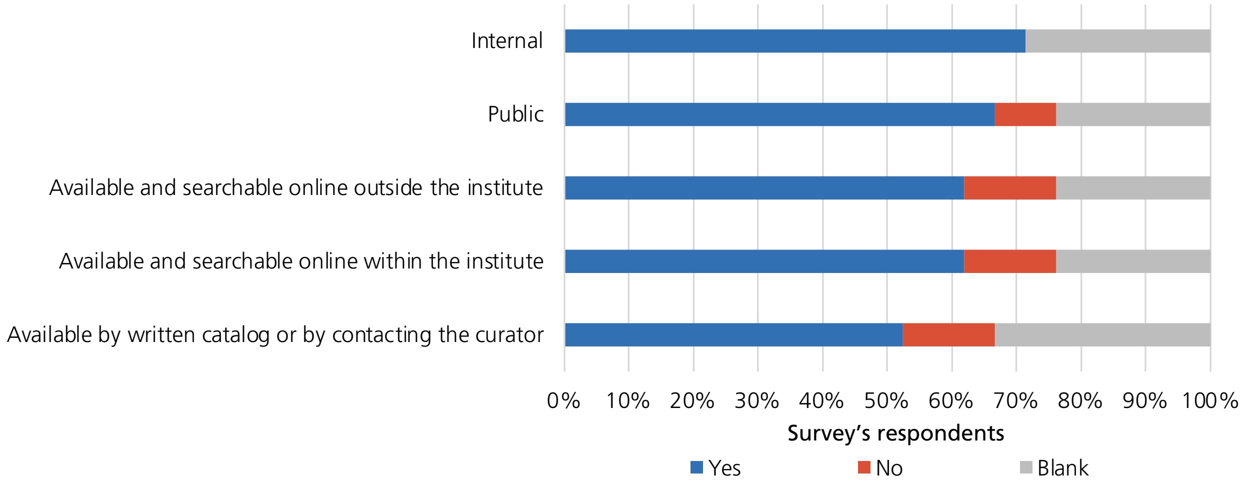


Figure 3.8 Availability of information about germplasm and the types of platforms used to store information in genebanks storing *Vigna* materials that answered the 2021-2022 survey (n = 21).

Table 3.9 Accession level information (%) for different species in the genus *Vigna* (2021–2022 Survey). Note: Values in parentheses show the number of species.

FAO code	Number of species	Passport data	Passport data in searchable database	Characterized with a minimum number of traits	Characterization data in searchable database	Georeference data
AUS165	62	100 (62)	100 (62)	17 (3)	17 (3)	35 (62)
BEL014	13	87 (13)	68 (13)	-	-	53 (13)
COL003	8	100 (8)	100 (8)	74 (8)	-	16 (8)
CAF010	3	-	-	11 (3)	-	-
ETH098	6	95 (39)	95 (39)	-	--	50 (39)
NPL069	6	83 (7)	53 (6)	-	-	78 (5)
NGA039	7	82 (7)	-	-	-	-
PHL018	6	57 (6)	70 (4)	27.5 (5)	12 (1)	-
RUS001	8	100 (8)	82 (8)	34 (3)	-	-
TWN001	14	100 (14)	100 (14)	50 (14)	51 (14)	-
VNM049	2	50 (1)		24 (2)	-	-
USA016	All available *Vigna* species	100	100	50	100	4

Overall, 57% of the genebank participants reported that they enter data into a database for genebank management: 48% reported that they enter data on seed inventory, regeneration, multiplication and characterization; 43% reported that they enter data on seed viability testing and re-testing, seed number and distribution; 38% reported that they enter data on seed or plant health status; and 33% reported that they enter data on packet weight (Figure 3.10).

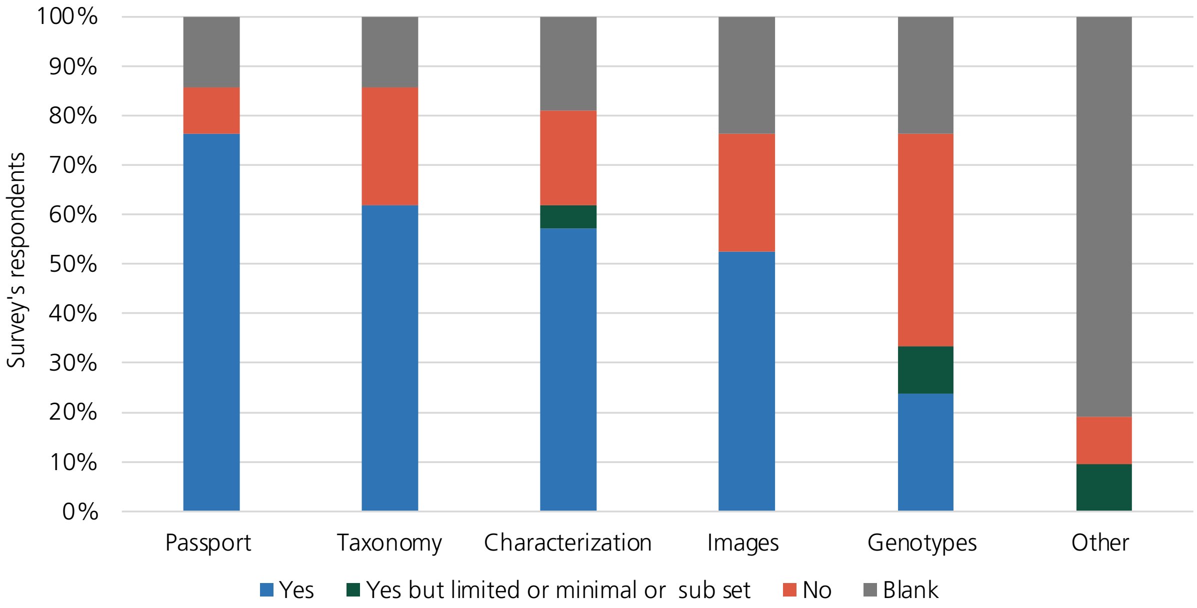


Figure 3.9 Types of data available for *Vigna* germplasm accessions stored in genebanks that answered the 2021-2022 survey (n = 21).

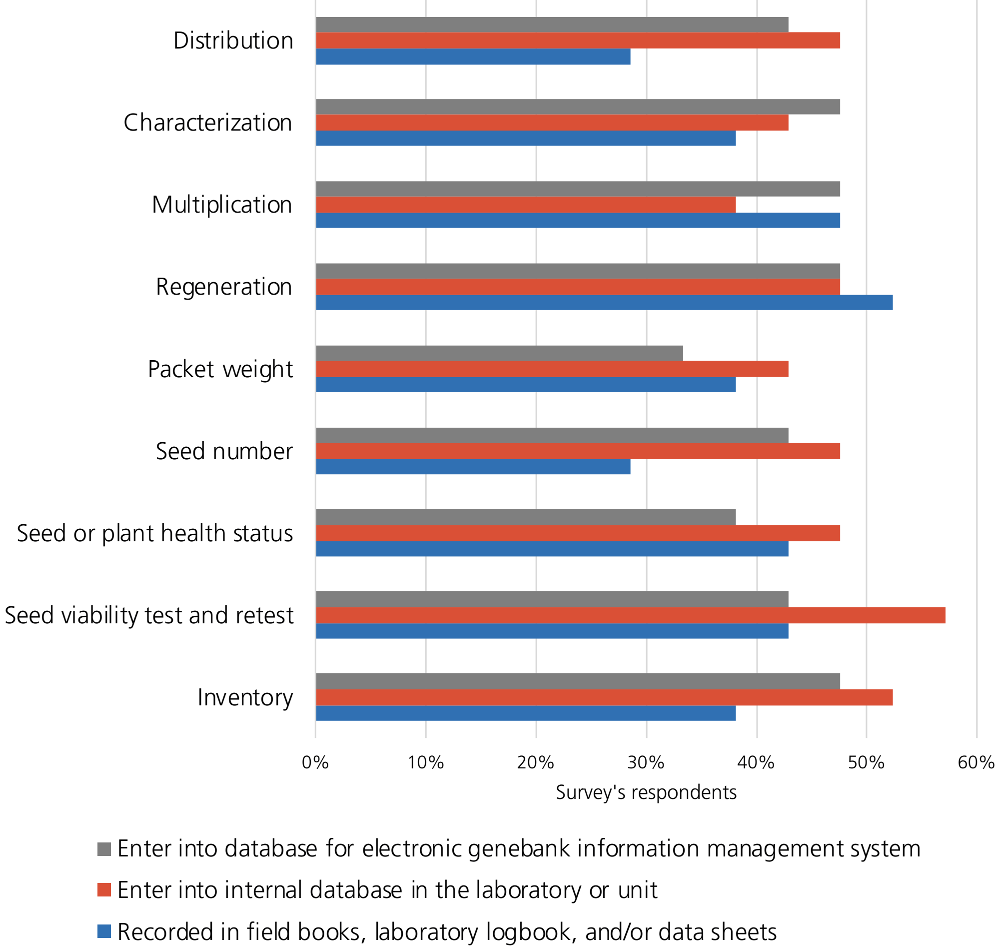


Figure 3.10 Types of data recorded by genebanks in field books, laboratory logbooks and/or data sheets; entered into an internal database in the laboratory or unit; and entered into the database of an electronic genebank information management system (n = 21, 2021-2022 Survey).

Of the 21 genebank respondents, eight reported that they have no barcoding facilities. Seven reported that they use barcodes to manage collections, conservation, storage, regeneration, and safety duplication. The Australian Grains Genebank reported that it uses QR codes to manage all genebank activities including storage, regeneration, distribution, viability testing and seed health testing. Seven respondents indicated that they use electronic tablets to collect data on characterization, harvesting, and threshing processes, seed viability, and accession requests by users. The electronic information system used to manage collections and share accession-level information was reported to be mostly adequate to meet the needs of the genebanks and users.

Most of the genebank respondents reported that they have their own standard operating protocols (SOPs) for characterization and data management. For example, WorldVeg uses its own SOP prepared under Worldveg-SOP-IM-V1 following the Key Performance Indicators of the Crop Trust for a Genebank Quality Management System. Regular characterization and the update of characterization data in the data management system are important in order to maintain the integrity of accessions and to avoid accumulating duplicates. The genebanks were asked about how often they update characterization data. A range of responses was obtained. Some genebanks reported that characterization data were updated every two years, every five years, and some reported even longer intervals of up to 10 years. Notably, some genebanks reported that they conduct characterization analyses every time an accession is regenerated. Others reported that they do not follow any specific schedule and tend to do it when funds are available

3.4.2 Major challenges in the characterization of *Vigna* collections

Funding, especially for labor and consumables, was reported as the major constraint to characterizing *Vigna* collections. The phenotyping and genotyping of a complete collection is a costly exercise that requires targeted funding. Some of the other challenges in the characterization of *Vigna* collections as reported in the survey include: insufficient staff time allocated to specific tasks such as regeneration, documentation, and sharing of genotypic and phenotypic data; a lack of screening facilities; inadequate laboratory facilities especially from a molecular characterization perspective; and inadequate expertise. A few genebanks also mentioned difficulties in the physicochemical characterization of seeds and agro-morphological characterization of *Vigna* varieties; in taxonomic identification; and in procuring materials from diverse altitudes. Some genebanks noted that not all morphological traits were expressed under different environmental conditions. Limited forages expertise, the lack of useful descriptors for characterization, and challenges with respect to crop management (fertilization, diseases and past pest management) and monitoring the growth habit in a changing environment were some of the other challenges reported in the survey.

3.4.3 Accuracy of passport information for *Vigna* collections

The survey asked the genebanks about the accuracy of the passport data for their *Vigna* collections. Of the 21 genebank respondents, 10 reported that their passport data is accurate. The Meise Botanic Garden reported that 87% of the collection has accurate passport data. According to the survey responses, accurate passport data are available for: more than 50% of the collection at CNRA; at least 40% of the collection at VIR; and 10% of the collection at the National Agriculture Genetic Resources Center (Nepal).

Some of the genebank respondents reported that they use the GRIN-Global genebank data management system to manage phenotypic and genotypic data. Some reported that they use Genesys for recording phenotypic data. Ten of the 21 genebank respondents have made some or all passport data (70% to 100%) available on Genesys. Some respondents reported that they use specific online platforms to store passport data information. These included:

- Meise Botanic Garden;
- WorldVeg;
- VIR;
- IITA;
- Australia;
- databases at the Alliance of Bioversity International & CIAT and the National Agriculture Genetic Resources Center (WIEWS-FAO and Genesys);
- ILRI - WIEWS; Genesys; GLIS; GRIN-Global
- USDA-ARS Plant Genetic Resources Conservation Unit.

3.4.4 Major challenges in data and information management for *Vigna* collections

As reported by the genebanks, the major challenges in data and information management for *Vigna* collections include:

- difficulty in exchanging passport data with other genebanks;
- non-uniformity of database systems among genebanks holding *Vigna* collections;
- insufficient time allocated to data management;
- lack of a modern database at a dedicated website; and
- no or poor access to genotypic data on online platforms.

In addition, the lack of expertise and capacity building for staff members in data management, inadequate time to acquire and store images of crop species, and inadequate funding were identified as constraints to data and information management for *Vigna* collections. Unlike some of the well-established genebanks, some smaller genebanks reported they do not have a database system and that data are instead stored in spreadsheets.

3.5 Germplasm evaluation

3.5.1 Traits evaluated

Accessions in collections are evaluated for multiple traits, including resistance to biotic and abiotic stresses. Such data are useful for breeding new varieties that are tolerant or resistant to one or more biotic and abiotic stresses. Genotype and molecular marker data for accessions will be helpful for documentation and identification of accessions. Most of the genebanks in the present survey did not provide information on biotic and abiotic stresses for which the accessions were screened, and also on the genotyping information of accessions that are available on public platform. However, five genebank respondents reported that phenotypic and genotypic characterization data and/or evaluation of the accessions obtained by other parties is available upon request.

Identification of duplicate accessions within a genebank collection is important, as it will help to minimize the effort and costs incurred in managing materials. The majority of the genebank respondents reported that duplicates are identified by morphological observation during field evaluation. Only a few genebanks reported using passport data and genotypic information to identify duplicates. Eight of the 21 genebank respondents reported that they analyze diversity among accessions using phenotypic and passport data, but only four reported that they make these diversity data available to users on an online platform.

3.5.2 Evaluation of biotic and abiotic stress resistance, and cross compatibility

According to the survey responses, drought, high temperature (heat) and water logging are the main abiotic stresses tested. The main tested biotic stresses reported include *Striga, Alectra,* aphids, pod borers, pod suckers, nematodes, powdery mildew, tan spot, halo blight and Mungbean Yellow Mosaic Virus (MYMD). Only three genebanks reported to have conducted cross-compatibility studies, with analyses of crossing between *V. vexillata* and *V. unguiculata,* and between *V. radiata* and *V. mungo*.

