

Global strategy for the conservation and use of *Vigna*: summary for ITPGRFA stakeholders

Cowpeas in Liberia Photo: Michael Major

This document is a concise summary of the [Global Strategy for the Conservation and Use of *Vigna*](#) (Nair et al. 2023). This summary supports decision making by the stakeholders of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) by providing evidence-based information in an accessible format.

Annex I crops: *Vigna unguiculata* (L.) Walp (cowpea), *V. subterranea* (L.) Verdc. (Bambara groundnut), *V. vexillata* (L.) A. Rich., *V. mungo* (L.) Hepper (urd bean), *V. angularis* (Willd.) Ohwi & Ohashi (adzuki bean), *V. umbellata* (Thunb.) Ohwi & Ohashi (rice bean), *V. radiata* (L.) Wilczek (mung bean), *V. aconitifolia* (Jacq.) Maréchal (moth bean), *V. reflexo-pilosa* Hayata (creole bean), *V. stipulacea* Kuntze (minni payaru)

International collections: International Institute of Tropical Agriculture (IITA), The World Vegetable Center (WorldVeg) and Alliance of Bioversity International and CIAT

Composition and gaps in *ex situ* collections

A total of 96,161 *Vigna* accessions belonging to 34 taxa including wild relatives and landraces were reported across the 21 genebanks participating in the 2021–2022 survey on global *Vigna* conservation. The largest collection of *Vigna* accessions were the International Institute of Tropical Agriculture (IITA) (19,020 accessions), the World Vegetable Center (WorldVeg), Taiwan (15,735 accessions), Indian Bureau of Plant Genetic Resources (NBPGR) (14,505 accessions), the USDA-ARS, USA (13,078 accessions) and NARO, Japan (7,177 accessions) and account for 72% of the *Vigna* accessions reported by the survey participants.

The species with the largest number of stored accessions was *V. unguiculata* subsp. *unguiculata* (33,015 accessions), followed by *V. radiata* (29,399 accessions). IITA conserves the largest collections of cowpea and Bambara groundnut. WorldVeg conserves the largest collection of mungbean and adzuki bean. NBPGR maintains the largest collections of urdbean, rice bean, and moth bean. CIAT holds the largest collection of 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 collec-

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tions of African wild *Vigna*, while the Japanese Agriculture and Food Science Organization and NBPGR hold important collections of wild Asian *Vigna*.

Meise Botanic Garden in Belgium has the largest number of wild species of *Vigna* (66 species). For *Vigna* crop wild relatives (CWRs) recent literature (van Zonneveld et al. 2020) identified taxa and regions that are priority for collecting, and the *Global Strategy for the Conservation and Use of Vigna* includes an overview of number of accessions of cowpea and Bambara groundnut conserved in genebanks by countries and regions where they were collected to identify gaps and underrepresented regions.

Routine operations, quality management system, and safety duplication

Sixty percent of the surveyed genebanks have storage units or freezers for long-term conservation. All of these genebanks use sealed aluminum packs or air-tight glass jars and have temperature monitors. Ninety percent of the surveyed genebanks have separate work areas for seed processing, over 71% have separate areas for packaging for storage and distribution with relative humidity control and a dedicated laboratory and trained staff for seed viability testing, and 57% have a low-temperature seed drying facility and a dedicated laboratory and trained staff for health testing. Eighty-six percent of the surveyed genebanks reported that they have access to at least one field site in a key agroecological zone for regeneration and multiplication.

The surveyed genebanks reported that they follow different standard operating protocols (SOPs) and proce-

dures. Most of the genebank respondents reported that they have their own SOPs for characterization and data management.

About one third of the surveyed genebanks reported to have at least partially duplicated their collection outside of the country, but there is variation among genebanks on the proportion of the collection duplicated. More than 40,000 *Vigna* accessions are duplicated at the SGSV representing 64 species and 142 taxa.

Documentation and information systems

About 10% of surveyed genebanks reported not having passport data for their *Vigna* collections, and about 24% do not have taxonomic information. About half of the surveyed genebanks make passport information openly available online. The percentage of accessions with passport data and the reported accuracy of these data vary among the different respondents. Fifty-seven percent of the surveyed genebanks reported that they enter data into a database for genebank management and some genebanks reported not having a database system and storing data in spreadsheets.

Fourteen percent of the respondents reported that they use GRIN-Global genebank data management system to manage phenotypic and/or genotypic data. The respondents identified a 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 as constraints to data and information management for *Vigna* collections.

Key metrics ¹	Data source	Value	%
Estimated global number of accessions <i>ex situ</i>	Genesys (2022) and WIEWS (2022)	129,903	
Estimated global number of accessions <i>ex situ</i>	Survey ² (2021-2022)	96,161	
Accessions with DOI	GLIS portal (2024)	52,405	40%
Global number of accessions notified as available in the MLS	GLIS portal (2024)	46,988	36%
Estimated number of accessions safety duplicated at a different genebank ³	Genesys (2022) and WIEWS (2022)	12,979	10%
Estimated number of accessions safety duplicated outside of the country ³	Genesys (2022) and WIEWS (2022)	5,476	4%
Number of accessions safety duplicated at Svalbard Global Seed Vault	SGSV web portal (2024)	41,894	34%
Number of accessions distributed per year	Plant Treaty Data Store (2015–2019) ⁴	4,738	
Number of samples distributed