3.5.3 Major constraints to evaluation of *Vigna* accessions

The major constraints to the evaluation of *Vigna* accessions, as reported by the genebank respondents, include difficulty in phenotyping and genotyping the entire collection, incidence of diseases affecting plant vigor, and the viability and quality of stored seeds. In addition, the distribution of germplasm without considering its health status could hinder the overall evaluation process. A few genebanks reported that some of the *Vigna* collections are not suitable for biochemical characterization of seeds and pods for practical reasons. Inadequate methods to screen for tolerance to major biotic and abiotic stresses, a lack of systematic phenotyping methods, and limited or no information on cross-compatibility of wild *Vigna* with cultivated varieties were some of the other reported constraints to the evaluation of *Vigna* accessions.

3.6 Distribution and use of genetic resources of *Vigna* collections

The objective of procuring *Vigna* germplasm accessions is to make them available to users now and in the future. The distribution of accessions in the form of seed is a critical and rigorous process, as it involves a lot of technical work which must meet legal requirements and the objectives of genebanks at national and international level.

3.6.1 Availability of collections for users

The survey asked about the availability of information on different *Vigna* species to users, and the responses were grouped into three levels:

1. Data available to users within the institute;
2. Data available to users at the national level; and
3. Data available to users at the international level.

This grouping highlighted the following key points (Figure 3.11): irrespective of whether the species is domesticated, a wild relative or a landrace, most collections make materials available to users from one or more genebanks by request. However, across all the crop species listed, cowpea and mungbean were reported to have relatively more genebank distributors, whether within the institute (16 and 14, respectively), at the national level (16 and 15, respectively) and at the international level (12 and 9, respectively). For minor crop species like *V. trilobata*, *Vigna glabrescens*, *V. luteola* and *V. marina,* only one genebank distributor reported that they share materials at the within-institute, national, and international levels.

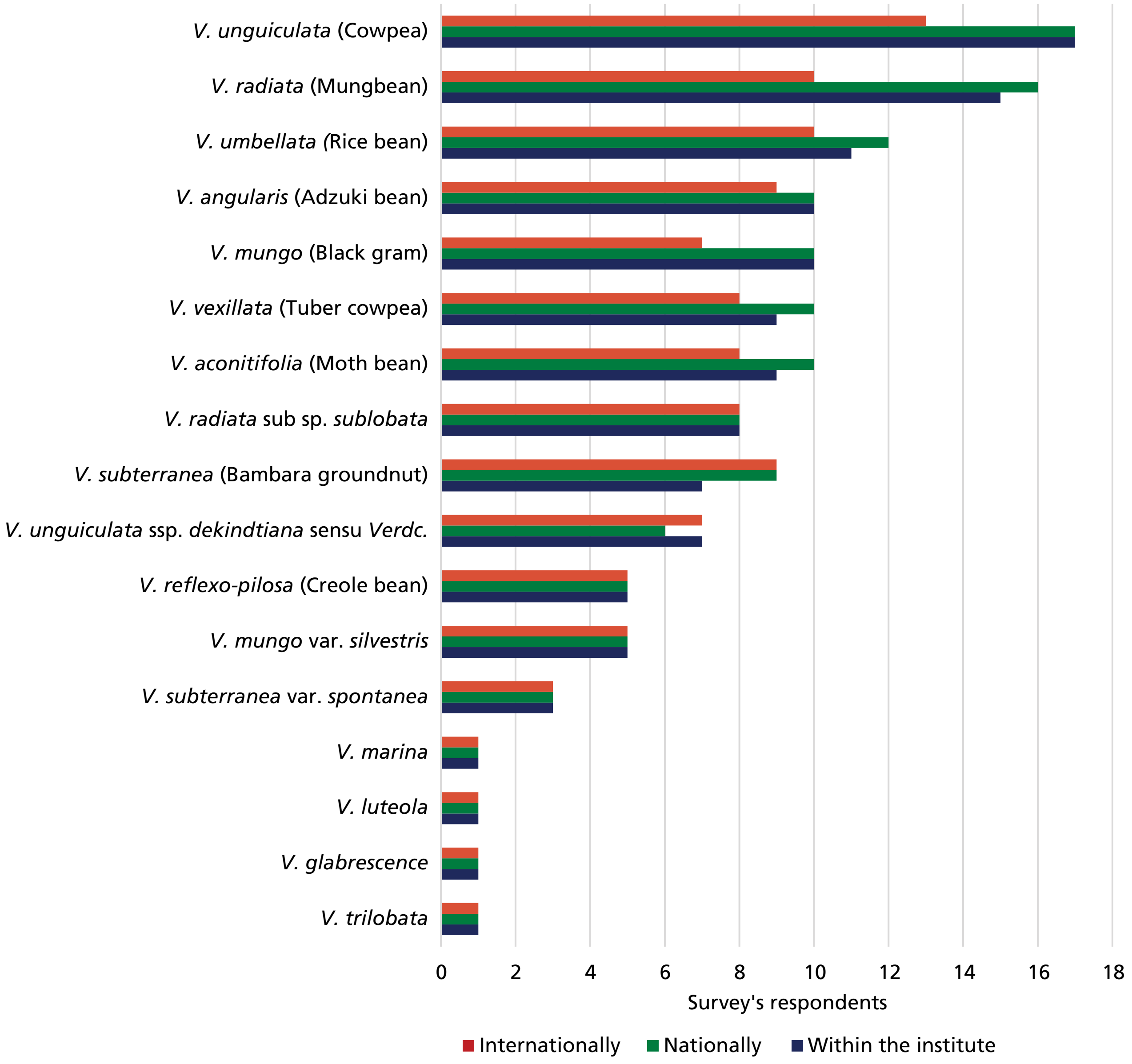


Figure 3.11 Number of genebank respondents making accessions of *Vigna* species available to users on request, internationally, nationally, and within the institute, (n = 21, Survey 2021–2022)

3.6.2 Conditions for distribution

The genebanks provided a range of responses to questions about restrictions of the distribution of collections. Some of the genebanks reported that accessions are included in the Multilateral System (MLS) and/or distributed under the framework of the Plant Treaty through a signing of a SMTA. Under these agreements, all the accessions with sufficient seeds are made available with an SMTA using the Easy-SMTA system for bona fide research, breeding and training. Some genebanks reported that they provide *Vigna* accessions only for research and direct use but not for commercial use. Some reported that they require a memorandum of understanding with private companies, and some reported that they distribute seeds only for non-profit research. In addition, some genebanks reported that they distribute accessions nationally for legitimate research/educational purposes and distribute seeds for research use internationally to countries with whom they have diplomatic relations.

Most of the genebank respondents reported that they have adequate procedures in place for the distribution of accessions to the requestor. Some of the procedures include signed material transfer agreement (MTA) or SMTA (14 genebank respondents), phytosanitary certification (17 genebank respondents), packaging (15 genebank respondents) and shipping (14 genebank respondents). However, some of the genebank respondents raised some concerns about the existing procedures. They reported that MTA/SMTA take a long time to process within the institute, and that phytosanitary certification is expensive and time-consuming. Some genebanks reported that it was difficult to distribute collections internationally because of limited funds for shipping and the lack of availability of small packets. A few genebank respondents also reported that there is a lack of proper legislation at the national level to distribute materials systematically.

3.6.3 Frequency of distribution

The survey asked about the frequency of distribution of *Vigna* accessions during the past 10 years. Analyses of the responses indicated that more than 90% of requests have been addressed successfully (number of requests received compared with number of requests addressed) (Figure 3.12). Only eight genebank respondents reported that it is fairly easy to share materials outside the country.

3.6.4 Routine follow-up and soliciting of feedback from germplasm recipients

Only about one-third (29%) of the genebank respondents reported that they collect feedback on the timeliness of distribution, the helpfulness of the information or advice from genebank staff in selecting accessions (Figure 3.13), and the quality and usefulness of the accessions. 33% of the genebanks reported that they collect feedback on the usefulness of the accessions received and the quality of the samples sent, and 19% reported that they collect feedback on the quality of packaging used and the sharing of evaluation or characterization data sets. A quarter of genebanks (24%) reported that they ask recipients to provide details of publications containing specific research results derived from the evaluation or use of the accession received; and 14% of the genebanks reported that they collect feedback on variety releases, adoption studies, or case studies on the use of an accession received.

According to the survey responses, collecting feedback is generally an informal process, rather than a systematic and mandatory one. The users can voluntarily provide feedback. Upon receiving feedback from users, a few genebanks reported that they use this information internally to improve seed management procedures and to understand whether the distributed germplasm has been useful. Some genebank respondents reported that feedback is taken seriously and necessary changes are made to the protocols/procedures upon reviewing, and then implemented within 6 months. A few genebanks reported that any feedback on integrity issues is investigated and any mixed/contaminated samples are removed from the active inventory.

3.6.5 Major challenges in the distribution of accessions

Some of the major challenges in distributing collections within and outside the country include:

- difficulty in obtaining phytosanitary certificates;
- limited availability/quantity of seeds because of damage caused by pests and disease; and
- reluctance of the requester to sign the SMTA and the long processing times for SMTA and MTA.

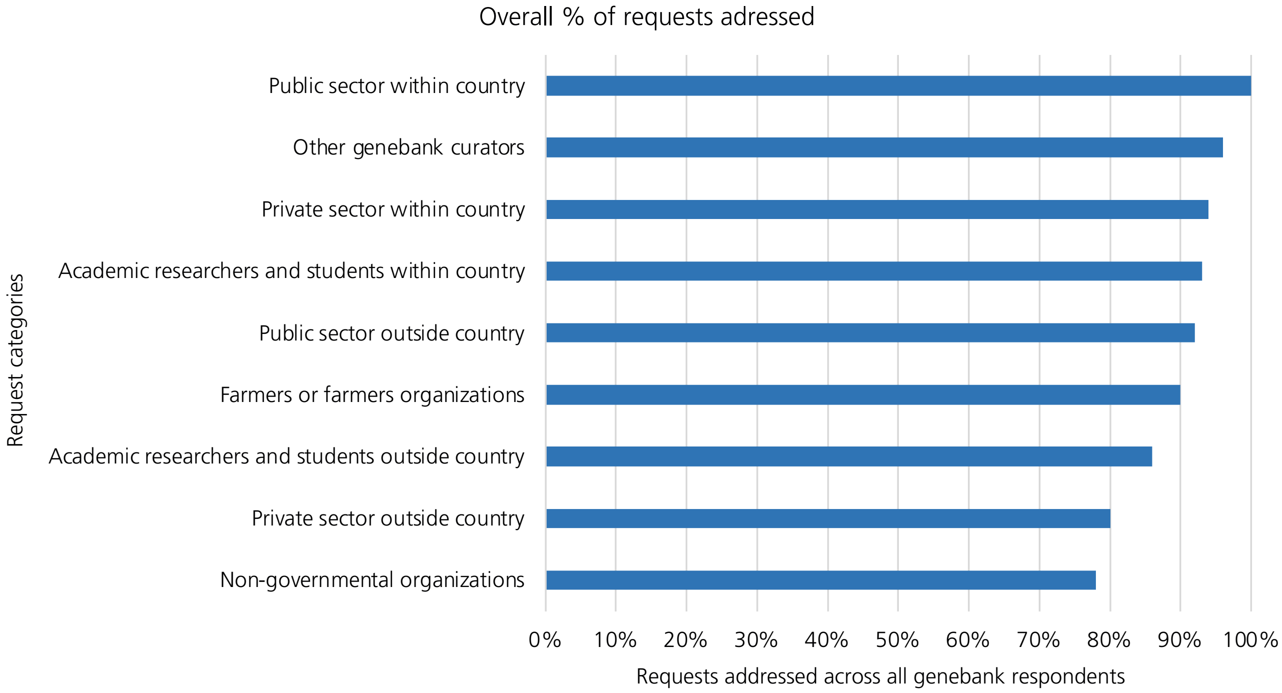


Figure 3.12 Overall percentage of requests addressed (across all genebank respondents) in specific request categories in the past 10 years. (n = 21, Survey 2021-2022).

A few genebanks reported that they did not have enough characterization data available for many available accessions, and hence could not share them with users. A few genebanks noted that shipping costs and the stringent restrictions of the host countries made it difficult to share materials internationally.

3.7 Safety duplication

Safety duplication is the replication of a genetically identical sub-sample of the accession to reduce the possibility of its partial or complete loss as a result of natural or man-made disasters (Engels and Visser, 2003). Safety duplicates are deposited in a base collection at a different location, typically in another country, and include both the duplicate of the material and its related data. The location is selected to reduce potential threats and on the basis of its ability to store the materials under suitable conditions. When asked if their collection of *Vigna* species was duplicated outside the country, five genebanks reported that part of their collection was safety duplicated, two reported that the entire collection was safety duplicated, and one reported that 90% of the collection was safety duplicated outside the country. Three genebanks reported that their collections were not safety duplicated. Most of the genebanks reported specific constraints to duplicating the collection elsewhere within or outside the country. These constraints included no or little active regeneration of the collection so that there are no duplicates to deposit elsewhere, limited budgets, and the low priority for *Vigna* species at their specific genebank. Nevertheless, many genebank respondents reported that they have already deposited some of their *Vigna* accessions at the SGSV under a black box agreement. As part of the agreement, the depositor must safety duplicate the same collection in another genebank that follows the similar international standards for conservation of germplasm. As of August 2022, 29 genebanks have deposited about 40,672 *Vigna* accessions at the SGSV, representing 64 species and 142 taxa.

3.8 Staff and training

3.8.1 Number of staff for conservation and distribution

Of the 21 genebank respondents, 16 reported that they allocate four staff on average to conduct routine annual operations for conservation; 15 reported that they allocate three staff on average to meet distribution requests annually; and 15 reported that they allocate three staff on average to supply accession-level information to users (Figure 3.14). Most of the genebanks reported that the staff had a high level of expertise in conservation and distribution activities, and usually consisted of curators, technicians, and farm supervisors. A few genebanks reported that training was provided as required to staff on methods of collection, conservation and distribution. One of the major concerns highlighted in the survey was

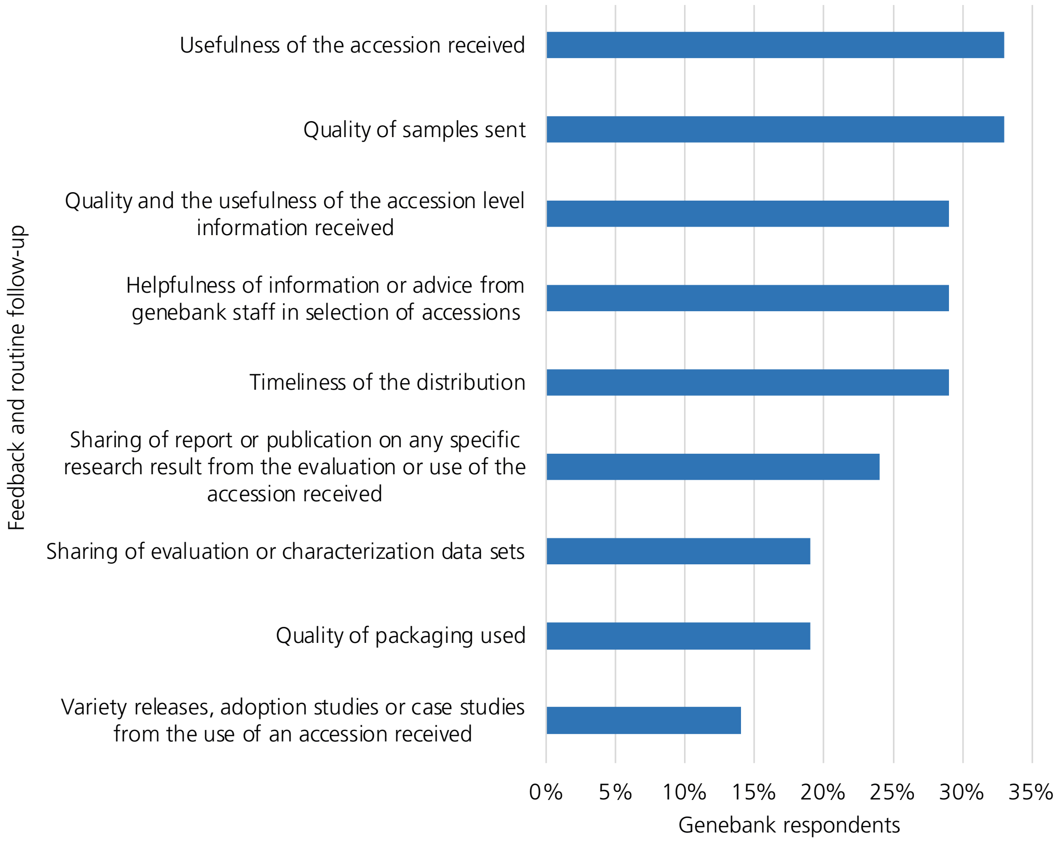


Figure 3.13 Types of feedback solicited by genebanks about the quality and use of distributed accessions (n = 21, Survey 2021-2022).

that only 38% of the genebank respondents have a dedicated curator for *Vigna* collections. This situation needs to be addressed.

3.8.2 Gaps in expertise and challenges for genebank staff

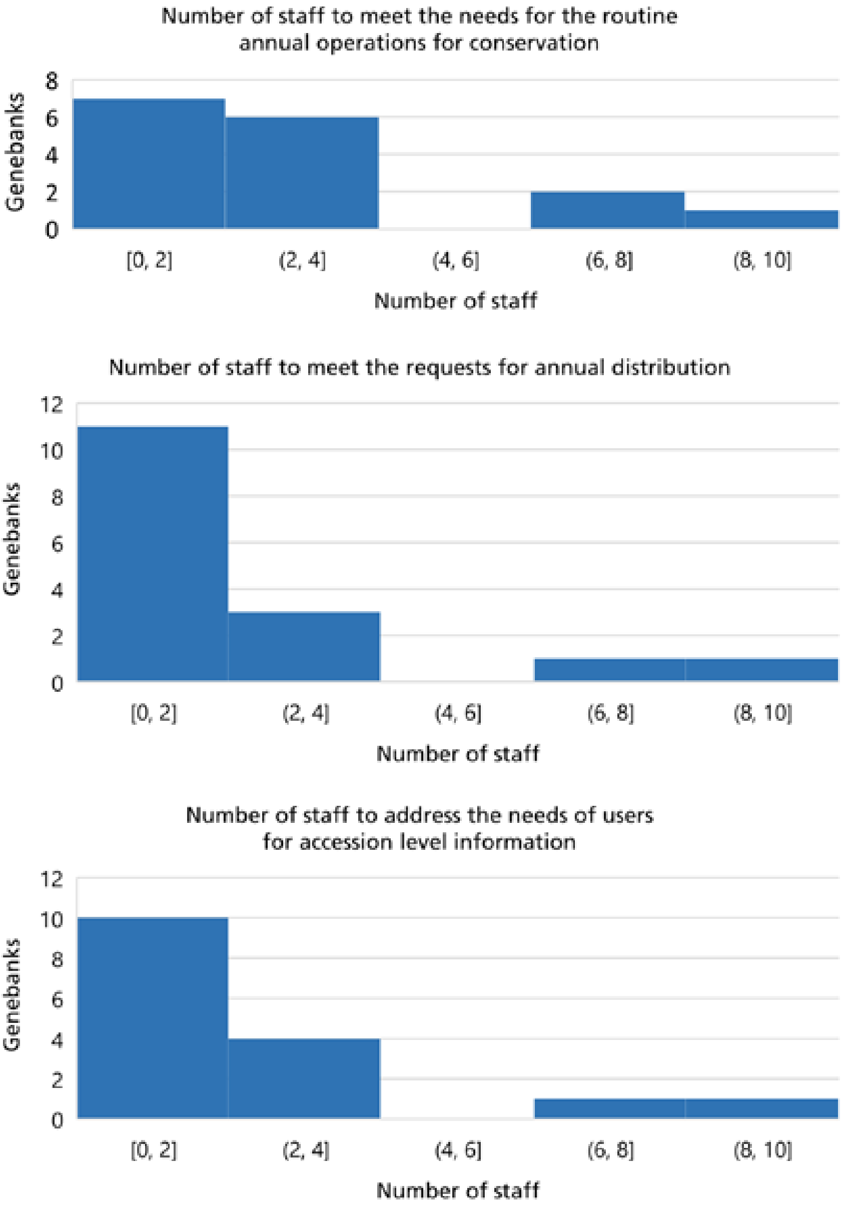
Some of the challenges reported by genebanks include untrained staff, and a lack of expertise in taxonomy, identification and characterization. Some genebanks reported that it is difficult to attract staff to work in regional centers, and some reported difficulties in retaining scientific and technical staff long term. Genebank staff were reported to face major challenges with respect to insufficient time for genotyping, phenotyping and regeneration of accessions.

3.9 Funding sources

Most of the genebanks reported that funding is not stable, and that short-term funding supports germplasm collection, conservation and distribution.

3.10 Risk management

Some genebank respondents (38%) reported that they have completed a risk assessment or it is underway. These risk assessments are performed by a committee involving one or more administrators. In addition, it was reported that the risk assessment plans will be reviewed annually, every two years, or every five or 10 years.



Number of staff to meet the needs for the routine annual operations for conservation

Number of staff to meet the requests for annual distribution

Number of staff to address the needs of users for accession level information

Figure 3.14 Histograms showing the distribution of the answers regarding the number of staff allocated to the conservation, distribution and to address the needs of users for accession level information of Vigna collections (n = 21, 2021–2022 survey).

3.10.1 Primary threats to the collections

According to the genebank responses, the primary threats to the collections include:

- lack of regeneration due to adverse conditions (climate conditions and/or insects/pests);
- loss of accessions due to conservation problems (e.g., fire in conservation facilities);
- genetic erosion;
- lack of funding to regenerate collections;
- inadequate power supply to the genebank;
- natural calamities; and
- uncertainty of funding, especially long-term funding.

Some of the major storage pests reported by the different genebanks include bruchids and weevils. In addition, fungal and bacterial diseases affect some stored materials. Some genebank respondents reported that thrips, aphids, pod bugs and spider mites are the predominant pests of concern during regeneration and multiplication. Leaf spot, charcoal rot, pot-viruses, *Curvalaria* sp., powdery mildew and leaf blight are some other diseases reported to affect materials during regeneration and multiplication.

3.10.3 Impacts of the COVID-19 pandemic during 2020-2021 on genebank operations

The survey asked about the impact of COVID-19 pandemic on genebank operations. The responses are summarized below:

- Some genebanks found that COVID-19 greatly impacted the collection and introduction of new accessions. Some noted that agricultural inputs have become more expensive. However, due to COVID-19, some conservation conditions have been improved to limit the loss of genetic material and the level of multiplication has increased, resulting in larger quantities of seeds.
- Inadequate staff availability for maintenance activities in the field and laboratory; specifically, <10% of staff were allowed to carry out necessary genebank activities during lockdown periods.
- A few genebanks reported that only senior staff were permitted to perform essential tasks. Some staff resided on the premises, but two-thirds of staff were on furlough and were not permitted to work.
- Some of the genebanks focused only on limited genebank operations while research staff focused on writing SOPs. In those genebanks, regeneration was conducted on a limited scale because of the frequent lockdowns.
- Many genebanks were forced to operate at half the normal staffing level to undertake activities related to distribution, regeneration, post-entry quarantine, seed conservation in long-term storage, packing for back-ups and viability testing. This was mitigated by reducing regeneration activities, reducing staff numbers, and focusing only on distribution and post-entry quarantine (client service activities). Viability testing and backing-up were paused, and processing of germplasm from a drying room to long-term storage was slowed.
- A few genebanks reported that COVID-19 had minimal impacts on their activities. Field work (regeneration) was able to continue, and field-grown plants were tended during lockdowns. Some genebanks reported that the pandemic mainly affected collection, on-farm trials and regeneration activities. Remote meetings and communication were used to support work on collection and on-farm activities.
- Some genebanks reported that they initially reduced staff numbers, but this resulted in the spread of diseases in regeneration plots, leading to the loss of about half of the accessions. No additional accessions were grown in the field for regeneration during the pandemic. Furthermore, COVID-19 disrupted seed order processing/shipping operations, resulting in significant backlogs.

Yard Long Bean. Photo: Amada44/ Wikimedia Commons

4 RECOMMENDATIONS

Here, we outline a list of recommendations to improve support the global system for the conservation of *Vigna* genetic diversity:

Global funding strategy

- Establish a long-term global funding strategy for the collection, conservation, characterization, and distribution of *Vigna* genetic resources.

Establish an International *Vigna* Advisory Group (IVAG)

- Establish an International *Vigna* Advisory Group (IVAG) to implement and review the Global *Vigna* Conservation Strategy periodically and engage key stakeholders to enhance the global conservation and use of *Vigna* genetic resources. This group should include crop genebanks with large *Vigna* collections. These organizations include the
  1. International Institute of Tropical Agriculture (IITA);
  2. WorldVeg;
  3. Indian Council of Agricultural Research (ICAR) -National Bureau of Plant Genetic Resources (NBPGR);
  4. USDA, and
  5. National Agriculture and Food Research Organization, Japan (NARO).
- The IVAG will need to work closely with the *Vigna* Crop Germplasm Committees (CGC) of the USDA.
- The IVAG should develop strategic *Vigna* germplasm conservation goals in collaboration with national partners and/or NGOs to collect new germplasm from threatened regions and manage native *Vigna* germplasm *in situ*.
- The IVAG, in consultation with the Crop Trust, should leverage funding for smaller national *Vigna* germplasm repositories that are underfunded and have insufficient infrastructure or staffing, to safeguard their *Vigna* collections. These genebanks/repositories must be integrated into a global system of germplasm conservation.
- The IVAG and the Crop Trust must explore opportunities for partnerships between the smaller genebanks and some of the leading *Vigna* genebanks for research and product (cultivar) development.

Identify and engage with *Vigna* key collections

- In addition to major crop genebank collections that are mentioned above, there are a several smaller collections. These smaller collections require further evaluation about their complementarity to the major collections and their roles in a global *Vigna* conservation strategy. It will especially be relevant to identify the complementary roles of crop genebanks and botanic gardens in conservation, characterization, and distribution of germplasm. Organizations that maintain smaller collections include:
  1. Nepal National Agriculture Genetic Resources Center;
  2. International Center for Tropical Agriculture (CIAT);
  3. Australian Pastures Genebank;

iv. South Australian Research and Development Institute (SARDI);
v. Royal Botanic Gardens, Kew – Millennium Seed Bank, UK; and
vi. Meise Botanic Garden, Belgium.

Complementary to the major crop genebanks, Meise Botanic Garden maintains the most species-rich *Vigna* collection globally, and is therefore an important organisation.

Policy implementation

- Support and encourage countries that ratified the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) with the inclusion of their *Vigna* collections in the Multilateral System of the ITPGRFA. Countries that ratified the ITPGRFA may not necessarily have done this yet despite the fact that all *Vigna* species are listed in the Annex 1 of the ITPGRFA.

Capacity building

- Conduct regular training programs, either in-person or virtually, for staff involved in *Vigna* conservation and train additional personnel in germplasm conservation and management activities. These training programs must also include taxonomic identification, morphological characterization, and genomic characterization. In addition, capacity building in international policy regulations for access to germplasm allows to bring more context to sharing seed and information with users nationally and internationally.

Characterization

- Systematically catalog all available *Vigna* accessions at each genebank in coordination with a well-established database system for *Vigna*. This will be helpful for prioritizing regeneration and multiplication of threatened germplasm. In addition, it will help to avoid losses of germplasm in the future, because most of the materials lost so far lacked taxa/species information.
- Phenotyping and genotyping of at least newly collected accessions should be conducted on a priority basis to identify unique materials. The *Vigna* collections in most genebanks overlap, but the level of redundancy is unknown because most genebanks do not have sufficient resources for characterization. We recommend that comprehensive genotypic information should be made available on a common online platform for future reference.
- Increase the number and availability of core and mini-core collections. The results of the survey revealed that there is an urgent need to develop such collections among the different species in *Vigna* and across genebanks. The genebank with the largest collection of a species may take the lead in this objective. For example, The International Mungbean Improvement Network (IMIN) led by World Vegetable Center has developed mini-core accessions of mungbean (Schafleitner et al. 2015) and shared with partners. A database management system (KDDart) is being used to share both phenotypic and genotypic data.
- Review the reproductive biology with a focus on self- and cross-pollination rates of *Vigna* crops to establish regeneration protocols that are cost-effective and up to standard to avoid inadvertent cross-pollination.
- As reported in the survey, genebanks have been using independent descriptors for characterization data. This has led to gaps in trait characterization and discrepancies in how data are recorded. Hence, for universal application, a standardized and comprehensive list of descriptors should be developed across *Vigna* species for consistency of data collection and data compatibility among genebanks and other *Vigna* germplasm repositories.
- Systematically evaluate the *Vigna* germplasm for resistance to biotic and abiotic stresses regionally and make the data available to the global *Vigna* research community.
- Systematically evaluate *Vigna* germplasm for nutritional/ health related compounds and make the data available to the global *Vigna* research community.

Collecting and *in situ* status of threatened germplasm

- Collect seed of threatened and endemic wild relatives of *Vigna,* which require urgent conservation. Priority should be on these rare species, which are more difficult to find and often endangered, and not yet well represented in genebank collections such as the endemic and endangered *V. keraudrenii* and *V. bosserii* in Madagascar, *V. monantha* and *V. somaliensis* in East Africa, and the endemic *V. o-wahuensis* in Hawaii, among others. Actively monitor and conserve the population of *Vigna* wild relatives *in situ* in protected areas and other areas and engage national conservation programs in collaboration with local communities and national universities to monitor their populations. This can be combined with germplasm collecting activity. Priority should be on conservation/collection of rare species as mentioned above. Monitoring is important as there is little evidence about the population trends while many populations are predicted to be extirpate due to climate change and other threats. This could be done by revisiting a location on a regular basis to describe the conservation status with standardized descriptors. Students from national universities could support these efforts as part of thesis research that can contribute to long-term research on population trends of rare crop wild relatives.

ACRONYMS AND ABBREVIATIONS

BARI	Bangladesh Agricultural Research Institute
BMEL	Government of Germany
CGIAR	Consultative Group on International Agricultural Research
CIAT	The International Center for Tropical Agriculture
CNRA	Centre National de Recherche Agronomique
DRC	Democratic Republic of the Congo
EMBRAPA	Brazilian Agricultural Research Corporation
FAO	Food and Agriculture Organization
FAO-WIEWS	FAO-World Information and Early Warning System
GLIS	Global Information System
GRIN-Global	Germplasm Resources Information Network-Global
GSCV	Global strategy for the conservation and use of *Vigna*
IAG	International Advisory Group
IITA	International Institute for Tropical Agriculture
ILRI	International Livestock Research Institute
INERA	Institut de l'Environnement et de Recherches Agricoles
IPGRI	International Plant Genetic Resources Institute
ITPGRFA	International Treaty for Plant Genetic Resources for Food and Agriculture
MCPD	Multi-Crop Passport Descriptors
MLS	Multilateral System
MTA	Material transfer agreement
NACGRAB	National Centre for Genetic Resources and Biotechnology
NARO	National Agriculture and Food Research Organization
NARS	National Agricultural Research System
NBPGR	National Bureau of Plant Genetic Resources, India
NPGS	National Plant Germplasm System
NGO	Non-Governmental Organization
PCR	Polymerase chain reaction
PGRCU	Plant Genetic Resources Conservation Unit
QTL	Quantitative trait loci
SARDI	South Australian Research and Development Institute
SGSV	Svalbard Global Seed Vault
SMTA	Standard material transfer agreement
SNP	Single nucleotide polymorphism
SOP	Standard operating procedure
SPGRC	SADC Plant Genetic Resources Center
USDA-ARS	United States Department of Agriculture-Agricultural Research Service
VIR	N. I. Vavilov Institute of Plant Genetic Resources, Russia
WorldVeg	World Vegetable Center, Taiwan
WIEWS	World Information and Early Warning System

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APPENDICES

Appendix 1. Maximum likelihood tree

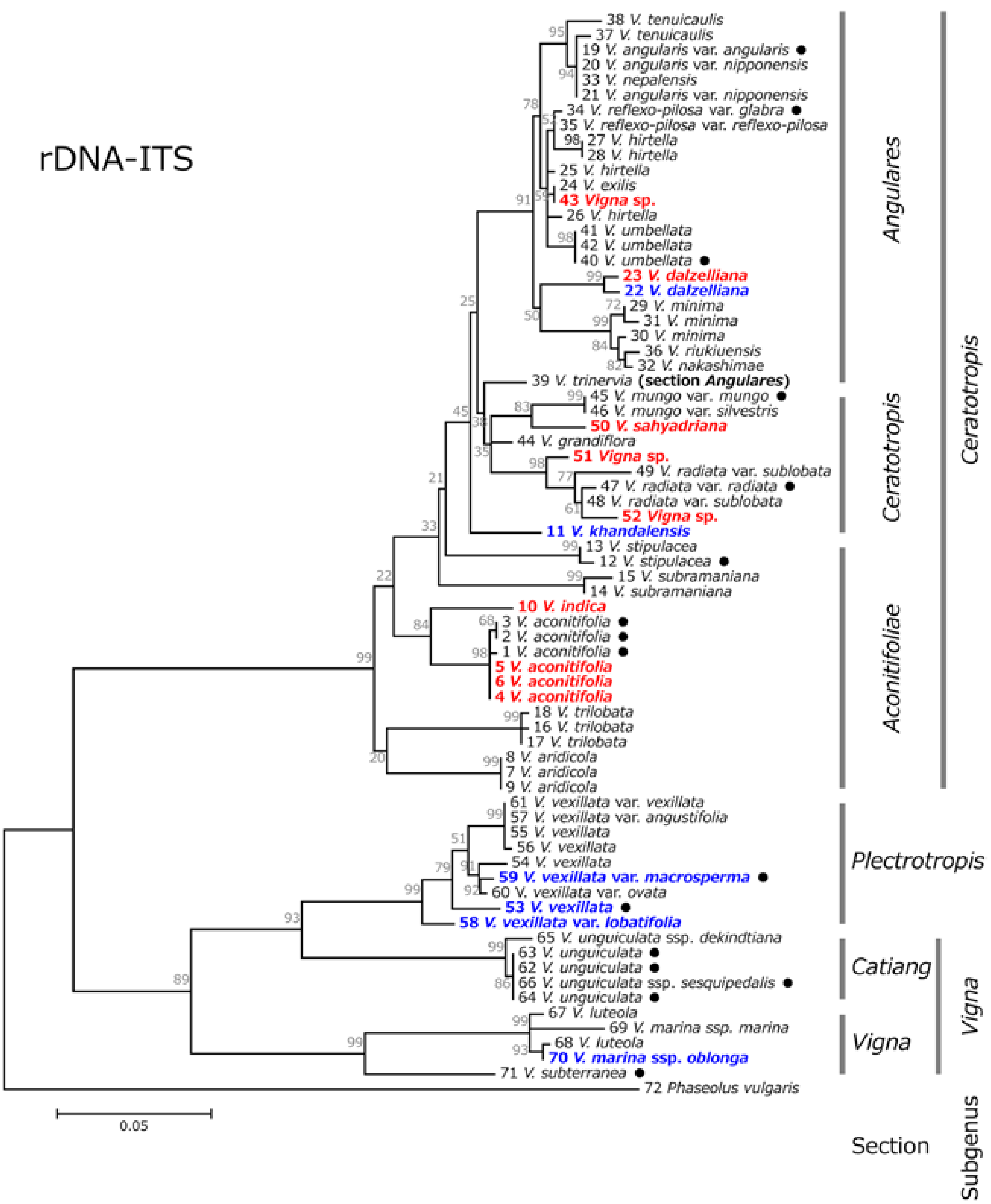


Figure 1. Maximum likelihood tree based on nuclear rDNA-ITS region for the genus *Vigna*, with *Phaseolus vulgaris* as an outgroup. Numbers beside branches represent bootstrap values (%) based on 1000 replications. Scale indicates genetic distance. Domesticated accessions are indicated with black circles, accessions which have been introduced as unidentified or misidentified accessions are indicated with red text, and taxa in which phylogenetic discussion using DNA sequences had not been conducted are indicated with blue text. (Source: Takahashi et al. 2016)

Appendix 2. Name of the genebanks and *Vigna* accessions available (Genesys and WIEWS, 2022) at different genebanks

Genebank Name	Acronym	Institution Code	Type Of Institution	*Vigna* Accessions
World Vegetable Center	AVRDC	TWN001	Non-Governmental	22,491
International Institute of Tropical Agriculture	IITA	NGA039	CGIAR	20,088
National Bureau of Plant Genetic Resources	NBPGR	IND001	Governmental	13,964
Plant Genetic Resources Conservation Unit, Southern Regional Plant Introduction Station, University of Georgia, USDA-ARS	S9	USA016	Governmental	13,060
NARO Genebank	NARO	JPN183	Governmental	12,038
Embrapa Recursos Geneticos e Biotecnologia	CENARGEN	BRA003	Governmental	5,107
Australian Grains Genebank, Department of Economic Development Jobs Transport and Resources	AGG	AUS165	Governmental	4,515
Embrapa Meio Norte	CPAMN	BRA142	Governmental	3,911
N.I. Vavilov Research Institute of Plant Industry	VIR	RUS001	Governmental	2,838
Institute of Plant Breeding-National Plant Genetic Resources Laboratory	IPB-NPGRL	PHL129	Governmental	2,386
Plant Genetic Resources Program	PGRP	PAK001	Governmental	1,991
Plant Genetic Resources Centre	PGRC	LKA036	Governmental	1,977
Genebank		THA300	Governmental	1,739
Genetic Resources Research Institute	GeRRI	KEN212	Parastatal	1,668
National Plant Genetic Resources Centre	NPGRC	BWA015	Governmental	1,610
SADC Plant Genetic Resources Centre	SRGB	ZMB030	Regional	1,397
Uzbek Research Institute of Plant Industry	UzRIPI	UZB006	Governmental	1,146
National Centre for Genetic Resources and Biotechnology	NACGRAB	NGA010	Governmental	1,140
International Livestock Research Institute	ILRI-Ethiopia	ETH013	CGIAR	1,113
Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development	ICABIOGRAD	IDN179	Governmental	1,019
National Plant Genetic Resources Centre	NPGRC	TZA016	Governmental	930
National Plant Genetic Resources Centre	NPGRC	ZMB048	Governmental	901
Botanic Garden Meise	BGM	BEL014	Governmental	888
Centro Internacional de Agricultura Tropical	CIAT	COL003	CGIAR	751
Institut national de la recherche agronomique du Niger	INRAN	NER001	Governmental	636
Agricultural Plant Genetic Resources Conservation and Research Centre	ARC	SDN002	Governmental	582
Genebank, Leibniz Institute of Plant Genetics and Crop Plant Research	IPK	DEU146	Governmental	550
Corporación Colombiana de Investigación Agropecuaria Tibaitata, CORPOICA	ICA/REGION 1	COL017	Governmental	493
Myanmar SeedBank	MSB	MMR015	Governmental	487
Centro Nacional de Recursos Fitogeneticos	INIA-CRF	ESP004	Governmental	485
Australian Pastures Genebank	APG	AUS167	Governmental	470
Bangladesh Agricultural Research Institute	BARI	BGD003	Governmental	455
International Center for Biosaline Agriculture	ICBA	ARE003	International	455
Institute for Plant Genetic Resources 'K.Malkov'	IPGR	BGR001	Governmental	401

Genebank Name	Acronym	Institution Code	Type Of Institution	*Vigna* Accessions
Genetic Resources and Biotechnology Institute, Department of Agricultural Research for Development, Ministry of Agriculture, Mechanization and Irrigation Development	GRBI	ZWE049	Governmental	396
Portuguese Bank of Plant Germplasm	BPGV-DRAEDM	PRT001	Governmental	357
Seed Savers Exchange	SSE	USA974	Non-Governmental	334
National Agriculture Genetic Resources Centre-Genebank	NAGRC	NPL069	Governmental	326
Plant Genetic Resources Research Institute	PGRRI	GHA091	Governmental	313
Plant Genetic Resources Department	AARI	TUR001	Governmental	307
Institute for Agrobotany	RCA	HUN003	Governmental	306
Malawi Plant Genetic Resources Centre	MPGRC	MWI041	Governmental	293
CREA-Centro di Ricerca Zootecnia e Acquacoltura, sede di Lodi	CREA-ZA-LO	ITA394	Governmental	289
Instituto de Investigaciones Fundamentales en Agricultura Tropical	INIFAT	CUB014	Governmental	235
Genetic Resources Directorate, Department of Agriculture, Forestry and Fisheries	DAFF	ZAF062	Governmental	220
Centro Agronómico Tropical de Investigación y Enseñanza	CATIE	CRI001	International	184
National Plant Genetic Resources Centre	NPGRC	NAM006	Governmental	165
Unité des Ressources Génétiques	URG	MLI070	Governmental	148
Millennium Seed Bank Project, Seed Conservation Department, Royal Botanic Gardens, Kew, Wakehurst Place	RBG	GBR004	Governmental	142
Centre de Recherche Agronomique Savane Sèche	CRA-SS	TGO044	Governmental	134
Research and Development Station for Plant Culture on Sands Dabuleni	SCDCPN Dabuleni	ROM021	Governmental	134
National Gene Bank	NGB	EGY087	Governmental	115
National Plant Genetic Resources Centre	NPGRC	SWZ015	Governmental	111
Ethiopian Biodiversity Institute	EBI	ETH085	Governmental	99
Bangladesh Institute of Nuclear Agriculture (BINA)	BINA	BGD028	Governmental	99
Lal Teer Seed Limited	LTS	BGD206	Private	88
National Center for Genetic Resources Preservation	NCGRP	USA995	Governmental	73
Dipartimento di Biologia Applicata, Università degli Studi Perugia	PERUG	ITA363	Governmental	73
Margot Forde Forage Germplasm Centre, AgResearch Ltd	AGRESEARCH	NZL001	Governmental	71
Republican National Genetic Resource Center	RNGRC	TJK027	Governmental	69
Suceava Genebank	BRGV Suceava	ROM007	Governmental	64
Station de Recherche Alaotra, FOFIFA	FOFIFA-CALA	MDG016	Governmental	64
Scientific Center of Agrobiotechnology	SC AB	ARM059	Governmental	63
Department of Agriculture - Region 2	DA-Region 2	PHL200	Governmental	62
Plant Genetic Resource Centre	PGRC	UGA132	Parastatal	61
National Agricultural Research Institute	NARI	ERI003	Governmental	51
Estacion Experimental de Toralapa	EE-Toralapa INIAF	BOL317	Governmental	49
Bureau of Plant Industry, Department of Agriculture	BPI	PHL008	Governmental	45

Genebank Name	Acronym	Institution Code	Type Of Institution	*Vigna* Accessions
Agricultural Research Service		JOR015		39
INIFAP, Centro Nacional de Recursos Genéticos (CNRG)	CNRG	MEX208		38
National Agricultural Research Center	NARC	JOR105	Governmental	38
Centro de Investigaciones Agropecuarias	CIAP	CUB284	Governmental	35
Genetic Resources Institute	GRI	AZE015	Governmental	33
Plant Gene Resources of Canada, Saskatoon Research and Development Centre	PGRC	CAN004	Governmental	33
Banco Activo de Germoplasma de La Consulta	BGLACONSULTA	ARG1350	Governmental	29
Unite de Recherche en Culture In-vitro (URCI)	ISRA-URCI	SEN075	Governmental	29
Institute of Plant Production n.a. V.Y. Yurjev of UAAS	IR	UKR001	Governmental	26
National Agricultural Research and Extension Institute	NAREI	GUY021	Governmental	25
Greek Genebank, Agricultural Research Center of Macedonia and Thrace, National Agricultural Research Foundation	GGB-NAGREF	GRC005	Governmental	24
Central Experiment Station, Research Division, Ministry of Agriculture, Land and Marine Resources		TTO010	Governmental	24
Desert Legume Program	DLEG	USA971	Governmental	23
INIA La Estanzuela	INIA LE	URY003	Governmental	22
Lesotho National Plant Genetic Resources Centre	LNPGRC	LSO015	Governmental	22
Ustymivka Experimental Station of Plant Production	UDS	UKR008	Governmental	19
Instituto de Investigaciones Agropecuarias Jorge Dimitrov	IIAJD	CUB251	Governmental	19
Centro de Investigacion Agropecuaria de Recursos Geneticos	CIARG	PAN075	Governmental	16
Research and Development Station for Vegetables - Bacau	SCDL Bacau	ROM055	Governmental	15
Station de la Reunion, CIRAD-FLHOR	CIRAD-FLHOR	FRA098	Governmental	11
Banco de Germoplasma - Universidade da Madeira	ISOPlexis	PRT102	Governmental	10
Instituto Nacional de Ciencias Agricolas	INCA	CUB005	Governmental	10
Research and Development Station for Vegetables Buzau	SCDL Buzau	ROM068	Governmental	8
National Semi Arid Agricultural Research Institute	NASARRI	UGA394	Parastatal	8
Estacion Experimental de Pastos y Forrajes Indio Hatuey	EEPF	CUB010	Governmental	7
Universidad Tecnica Nacional - Sede Atenas	UTN	CRI141	Parastatal	7
Israel Gene Bank for Agricultural Crops, Agricultural Research Organisation, Volcani Center	IGB	ISR002	Governmental	7
Centro Nacional de Investigacion Agropecuaria y Biotecnologia (INTA-CNIAB)	INTA - CNIAB	NIC014	Governmental	7
UACh, Centro Regional Universitario Sur (CRUS)	CRUS	MEX201		7
International Centre for Agricultural Research in Dry Areas	ICARDA	LBN002	CGIAR	6
Embrapa Clima Temperado	CPACT/EMBRAP	BRA020	Governmental	6
Consejo Superior de Investigaciones Cientificas. Mision Biologica de Galicia	CSICMBG	ESP009	Governmental	6
National (CYPARI) Genebank, Agricultural Research Institute, Ministry of Agriculture, Rural Development and Environment	ARI	CYP004	Governmental	5
Instituto de Investigación y Capacitación Agropecuaria, Acuícola y Forestal del Estado de México (ICAMEX)	ICAMEX	MEX194		5

Genebank Name	Acronym	Institution Code	Type Of Institution	*Vigna* Accessions
Centre National de Recherche Agronomique et de Developpement Agricole	CNRA	MRT002	Governmental	5
Republican Unitary Enterprise ‘Scientific Practical Centre of the National Academy of Sciences of Belarus for Arable Farming’		BLR011	Governmental	4
Office of the Styrian Regional Government, Department for Plant Health and Special Crops	WIES	AUT025	Governmental	4
Departamento Nacional de Recursos Fitogenéticos	DENAREF	ECU023	Governmental	4
Banco de Germoplasma de Especies Nativas de Oaxaca (BAGENO)	BAGENO	MEX287		3
Gene bank	CRI	CZE122	Governmental	3
Agricultural Institute Osijek	AIOS	HRV021	Governmental	3
Banco de Germoplasma, Centro Nacional de Investigaciones Agropecuarias, Instituto Nacional de Tecnología Agropecuaria	BBC-INTA	ARG1342	Governmental	3
Generalidad Valenciana. Universidad Politécnica de Valencia. Escuela Técnica Superior de Ingenieros Agrónomos. Banco de Germoplasma	BGUPV	ESP026	Governmental	2
Gobierno de Aragón. Centro de Investigación y Tecnología Agroalimentaria. Banco de Germoplasma de Hortícolas	CITA-HOR	ESP027	Governmental	2
RSA Plant Genetic Resources Centre		ZAF064		2
Centre de Recherche Agronomique de Foulaya	CRAF-IRAG	GIN009	Governmental	2
Bangladesh Livestock Research Institute	BLRI	BGD189	Governmental	2
Plant Production Research Center Piestany	SVKPIEST	SVK001	Governmental	2
Plant Breeding and Acclimatization Institute	IHAR	POL003	Governmental	2
Faculty of Agriculture, University Ss. Cyril and Methodius		MKD001	Governmental	2
Niko Ketskhoveli Institute of Botany		GEO013	Governmental	2
Advanced Seed Research & Biotech Centre	ASRBC	BGD215	Private	2
Plant Genetic Bank of the Kyrgyz Republic	KYRGGEN	KGZ040	Governmental	1
Gembloux agro-biotech, Université de Liège, département des Sciences agronomiques, Phytotechnie tropicale et Horticulture	GxABT	BEL002	Governmental	1
INIFAP, Campo Experimental Iguala (CEIGUA)	CEIGUA	MEX014	Governmental	1
Field Crop Central Research Institute	FCCRI	TUR034	Governmental	1
National Bank for Plant Genetic Resources	NBPGR	LBY006	Governmental	1
Banco de Germoplasma de la Universidad TÃ©cnica Particular de Loja	BG-UNPL	ECU167	Private	1
Banca del germoplasma autoctono vegetale regionale	BAGAV	ITA368	Governmental	1
Estación Central de Pastos y Forrajes de Sancti Spiritus	ECPFSS	CUB126	Governmental	1
Instituto de Ciencia Animal	ICA	CUB287	Governmental	1
Davao Experiment Station Bureau of Plant Industry	DAVAO-ES	PHL024	Governmental	1
Nordic Genetic Resource Center	NORDGEN	SWE054	Regional	1
Plant Genetic Resources Center	PGRC	ALB026	Governmental	1
Crops and Seed Production Department, Agricultural Institute of Slovenia	AISLJ	SVN019	Governmental	1

Appendix 3. Reported accessions conserved *ex situ* in 2017

Gene-pool	Subgenus	Section	Species	Meise, Belgium	IITA	Australian Grains Genebank	CIAT	NARO, Japan	NBPGR, India	WorldVeg	Subtotal	Total
A	*Ceratotropis*	*Angulares*	*V. angularis*	9		349	3	1492	175	2350	4378	5082
A	*Ceratotropis*	*Angulares*	*V. dalzelliana*			4	4		21		29	36
A	*Ceratotropis*	*Angulares*	*V. exilis*	1							1	1
A	*Ceratotropis*	*Angulares*	*V. hirtella*	3				4			7	7
A	*Ceratotropis*	*Angulares*	*V. minima*	2	1		2	5	1		11	12
A	*Ceratotropis*	*Angulares*	*V. nakashimae*	2				21			23	24
A	*Ceratotropis*	*Angulares*	*V. nepalensis*	3				4	3		10	10
A	*Ceratotropis*	*Angulares*	*V. reflexopilosa*	3	2	1	2	37		3	48	50
A	*Ceratotropis*	*Angulares*	*V. riukiuensis*	1				63			64	64
A	*Ceratotropis*	*Angulares*	*V. tenuicaulis*	1				2			3	3
A	*Ceratotropis*	*Angulares*	*V. trinervia*	2				6	8		16	16
A	*Ceratotropis*	*Angulares*	*V. umbellata*	13	1	59	39	214	2050	320	2696	3003
A	*Ceratotropis*	*Ceratotropis*	*V. grandiflora*	1				1			2	2
A	*Ceratotropis*	*Ceratotropis*	*V. hainiana*						2		2	2
A	*Ceratotropis*	*Ceratotropis*	*V. mungo*	12	11	104	96	145	1751	849	2968	5987
A	*Ceratotropis*	*Ceratotropis*	*V. radiata*	34	124	1385	69	922	4024	6752	13310	21161
A	*Ceratotropis*	*Ceratotropis*	*V. sahyadriana*								0	0
A	*Ceratotropis*	*Aconitifoliae*	*V. aconitifolia*	7		35	8	6	1486	26	1568	1849
A	*Ceratotropis*	*Aconitifoliae*	*V. aridicola*	1							1	1
A	*Ceratotropis*	*Aconitifoliae*	*V. indica*								0	0
A	*Ceratotropis*	*Aconitifoliae*	*V. khandalensis*						1		1	1
A	*Ceratotropis*	*Aconitifoliae*	*V. stipulacea*	4				1			5	5
A	*Ceratotropis*	*Aconitifoliae*	*V. subramaniana*	1		2		1			4	6
A	*Ceratotropis*	*Aconitifoliae*	*V. trilobata*	4	7	53	4		130	2	200	336
B	*Plectrotropis*	*Plectotropis*	*V. kirkii*	1	6	1					8	9
B	*Plectrotropis*	*Plectotropis*	*V. vexillata*	135	195	187	201	6	110	2	836	1068
B	*Plectrotropis*	*Pseudoliebrechtsia*	*V. lobatifolia*		3	1					4	5
C	*Vigna*	*Catiang*	*V. keraudrenii*								0	0
C	*Vigna*	*Catiang*	*V. monantha*								0	0
C	*Vigna*	*Catiang*	*V. slechteri*		9						9	9
C	*Vigna*	*Catiang*	*V. unguiculata*	332	16127	935	94	1371	3649	1610	24118	44694

Gene-pool	Subgenus	Section	Species	Meise, Belgium	IITA	Australian Grains Genebank	CIAT	NARO, Japan	NBPGR, India	WorldVeg	Subtotal	Total
C	*Vigna*	*Macrodontae*	*V. friesiorum*	1	6	1	1				9	11
C	*Vigna*	*Macrodontae*	*V. frutescens*	14	7	10	3				34	46
C	*Vigna*	*Macrodontae*	*V. membranacea*	32	13	3	1				49	96
C	*Vigna*	*Macrodontae*	*V. somaliensis*								0	0
C	*Vigna*	*Reticulatae*	*V. reticulata*	28	116	3					147	202
C	*Vigna*	*Reticulatae*	*V. wittei*		29		1				30	30
D	*Vigna*	*Vigna*	*V. ambacensis*	36	151	4	1				192	195
D	*Vigna*	*Vigna*	*V. angivensis*	3	1	1					5	6
D	*Vigna*	*Vigna*	*V. bequaertii*								0	0
D	*Vigna*	*Vigna*	*V. comosa*	1	11						12	13
D	*Vigna*	*Vigna*	*V. filicaulis*	5	4	2					11	14
D	*Vigna*	*Vigna*	*V. fischeri*		1						1	1
D	*Vigna*	*Vigna*	*V. gazensis*								0	0
D	*Vigna*	*Vigna*	*V. gracilis*	14	24						38	49
D	*Vigna*	*Vigna*	*V. heterophylla*	2	1	4					7	32
D	*Vigna*	*Vigna*	*V. hosei*	5	44	4	7				60	65
D	*Vigna*	*Vigna*	*V. laurentii*	2	1	1					4	6
D	*Vigna*	*Vigna*	*V. luteola*	24	66	39	69			4	202	257
D	*Vigna*	*Vigna*	*V. marina*	6	8	39		1	2	43	99	129
D	*Vigna*	*Vigna*	*V. multinervis*	5	17						22	23
D	*Vigna*	*Vigna*	*V. oblongifolia*	31	55	42	31				159	256
D	*Vigna*	*Vigna*	*V. o-wahuensis*	1							1	1
D	*Vigna*	*Vigna*	*V. parkeri*	6	2	20	1			1	30	80
D	*Vigna*	*Vigna*	*V. racemosa*	43	131	6	1				181	208
D	*Vigna*	*Vigna*	*V. subterranea*		2088	47					2135	4125
	Number of accessions			**831**	**19262**	**3342**	**638**	**4302**	**13413**	**11962**	**53750**	**89288**
	Number of taxa			**41**	**32**	**29**	**21**	**19**	**15**	**12**	**55**	**55**

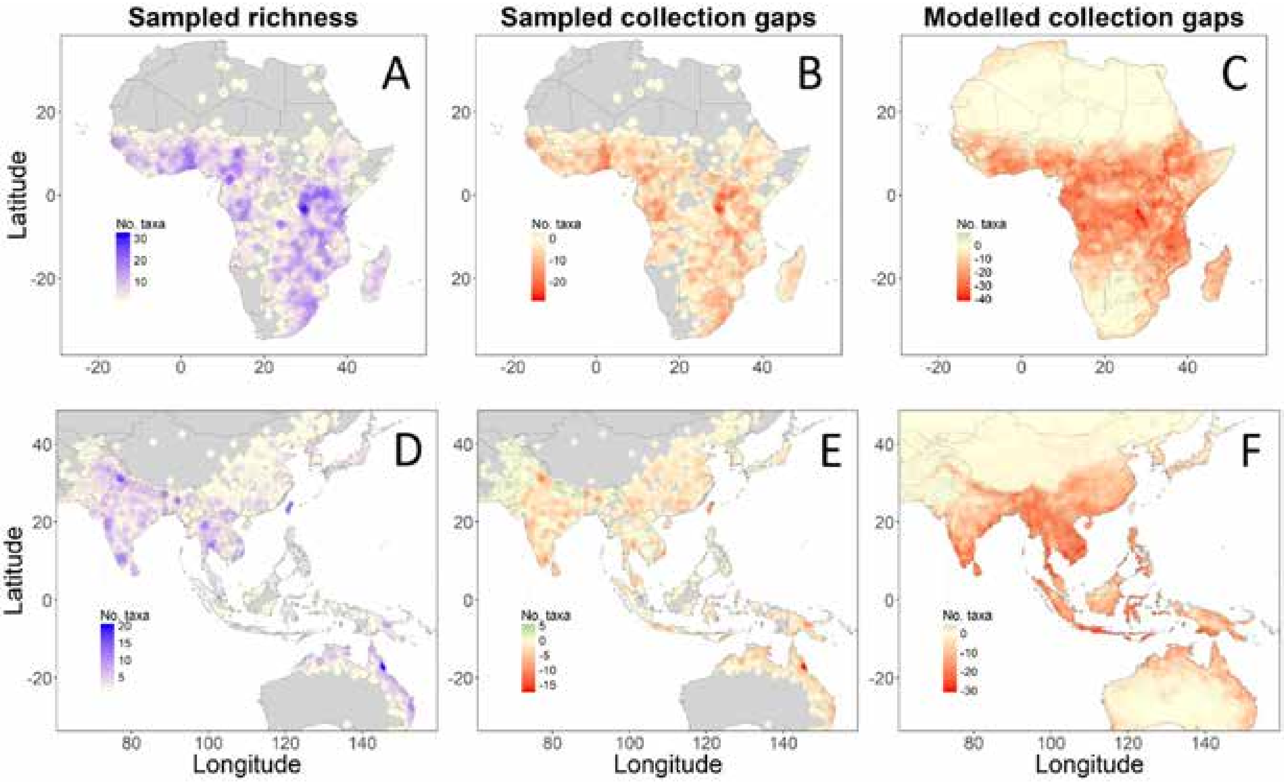
Appendix 4. Targeted countries for collection of *Vigna* species with less than 10 accessions stored in genebanks

Subgenus	Section	Taxa	Reported occurrence	Modelled occurrence
Ceratotropis	*Angulares*	*V. exilis*	**Thailand**[i]	**Thailand**, Myanmar
Ceratotropis	*Angulares*	*V. hirtella*	**Thailand**, India, Myanmar, Malaysia, Vietnam, China, Lao People's Democratic Republic	**Myanmar**, Thailand, India, Cambodia, China, Malaysia, Indonesia, Bhutan, Nepal, Bangladesh
Ceratotropis	*Angulares*	*V. tenuicaulis*	**Thailand**	**Thailand**
Ceratotropis	*Ceratotropis*	*V. grandiflora*	**Thailand**, Cambodia	**Thailand**, Cambodia
Ceratotropis	*Ceratotropis*	*V. hainiana*	**India**	**India**, Nepal
Ceratotropis	*Ceratotropis*	*V. sahyadriana*	na	na
Ceratotropis	*Aconitifoliae*	*V. aridicola*	**Sri Lanka**	**Sri Lanka**
Ceratotropis	*Aconitifoliae*	*V. indica*	na	na
Ceratotropis	*Aconitifoliae*	*V. khandalensis*	**India**	**India**
Ceratotropis	*Aconitifoliae*	*V. stipulacea*	**India**, Indonesia, Sri Lanka, Spain, Vietnam	**India**, Thailand, Myanmar, Indonesia, Cambodia, Australia, Philippines, Sri Lanka, Ethiopia, Bangladesh, South Sudan, Malaysia, Sudan, China, Maldives
Ceratotropis	*Aconitifoliae*	*V. subramaniana*	**India**	**India**, Pakistan, Nepal, China
Plectrotropis	*Plectotropis*	*V. kirkii*	**Tanzania**, DRC, Uganda, Mozambique, Malawi, Burundi, Cameroon, Guinea-Bissau, Guinea, Kenya, Senegal, South Sudan, Zambia	**DRC**, Central African Republic, Mozambique, Cameroon, Congo, Nigeria, Uganda, Ghana, South Sudan, Angola, Gabon, Malawi, Kenya, Zambia, Guinea, Ethiopia, Senegal, Guinea-Bissau, Mali, Togo, Benin, Liberia, Burundi, Burkina Faso, Rwanda, Madagascar, Chad, Equatorial Guinea, Zimbabwe, Sierra Leone, Gambia, Comoros
Plectrotropis	*Pseudoliebrechtsia*	*V. lobatifolia*	**Namibia**	na
Vigna	*Catiang*	*V. keraudrenii*	**Madagascar**	**Madagascar**
Vigna	*Catiang*	*V. monantha*	**Somalia**	**Somalia**
Vigna	*Catiang*	*V. schlechteri*	**South Africa**, Zimbabwe, Swaziland, Mozambique	**South Africa**, Zimbabwe, Swaziland, Mozambique, Lesotho
Vigna	*Macrodontae*	*V. somaliensis*	na	na
Vigna	*Vigna*	*V. angivensis*	**Madagascar**, Burundi, Russian Federation	**Madagascar**, Nepal, India, Mozambique, DRC, Reunion (France), Comoros, Mauritius, Zimbabwe, Kenya, China, Uganda, Malawi, Ethiopia, Rwanda
Vigna	*Vigna*	*V. bequaertii*	**DRC**, Burundi, Rwanda	**DRC**, Central African Republic, Rwanda, Uganda, Burundi, South Sudan, Angola
Vigna	*Vigna*	*V. fischeri*	**Burundi**, Malawi	na
Vigna	*Vigna*	*V. gazensis*	**Mozambique**, Malawi, Madagascar, Zimbabwe	**Madagascar**, Mozambique, Zimbabwe, Malawi, Zambia
Vigna	*Vigna*	*V. laurentii*	**Benin**, DRC, Cameroon, Burundi, Togo, Central African Republic, Gabon, Guinea-Bissau, South Sudan	**DRC**, Nigeria, Central African Republic, Cameroon, Angola, South Sudan, Zambia, Ghana, Gabon, Congo, Uganda, Chad, Benin, Togo, Guinea, Burundi, Guinea-Bissau, Rwanda, Burkina Faso, Senegal, Mali, Equatorial Guinea, Sudan, Kenya, Sao Tome and Principe, Malawi, Sierra Leone
Vigna	*Vigna*	*V. o-wahuensis*	**United States**	**United States**, Canada, Mexico

[i] Countries are presented in order of occurrence. **Countries in bold** reported most records of the corresponding species and greatest coverage of its modelled distribution.

Appendix 5. Sampled taxonomic richness and sampled and modelled collection gaps.

Panel A and D show sampled taxonomic richness; Panel B and E show sampled taxonomic richness that is not conserved ex situ; Panel C and F show gaps where a high number of taxa are modelled to occur but are not reported in herbaria, living collections, or genebanks. Maps were made by Maarten van Zonneveld in R version 3.3.3 with ggplot2 version 3.1.0. (Source: van Zonneveld et al. 2020)



Appendix 6. Survey Questionnaire "Global *Vigna* Conservation Strategy"

Survey Disclaimer: The main objective of this survey is to assess the current status of *Vigna* conservation across the world to identify the gaps and prepare a Global *Vigna* Conservation Strategy (GVCS). The initiative to prepare GVCS is being led by the World Vegetable Center (WorldVeg), Taiwan in association with all the participating institutes/gene banks in this survey. The Global Crop Diversity Trust (the Crop Trust) provided support for this initiative. The outcome of this work in the form of GVCS will be available in open access for research across the world. You are invited to participate in this survey as you are one of the *Vigna* curators, researchers, or gene bank managers actively working on *Vigna* conservation and improvement. The information collected through this survey will be analyzed and interpreted to prepare GVCS. Your participation in this initiative and survey is voluntary. You may choose not to participate.

We are expecting your response on questions that apply to the relevant *Vigna* species being conserved at your gene bank/research program latest by 31st January 2022. If you have any questions about this survey or need any clarifications, please feel free to contact Ramakrishnan M Nair, Regional Director and Global Pant Breeder (Legumes), WorldVeg, South Asia Regional Headquarters, ICRISAT Campus, India (ramakrishnan.nair@worldveg.org) or Sunil Chaudhari (sunil.chaudhari@worldveg.org), Associate Scientist, Legume Breeding, WorldVeg, South Asia.

ORGANIZATION INFORMATION

1.1 Name and address of organization holding/maintaining *Vigna* collection

Name of the organization	
Address	
Postal Code	
Country	
Web site	
Institute type (Governmental, NGO, Public- non-profitable or Private organization)	

1.2 Curator of *Vigna* collection

Name of Curator	
Contact Number	
Email ID	

1.3 Name of the respondent to this questionnaire (if not curator)

Name of respondent	
Designation	
Institute	
Contact details	
Date of response	

1.4 Additional key contact persons for *Vigna* collections in the country

Name of respondent	Designation	Email ID

1.5 Does the collection operate under a national conservation strategy, policy, or plan? If yes, please specify?

1.6 Who decides the priorities for your genebank objectives, species focus, and activities? (Curator, management of the institute, governing committee or others)

2. COMPOSITION OF *VIGNA* COLLECTION

2.1 In which year the genebank was established the *Vigna* collection was established/started:

2.2 Total number of accessions available at your genebank?

Particulars	When gene bank established	What is the status today
Total number of accessions across the crops		
How many total crops (across genus/species) genetic resource is available		
Total number of *Vigna* accessions (all the taxa)		
Total number of *Vigna* taxa available		
Total number of sections		

2.3 What are the mandate crops of your genebank? The main objective of the collection includes (Yes/No)

Long term conservation for public organizations	
Working collection for public breeding programs and research institutes	
Working collection for private breeding programs	
Others (please specify below)	

2.4 The current composition of the accessions in the specific Vigna species overall and in the various accession types?

Vigna spp.	Total No. of accessions	Number of accessions					
		Landraces or farmer's varieties collected within country	Landraces or farmer's varieties acquired from outside country	Old cultivars and released varieties	Advanced breeding lines or genetic stocks	Wild relatives	Others/ known
V. radiata (Mungbean)							
Vigna radiata sub sp. sublobata							
V. mungo (Blackgram)							
Vigna mungo var. silvestris							
V. acontifolia (Moth bean)							
V. angularis (Azuki bean)							
V. umbellata (Rice bean)							
V. reflexo-pilosa (Creole bean)							
V. unguiculata (Cowpea)							
V. unguiculata ssp. dekindtiana sensu Verdc.							
V. vexillata (Tuber cowpea)							
V. subterranea (Bambara groundnut)							
Vigna subterranea var. spontanea							
Add other species when relevant							

2.5 How many other wild *Vigna* species are available at your genebank?

***Vigna* wild species**	**Total no. of accessions**

2.6 The number of *Vigna* accessions have been:

Particulars	**Number of accessions**	**Number of species these accession belongs to**
How many accessions have been lost from the collection in the past 10 years		
How many of these accessions have been replaced with a re-collection or repatriation from others?		
How many accessions have been collected in the past 10 years?		

2.7 To what extent do you consider the *Vigna* accessions in your collection to be unique and not duplicated extensively elsewhere within the country or outside the country (*i.e.* excluding safety-duplication)?

Vigna spp.	100% Unique	More than 50% unique	Less than 50% unique
V. radiata (Mungbean)			
Vigna radiata sub sp. *sublobata*			
V. mungo (Blackgram)			
Vigna mungo var. *silvestris*			
V. acontifolia (Moth bean)			
V. angularis (Azuki bean)			
V. umbellata (Rice bean)			
V. reflexo-pilosa (Creole bean)			
V. unguiculata (Cowpea)			
V. unguiculata ssp. *dekindtiana* sensu Verdc.			
V. vexillata (Tuber cowpea)			
V. subterranea (Bambara groundnut)			
Vigna subterranea var. *spontanea*			
Add other species when relevant			

2.8 Is the passport information for all the accessions are available? if not specify the percent of accession with accurate passport information?

2.9 Which passport descriptor is being followed?

2.10 Has your institution been involved in collaboration with other international or national institutions to collect *Vigna* germplasm? If yes, please describe.

2.11 Can you describe any core or mini core collection or other trait-specific subsets of accessions that have been established for the collection? If yes, please specify the number of accessions in the below table.

Vigna spp.	Core collection	Mini core collection	Other traits specific subset if any (trait)
V. radiata (MungbeanMungbean)			
V. mungo (Blackgram)			
V. acontifolia (Moth bean)			
V. angularis (Azuki bean)			
V. umbellata (Rice bean)			
V. reflexo-pilosa (Creole bean)			
V. unguiculata (Cowpea)			
V. vexillata (Tuber cowpea)			
V. subterranea (Bambara groundnut)			
Add other species when relevant			

2.12 Is this subset being distributed or requested by users? How many countries, the subset has been distributed so far? Please mentioned the number of countries, these subsets are shared so far.

Vigna spp.	Core collection	Mini core collection	Other traits specific subset if any (trait)
V. radiata (Mungbean)			
V. mungo (Blackgram)			
V. acontifolia (Moth bean)			
V. angularis (Azuki bean)			
V. umbellata (Rice bean)			
V. reflexo-pilosa (Creole bean)			
V. unguiculata (Cowpea)			
V. vexillata (Tuber cowpea)			
V. subterranea (Bambara groundnut)			
Add other species when relevant			

2. 13 Have the significant gaps or redundancies in diversity, or national or regional representation, or specific traits in the collection been determined? How?

2. 14 What are the major gaps composition of collection to fill and how you are planning to fill them?

3. CONSERVATION OF *VIGNA* COLLECTION

3.1 What is the status of conservation for the collection?

Vigna spp.	Accessions in long-term storage	Accessions on medium-term storage	Accessions with baseline seed viability	Accessions with baseline seed health status	Accessions with baseline seed number	Accessions that have been regenerated
V. radiata (Mungbean)						
Vigna radiata sub sp. sublobata						
V. mungo (Blackgram)						
Vigna mungo var. silvestris						
V. acontifolia (Moth bean)						
V. angularis (Azuki bean)						
V. umbellata (Rice bean)						
V. reflexo-pilosa (Creole bean)						
V. unguiculata (Cowpea)						
V. unguiculata ssp. dekindtiana sensu Verdc.						
V. vexillata (Tuber cowpea)						
V. subterranea (Bambara groundnut)						
Vigna subterranea var. spontanea						
Add other species when relevant						

3.2 The long-term, medium-term, and short-term storage facility at your institute for *Vigna* collection has (specify in numbers)

Particulars	Long term	Medium term	Short term
Cold storage units			
Individual freezers			
Air-conditioned rooms			
Air-conditioned room with dehumidifiers			
Back-up generator			
Other (please specify)			

3.3 What type of packaging is used for long term, medium term, and short-term storage? (✓)

Type of packaging	Long term	Medium term	Short term
Sealed Aluminum packs			
Sealed and vacuum-packed aluminum packs			
Air tight plastic containers			
Air tight glass containers			
Non-air tight plastic/glass containers			
Paper envelopes or bags			
Cloth bags			
Others (please specify)			

3.4 The temperature and relative humidity in the long-term, medium term, and short-term storage units are monitored by (Please specify the storage conditions)

Particulars	Long term	Medium term	Short term
Temperature monitors (°C)			
Relative humidity monitors (%)			
Availability of external sounding alarms if temperature and RH goes above limit (Yes/No)			
Automated monitoring system with link to security or curator (Yes/No)			
Daily visit by genebank staff or security staff (Yes/No)			
Others (please specify)			

3.5 The genebank facilities include: (Yes/No)

Separate work areas for seed processing *(threshing, cleaning etc.) and 'clean' seed handling	
Separate work areas for seed packaging for storage and distribution with relative humidity control	
Dedicated laboratory and trained staff for seed viability testing	
Dedicated laboratory and trained staff for seed health testing	
Low-temperature seed dryer	
Access to at least one field sites in key agro-ecological zones for regeneration and multiplication	
Access to field site or greenhouse/glasshouse near genebank for regeneration and multiplication	
Access to the irrigated field site for rainy season or off-season for regeneration and multiplication	
Other (please specify)	

3.6 What is the average age, status, and main constraint for upgrading or improving the key conservation facilities and equipment?

Item	Average age	Status (✓)			Main constraint to improvement
		Excellent	Adequate	Inadequate	
Genebank building and facilities					
Storage facilities					
Laboratory facilities					
Laboratory equipment					
Field equipment					
Generator					
Other (please specify)					

3.7 Does the genebank make use of any alternative energy option, such as solar panels, to power a portion of the electricity needs for seed storage or seed processing? If yes, please be specific.

3.8 Does the genebank give a priority to energy efficiency in the procurement of new and replacement facilities and equipment? If yes, please be specific.

3.9 The genebank utilizes written procedures and protocols from (Check all that apply): If yes, please specify the SOP/Manual being followed.

3.10 Do you have ongoing research or the resources and expertise to research in the future on the conservation of *Vigna*, such as (Check all those that apply)?

Research area	Ongoing research	Future research need
Improve procedures or protocols		
Increase efficiency of conservation		
Increase the security of conservation		
Address crop-specific constraints, such as seed dormancy, seed heath, seed longevity, etc.		
Crossability among crop wild relatives		
Genetic diversity and/or phylogenetic relationships		
Others (please specify)		

3.11 Are you using cryo-preservation for the *Vigna* collection? If yes, please specify

3.12 What are the major gaps in *Vigna* conservation and your plans to overcome them?

4. CHARACTERIZATION AND INFORMATION MANAGEMENT

4.1 What is the status of accession level information in your collection?

Vigna spp.	% of accessions				
	With passport data	With passport data in searchable database	Characterized with a minimum number of traits	Characterization data in searchable database	Georeferenced
V. radiata (Mungbean)					
Vigna radiata sub sp. sublobata					
V. mungo (Blackgram)					
Vigna mungo var. silvestris					
V. acontifolia (Moth bean)					
V. angularis (Azuki bean)					
V. umbellata (Rice bean)					
V. reflexo-pilosa (Creole bean)					
V. unguiculata (Cowpea)					
V. unguiculata ssp. dekindtiana sensu Verdc.					
V. vexillata (Tuber cowpea)					
V. subterranea (Bambara groundnut)					
Vigna subterranea var. spontanea					
Add other species when relevant					

4.2 The information/database is (check all that apply):

Information available to	Status (Yes/No)
Public	
Internal	
Available by written catalog or by contacting the curator	
Available and searchable online within the institute	
Available and searchable online outside the institute	

4.3 The accession level information/database provides data about (check all that apply):

Information	Status (yes/No)
Passport	
Taxonomy	
Characterization	
Genotypes	
Images	
Other (Please specify)	

4.4. Where is various accession level management data recorded, used and shared?

Operation	Recorded in field books, laboratory logbook, and/or data sheets	Enter into internal database in the laboratory or unit	Enter into database for electronic genebank information management system
Inventory			
Seed viability test and retest			
Seed or plant health status			
Seed number			
Packet weight			
Regeneration			
Multiplication			
Characterization			
Distribution			

4.5 Do you use barcoding for managing the identity of the accessions? In what operations?

4.6 Has the genebank automated any of the seed handling processes or data collection (such as using electronic tablets for data collection)? If yes, please describe what process is now being done with automation.

4.7 If you use an electronic information system for managing the collection and sharing accession level information, is it adequate to meet the needs of the genebank and users? If not adequate, what are the plans to upgrade or improve this system?

4.8 How often do you repeat the characterization of the collection to confirm and curate the information?

4.9 Do you have written SOPs for characterization and data management? If yes please specify

4.10 What are the major challenges in the characterization of *Vigna* collection?

4.11 Is the passport information accurate for the entire collection to the best of your knowledge? If not what percent of accession required confirmation on passport information?

4.12 Is the passport information is available in open access? If yes, where the users can get the information (mention the link)?

4.13 The passport data format being used is of global standards? please specify

4.14 Which gene bank data management system is being used to manage phenotypic and genotypic data? If not, please specify the challenges if any.

4.15 Is the passport data information is available at Genesys or WIEWS or Any other platform? If yes, where and what % of accessions information is available? How often do you update the information on the platform?

4.16 Highlight the major gaps/challenges in characterization of *Vigna* collection if any

4.17 Highlight the major gaps/challenges in management of data and information of *Vigna* collections

5. EVALUATION

5.1 Has your *Vigna* collection been evaluated/screened for biotic and abiotic stresses? (mention the names of biotic and abiotic stresses)

	Biotic stresses	Abiotic Stresses	Genotyping or marker studies (yes/no)	Data publicly available? (yes/no)
Partial				
Core collection				
Focused trait-specific subsets				
Majority of the complete collection				

If yes, please list the specific crop and specific biotic or abiotic stresses that have been evaluated?

5.2 Has there been any genotyping done on your *Vigna* collection?

***Vigna* spp.**	**% of accessions**			
	Total collection	**Core collection**	**Minicore collection**	**Type of genotyping** **(SSR, SNPs, GBS, WGRS etc.)**
V. radiata (Mungbean)				
V. mungo (Blackgram)				
V. acontifolia (Moth bean)				
V. angularis (Azuki bean)				
V. umbellata (Rice bean)				
V. reflexo-pilosa (Creole bean)				
V. unguiculata (Cowpea)				
V. vexillata (Tuber cowpea)				
V. subterranea (Bambara groundnut)				
Add other species when relevant				

5.3. Does your genebank conserve the data generated from the phenotypic or genotypic characterization or evaluation of the accessions by others? Please describe how this is formally or informally requested.

5.4 Have you studies cross-compatibility among the *Vigna* species? if yes please summarize?

5.5 Do you have written SOP or Manuals for germplasm collections, *ex-situ* **conservation, characterization, etc.? If yes, please specify**

5.6 How the duplicate accessions are being identified? Morphologically or at the genomic level?

5.7 Have you assessed diversity among germplasm using phenotypic, genotypic or passport information? If yes is the information available for the users?

5.8 Which are the major biotic and abiotic stresses, the collection was evaluated?

5.9 What are the major gaps in the evaluation of *Vigna* **collection?**

6. DISTRIBUTION

6.1 Are the accession in the collection available for use to requestors?

Vigna spp.	Within the institute	Nationally	Internationally	% of accession available with an SMTA
V. radiata (Mungbean)				
Vigna radiata sub sp. sublobata				
V. mungo (Blackgram)				
Vigna mungo var. silvestris				
V. acontifolia (Moth bean)				
V. angularis (Azuki bean)				
V. umbellata (Rice bean)				
V. reflexo-pilosa (Creole bean)				
V. unguiculata (Cowpea)				
V. unguiculata ssp. dekindtiana sensu Verdc.				
V. vexillata (Tuber cowpea)				
V. subterranea (Bambara groundnut)				
Vigna subterranea var. spontanea				
Add other species when relevant				

6.2 Do you have any restrictions on who can receive materials? If yes, please specify

6.3 Do you have adequate procedures in place for distribution?

	Adequate	Inadequate	Main constraints
MTA or SMTA			
Phytosanitary certification			
Packaging			
Shipping			
Other, please specify:			

6.4 For the following users, how would you describe the frequency of distribution of accessions of *Vigna* in the past 10 years?

Users	Number of request received	Number of requests addressed	Specific remarks/ challenges for not addressing the request (if any)
Farmers or farmers organizations			
Other genebank curators			
Academic researchers and students within country			
Academic researchers and students outside country			
Public sector within country			
Private sector within country			
Public sector outside country			
Private sector outside country			
Non-governmental organizations			
Other (specify below)			

6.5 Do you routinely follow-up and solicit feedback from recipients on the quality and use of the accession received (Check all that apply):

Timeliness of the distribution
Helpfulness of information or advice from genebank staff in selection of accessions
Quality of samples sent
Quality of packaging used
Quality and the usefulness of the accession level information received
Usefulness of the accession received
Sharing of report or publication on any specific research result from the evaluation or use of the accession received
Sharing of evaluation or characterization data sets
Variety releases, adoption studies or case studies from the use of an accession received
Other feedback (Please specify)

6.6 Is this a formal mandatory survey to have user's feedback or informal process?

6.7 How do you use the feedback obtained?

6.8 How do you rate genebank on ease of sharing the material outside the country?

6.9 What are the major challenges in distribution of collection within country and outside the country?

7. SAFETY DUPLICATION

7.1 Is the collection (complete or partially) duplicated outside the country for all the available *Vigna* species?

7.2 What is the status of safety duplication?

***Vigna* spp.**	**Number of accessions**				
	Safety duplicated in Svalbard GSV	**Safety duplicated in a black box arrangement outside country**	**Safety duplicated in another collection in the country**	**Safety duplicated in another research site in the country**	**Safety duplicated in another collection outside the country**
V. radiata (Mungbean)					
Vigna radiata sub sp. *sublobata*					
V. mungo (Blackgram)					
Vigna mungo var. *silvestris*					
V. acontifolia (Moth bean)					
V. angularis (Azuki bean)					
V. umbellata (Rice bean)					
V. reflexo-pilosa (Creole bean)					
V. unguiculata (Cowpea)					
V. unguiculata ssp. *dekindtiana sensu* Verdc.					
V. vexillata (Tuber cowpea)					
V. subterranea (Bambara groundnut)					
Vigna subterranea var. *spontanea*					
Add other species if relevant					

7.3 How many times the partial or complete set of safety duplicate was withdrawn from Global Seed Vault?

7.4 If the collection is not safety duplicated, are there any specific constraints to duplicating the collection elsewhere within or outside your country? If yes, please specify.

7.5 Can you generally describe the terms of conservation and the obligations for both organizations in any formal or informal agreement for safety duplication?

8. STAFF AND TRAINING

8.1 What is the number of staff allocated for the conservation and distribution of *Vigna* collections?

	Number of staff	Level of expertise	Training
To meet the needs for the routine annual operations for conservation			
To meet the request for annual distribution			
To address the needs of users for accession level information			

8.2 Do you have dedicated *Vigna* curators at your gene bank?

8.3 Is the number of staff, level of expertise, and training adequate? If inadequate, how is this being addressed?

8.4 Please highlight the gaps and challenges for gene bank staff if any

9. FUNDING

9.1 Who provides most or all of the annual recurrent costs for the conservation of the collection?

9.2 Are there other sources of funds or significant revenue-producing activities used to support the conservation of the collection? If yes, what percentage of the collection cost is covered by these activities?

9.3 What is the status of funding for the main conservation and use activities and who is providing this?

Operation	Source of funds		Status of funding (✓)		
	Annual allocation	Project funded	Increasing	Stable	Decreasing
Annual routine conservation activities					
Regeneration					
Multiplication					
Characterization					
Conservation Research					
Evaluation					
Collection					
Upgrade facilities or equipment					

10. RISK MANAGEMENT

10.1 Has there been a risk assessment done specifically for the genebank? Who is in charge of the assessment of risk and the development of a risk management plan for the institute and genebank?

10.2 Is the risk assessment and management plan reviewed on an annual basis? How?

10.3 What are the primary threats to the collection?

10.4. What are the primary diseases/pathogens concerns for?

Seed storage	
Distribution	
Regeneration/multiplication	

10.5 How has the COVID-19 pandemic impacted your genebank operations? How you have mitigated?

10.6 Is there any long-term measures taken to deal with such concerns in the future?

***********Thank you for your kind consideration to complete this survey**********

Appendix 7. The plants that feed the world: baseline data and indicators for PGRFA, with specific reference to *Vigna* crops

Khoury et al. (2022) compiled a comprehensive dataset as part of a project funded by the International Treaty on Plant Genetic Resources for Food and Agriculture and with the collaboration Crop Trust, and implemented by the Alliance of Bioversity International and the International Center for Tropical Agriculture (CIAT).

The aim was to introduce normalized, reproducible indicators to serve as an evidence base when prioritizing actions on the conservation and use of plant genetic resources for food and agriculture. The indicators encompass metrics associated with the USE of a crop (Global importance), the INTERDEPENDENCE between countries with respect to genetic resources, the DEMAND for genetic resources, the SUPPLY of germplasm by genebanks and the SECURITY of germplasm conservation. To generate the indicators, Khoury et al. (2022) collected a comprehensive dataset from multiple sources. We do not present those indicators here, but rather we present a small subset of the variables used in this study.

To put numbers into context, for some indicators (when the data allow), we compare the values for *Vigna* crops with the values for common bean (Table 1). Both crops or crop groups are herbaceous annual legumes and thus, they are comparable with respect to type of growth and use, as in both cases the dry seed is used for human consumption.

There are many *Vigna* crop species including adzuki bean (*V. angularis*), Bambara groundnut (*V. subterranea*), blackgram (*V. mungo*), cowpea (*V. unguiculata*), mat bean (*V. aconitifolia*), mungbean (*V. radiata*) and rice bean (*V. umbellata*). The genus and species name of common bean is *Phaseolus vulgaris*.

The metrics for “Global production,” “Food supply” and “Quantity exported globally” under the indicator domain USE are annual average values drawn from FAOSTAT for the years 2015–2018 (Khoury et al. 2022). 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 that report respective numbers (can be different between metrics and crops). FAOSTAT reports numbers for common bean (*P. vulgaris)* and several *Vigna* crops (adzuki bean, blackgram, mat bean, mungbean and rice bean) in one combined category referred to as “Beans”, while only Bambara groundnut (*V. subterranea*) and cowpea (*V. unguiculata*) are reported separately. Therefore, here we will not discuss the FAOSTAT-derived indicators.

The crop use metrics with respect to research were assessed by manual searches on Google Scholar, searching for the respective genus or species in the titles of publications, including patents and citations, between the years 2009 and 2019 (Khoury et al. 2022). Search hits on Google Scholar indicate the level of scientific interest in a crop. As a comparison, the genus name *Vigna* is found in more titles (11,300 publication titles) than is the common bean genus *Phaseolus* (9,870 publication titles). However, we note that the term “Vigna” is not only used for the scientific genus name of vigna crop plants, but also as a common generic term for the crop group, whereas *Phaseolus* designates exclusively the genus of common bean. The scientific names of vigna crops appear in 9,676 publication titles, while *Phaseolus vulgaris* is included in 8,220 publication titles. However, we note that the vigna crops encompass seven species, but there is only one common bean species.

DEMAND for germplasm is defined by various metrics (Khoury et al., 2022), including: (1) the number of distributions of accessions by genebanks, as an annual average between 2015 and 2019, drawn from the Plant Treaty’s Global Information System; (2) the number of accessions distributed by national genebanks as reported to the FAO WIEWS system as an annual average between 2014 and 2019, (3) the annual average 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).

According to the distribution metric from the Plant Treaty’s Data Store, on average 4738 accessions of vigna crops were distributed annually between 2015 and 2019. In the FAO WIEWS dataset 18,099 accessions per year (Annual average 2014–2019) were distributed by genebanks. On average seven varieties of vigna crops per year were registered at UPOV during a five-year period, a small number when compared to 194 common bean varieties registered in the same period.

Khoury et al. (2022) illustrated the SUPPLY of germplasm by quantifying 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. They also assessed the number of accessions (again with respect to genus and species) available under the multilateral system (MLS) of the Plant Treaty. This MLS assessment was done first, directly, as noted (in MLS/not in MLS) in the public online databases Genesys, FAO WIEWS and GBIF. Secondly, the availability of accessions was assessed by considering whether the country hosting the institution that held the respective germplasm collection was a signatory to the Plant Treaty, as well as whether the crop was listed in Annex 1 of the Treaty; if both conditions were met,the accession was regarded as available via the MLS.

According to Khoury et al. (2022), globally databases records 103,630 *ex situ* accessions in the *Vigna* genus. However, search on FAO-WIEWS and Genesys conducted in 2022 for the Global strategy for the conservation and use of *Vigna*, found records of 129,903 *Vigna* accessions. The discrepancy may be because the database data used in Khoury et al. (2022) was acquired in late 2018 while the data used for the strategy was acquired in 2022. In other words, additional genebanks may have added their data to open databases between 2018 and 2022.

Vigna crops are listed in Annex I of the Plant Treaty (FAO 2009). As stated in respective databases, 17% of *Vigna* accessions are available under the MLS. At the species level, the proportion of available accessions ranges from less than 1% (Bambara groundnut) to 47% (adzuki bean). For the common bean, 34% and 33% of accessions are available directly under the MLS, by genus and species, respectively. If counting accessions available indirectly by matching institute countries with party status, at the genus level, 86% of accessions of vigna crops and 86% of common bean accessions are available. At the species level, 68% (Bambara groundnut) to 97% (rice bean) of vigna crop accessions are available, while 86% of common bean accessions are available. The discrepancy, between the indicator calculated with passport data from databases and the indicator calculated indirectly by matching institute countries with party status, suggests that in FAO-WIEWS and in Genesys the passport data of many *Vigna* accessions the MLS status was either not recorded or it was incorrectly recorded.

SECURITY of germplasm conservation is represented here by one metric: safety duplication at the Svalbard Global Seed Vault (SGSV). The numbers of accessions, by genus and species, safety duplicated were taken from the SGSV website and divided by the total number of accessions stored in global ex situ collections (see above), with the result giving the percentage of germplasm that is safety duplicated. These analyses revealed that 31% of crops of the genus *Vigna* and 27% of the genus *Phaseolus* are safety duplicated at the SGSV. At the species level, the proportion of vigna crop accessions safety duplicated at the SGSV ranges from 0% (Mat bean) up to 38% (Mung bean). 27% of *P. vulgaris* accessions are safety duplicated at the SGSV.

Literature cited in this annex.

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FAOSTAT 2021. Statistics for 2015-2019 (production). www.fao.org. Accessed July 19, 2021.

Khoury CK, Amariles D, Sotelo S , Hawtin G, Wibisono J, Gallo P. (2022) Plants That Feed the World: baseline data and metrics to inform strategies for the conservation and use of plant genetic resources for food and agriculture. International Treaty on Plant Genetic Resources for Food and Agriculture Background Study Paper X. Rome: Food and Agricultural Organization of the United Nations. https://www.fao.org/3/cc1988en/cc1988en.pdf

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 Science 283(1832): 20160792. DOI:10.1098/rspb.2016.0792

Table 1. Selected indicators for *Vigna* crops and common bean (as a comparison) mentioned in this annex.

	Cowpea	**Mung bean**	**Adzuki bean**	**Bambara groundnut**	**Rice bean**	**Black gram**	**Mat bean**	**Aggregated *Vigna* crops**	**Common bean (as a comparison)**
Number of publications between 2009–2019, including patents and citations, searching title of publication (Google scholar search hits) for genus **	11,300	9,870							
Number of publications between 2009–2019, including patents and citations, searching title of publication (Google scholar search hits) for species	3,800	3,600	277	391	138	1,350	120	9,676	8,220
Annual average of variety releases (2014–2018, registered at UPOV)	2.25	2	2.75	0	0	0.25	0		194
Accessions distributed from gene banks (Plant Treaty Data Store, annual average 2015-2019)	4,316	60	0	359	1.5	1.5	0	4,738	8,187
Accessions distributed from gene banks (FAO-WIEWS, Annual average 2014–2019)	10,068	3,176	63	475	2,581	1,421	315	18,099	27,454
Number of accessions in *ex situ* collections of genus (open databases data)	103,630	180,615							
Number of accessions in *ex situ* collections of species (open databases data)	52,590	22,384	5,313	4,739	3,423	6,505	1,921	96,875	157,632
Accessions of the genus available through Multilateral System (MLS) directly noted in databases	17,151 (17%)	61,253 (34%)							
Accessions of the genus available through Multilateral System (MLS) indirectly by matching institute countries with party status [total and %]	90,009 (87%)	155,305 (86%)							
Accessions of the species available through Multilateral System (MLS) directly noted in databases	3636 (7%)	7,142 (32%)	2491 (47%)	37 (1%)	468 (14%)	991 (15%)	78 (4%)	14,843 (15%)	52,244 (33%)
Accessions of the species available through Multilateral System (MLS) indirectly by matching institute countries with party status [total and %]	46,234 (88%)	19,725 (88%)	4,968 (94%)	3,226 (68%)	3,322 (97%)	4,542 (70%)	1,779 (93%)	83,796 (86%)	135,200 (86%)
Accessions of genus safety duplicated in Svalbard Global Seed Vault [total and %]	32,569 (31%)	18341 (27%)							
Accessions of species safety duplicated in Svalbard Global Seed Vault [total and %]	17,959 (34%)	8,598 (38%)	1,562 (29%)	1,208 (25%)	415 (12%)	313 (5%)	4 (0%)	30,059 (31%)	41,995 (27%)

Appendix 8. Accepted *Vigna* names and taxonomic classification

Following GRIN taxonomy[1] and Iseki et al. 2016[2]. Source: van Zonneveld et al. 2020

Subgenus	Section	Species	Complete scientific name	Taxonomy
Ceratotropis	*Angulares*	*V. angularis*	*V. angularis* (Willd.) Ohwi & H. Ohashi	1
Ceratotropis	*Angulares*	*V. angularis* var. *nipponensis*	*V. angularis* var. *nipponensis* (Ohwi) Ohwi & H. Ohashi	1
Ceratotropis	*Angulares*	*V. dalzelliana*	*V. dalzelliana* (Kuntze) Verdc.	1
Ceratotropis	*Angulares*	*V. exilis*	*V. exilis* Tateishi & Maxted	1
Ceratotropis	*Angulares*	*V. hirtella*	*V. hirtella* Ridl.	1
Ceratotropis	*Angulares*	*V. minima*	*V. minima* (Roxb.) Ohwi & H. Ohashi	1
Ceratotropis	*Angulares*	*V. nakashimae*	*V. nakashimae* (Ohwi) Ohwi & H. Ohashi	1
Ceratotropis	*Angulares*	*V. nepalensis*	*V. nepalensis* Tateishi & Maxted	1
Ceratotropis	*Angulares*	*V. reflexopilosa*	*V. reflexopilosa* Hayata	1
Ceratotropis	*Angulares*	*V. reflexopilosa* subsp. *glabra*	*V. reflexopilosa* subsp. *glabra* (Roxb.) N. Tomooka & Maxted	1
Ceratotropis	*Angulares*	*V. riukiuensis*	*V. riukiuensis* (Ohwi) Ohwi & H. Ohashi	1
Ceratotropis	*Angulares*	*V. tenuicaulis*	*V. tenuicaulis* N. Tomooka & Maxted	1
Ceratotropis	*Angulares*	*V. trinervia*	*V. trinervia* (B. Heyne ex Wight & Arn.) Tateishi & Maxted	1
Ceratotropis	*Angulares*	*V. umbellata*	*V. umbellata* (Thunb.) Ohwi & H. Ohashi	1
Ceratotropis	*Ceratotropis*	*V. grandiflora*	*V. grandiflora* (Prain) Tateishi & Maxted	1
Ceratotropis	*Ceratotropis*	*V. hainiana*		2
Ceratotropis	*Ceratotropis*	*V. mungo*	*V. mungo* (L.) Hepper	1
Ceratotropis	*Ceratotropis*	*V. mungo* var. *silvestris*	*V. mungo* var. *silvestris* Lukoki et al.	1
Ceratotropis	*Ceratotropis*	*V. radiata*	*V. radiata* (L.) R. Wilczek	1
Ceratotropis	*Ceratotropis*	*V. radiata* var. *sublobata*	*V. radiata* var. *sublobata* (Roxb.) Verdc.	1
Ceratotropis	*Ceratotropis*	*V. sahyadriana*		2
Ceratotropis	*Aconitifoliae*	*V. aconitifolia*	*V. aconitifolia* (Jacq.) Maréchal	1
Ceratotropis	*Aconitifoliae*	*V. aridicola*	*V. aridicola* N. Tomooka & Maxted	1
Ceratotropis	*Aconitifoliae*	*V. indica*		2
Ceratotropis	*Aconitifoliae*	*V. khandalensis*	*V. khandalensis* (Santapau) Sundararagh. & Wadhwa	1
Ceratotropis	*Aconitifoliae*	*V. stipulacea*	*V. stipulacea* (Lam.) Kuntze	1
Ceratotropis	*Aconitifoliae*	*V. subramaniana*	*V. subramaniana* (Babu ex Raizada) Raizada	1
Ceratotropis	*Aconitifoliae*	*V. trilobata*	*V. trilobata* (L.) Verdc.	1
Plectrotropis	*Plectotropis*	*V. kirkii*	*V. kirkii* (Baker) J. B. Gillett	1
Plectrotropis	*Plectotropis*	*V. vexillata*	*V. vexillata* (L.) A. Rich.	1
Plectrotropis	*Plectotropis*	*V. vexillata* var. *angustifolia*	*V. vexillata* var. *angustifolia* (Schumach.) Baker	1
Plectrotropis	*Plectotropis*	*V. vexillata* var. *davyi*	*V. vexillata* var. *davyi* (Bolus) B. J. Pienaar	1
Plectrotropis	*Plectotropis*	*V. vexillata* var. *macrosperma*	*V. vexillata* var. *macrosperma* Maréchal et al.	1
Plectrotropis	*Plectotropis*	*V. vexillata* var. *ovata*	*V. vexillata* var. *ovata* (E. Mey.) B. J. Pienaar, nom. inval.	1
Plectrotropis	*Plectotropis*	*V. vexillata* var. *vexillata*	*V. vexillata* var. *vexillata*	1
Plectrotropis	*Plectotropis*	*V. vexillata* var. *youngiana*	*V. vexillata* var. *youngiana* F. M. Bailey	1
Plectrotropis	*Pseudoliebrechtsia*	*V. lobatifolia*	*V. lobatifolia* Baker	1
Vigna	*Catiang*	*V. keraudrenii*	*V. keraudrenii* Du Puy & Labat	1
Vigna	*Catiang*	*V. monantha*	*V. monantha* Thulin	1
Vigna	*Catiang*	*V. schlechteri*	*V. schlechteri* Harms	1
Vigna	*Catiang*	*V. unguiculata*	*V. unguiculata* (L.) Walp.	1
Vigna	*Catiang*	*V. unguiculata* group *biflora*	*V. unguiculata* (L.) Walp. group *biflora*	1
Vigna	*Catiang*	*V. unguiculata* subsp. *baoulensis*	*V. unguiculata* (L.) Walp. subsp. *baoulensis* (A. Chev.) Pasquet	1
Vigna	*Catiang*	*V. unguiculata* subsp. *protracta*	*V. unguiculata* (L.) Walp. subsp. *protracta* (E. Mey.) B. J. Pienaar	1

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[1] USDA, ARS & NPGS. GRIN-Taxonomy. (2018). Available at: https://npgsweb.ars-grin.gov/gringlobal/taxon/taxonomysearch.aspx.

[2] Iseki, K., Takahashi, Y., Muto, C., Naito, K. & Tomooka, N. Diversity and evolution of salt tolerance in the genus *Vigna*. *PLoS One* 11, e0164711 (2016).

Subgenus	Section	Species	Complete scientific name	Taxonomy
Vigna	*Catiang*	*V. unguiculata* group *melanophthalmus*	*V. unguiculata* (L.) Walp. group *melanophthalmus*	1
Vigna	*Catiang*	*V. unguiculata* group *unguiculata*	*V. unguiculata* (L.) Walp. group *unguiculata*	1
Vigna	*Catiang*	*V. unguiculata* subsp. *aduensis*	*V. unguiculata* subsp. *aduensis* Pasquet	1
Vigna	*Catiang*	*V. unguiculata* subsp. *burundiensis*	*V. unguiculata* (L.) Walp. subsp. *burundiensis* Pasquet	1
Vigna	*Catiang*	*V. unguiculata subsp. letouzeyi*	*V. unguiculata* (L.) Walp. subsp. *letouzeyi* Pasquet	1
Vigna	*Catiang*	*V. unguiculata subsp. pawekiae*	*V. unguiculata* (L.) Walp. subsp. *pawekiae* Pasquet	1
Vigna	*Catiang*	*V. unguiculata* subsp. *tenuis*	*V. unguiculata* subsp. *tenuis* (E. Mey.) Maréchal et al.	1
Vigna	*Catiang*	*V. unguiculata* subsp. *unguiculata*	*V. unguiculata* subsp. *unguiculata*	1
Vigna	*Catiang*	*V. unguiculata* subsp. *stenophylla*	*V. unguiculata* subsp. *stenophylla* (Harv.) Maréchal et al.	1
Vigna	*Catiang*	*V. unguiculata* var. *spontanea*	*V. unguiculata* var. *spontanea* (Schweinf.) Pasquet	1
Vigna	*Catiang*	*V. unguiculata* group *sesquipedalis*	*V. unguiculata* group *sesquipedalis*	1
Vigna	*Catiang*	*V. unguiculata* subsp. *alba*	*V. unguiculata* subsp. *alba* (G. Don) Pasquet	1
Vigna	*Catiang*	*V. unguiculata* subsp. *dekindtiana*	*V. unguiculata* subsp. *dekindtiana* (Harms) Verdc.	1
Vigna	*Catiang*	*V. unguiculata* subsp. *pubescens*	*V. unguiculata* subsp. *pubescens* (R. Wilczek) Pasquet	1
Vigna	*Macrodontae*	*V. friesiorum*	*V. friesiorum* Harms	1
Vigna	*Macrodontae*	*V. frutescens*	*V. frutescens* A. Rich.	1
Vigna	*Macrodontae*	*V. frutescens* subsp. *incana*	*V. frutescens* subsp. incana (Taub.) Verdc.	1
Vigna	*Macrodontae*	*V. frutescens* var. *buchneri*	*V. frutescens* var. *buchneri* (Harms) Verdc.	1
Vigna	*Macrodontae*	*V. membranacea*	*V. membranacea* A. Rich.	1
Vigna	*Macrodontae*	*V. somaliensis*	*V. somaliensis* Baker f.	1
Vigna	*Reticulatae*	*V. reticulate*	*V. reticulata* Hook. f.	1
Vigna	*Reticulatae*	*V. wittei*	*V. wittei* Baker f.	1
Vigna	*Vigna*	*V. ambacensis*	*V. ambacensis* Welw. ex Baker	1
Vigna	*Vigna*	*V. angivensis*	*V. angivensis* Baker	1
Vigna	*Vigna*	*V. bequaertii*	*V. bequaertii* R. Wilczek	1
Vigna	*Vigna*	*V. comosa*	*V. comosa* Baker	1
Vigna	*Vigna*	*V. comosa* var. *lebrunii*	*V. comosa* var. *lebrunii*	1
Vigna	*Vigna*	*V. filicaulis*	*V. filicaulis* Hepper	1
Vigna	*Vigna*	*V. filicaulis* var. *pseudovenulosa*	*V. filicaulis* var. *pseudovenulosa* Maréchal et al.	1
Vigna	*Vigna*	*V. fischeri*	*V. fischeri* Harms	1
Vigna	*Vigna*	*V. gazensis*	*V. gazensis* Baker f.	1
Vigna	*Vigna*	*V. gracilis*	*V. gracilis* (Guill. & Perr.) Hook. f.	1
Vigna	*Vigna*	*V. heterophylla*	*V. heterophylla* A. Rich.	1
Vigna	*Vigna*	*V. hosei*	*V. hosei* (Craib) Backer	1
Vigna	*Vigna*	*V. laurentii*	*V. laurentii* De Wild.	1
Vigna	*Vigna*	*V. luteola*	*V. luteola* (Jacq.) Benth.	1
Vigna	*Vigna*	*V. marina*	*V. marina* (Burm.) Merr.	1
Vigna	*Vigna*	*V. multinervis*	*V. multinervis* Hutch. & Dalziel	1
Vigna	*Vigna*	*V. oblongifolia*	*V. oblongifolia* A. Rich.	1
Vigna	*Vigna*	*V. o-wahuensis*	*V. o-wahuensis* Vogel	1
Vigna	*Vigna*	*V. parkeri*	*V. parkeri* Baker	1
Vigna	*Vigna*	*V. parkeri* subsp. *acutifolia*	*V. parkeri* subsp. *acutifolia* Verdc.	1
Vigna	*Vigna*	*V. parkeri* subsp. *maranguensis*	*V. parkeri* subsp. *maranguensis* (Taub.) Verdc.	1
Vigna	*Vigna*	*V. racemosa*	*V. racemosa* (G. Don) Hutch. & Dalziel	1
Vigna	*Vigna*	*V. subterranea*	*V. subterranea* (L.) Verdc.	1
Vigna	*Vigna*	*V. subterranea* var. *spontanea*	*V. subterranea* var. *spontanea* (Harms) Pasquet	1
Vigna	*Vigna*	*V. oblongifolia* var. *parviflora*	*V. oblongifolia* A. Rich. var. *parviflora* (Welw. ex Baker) Verdc.	1

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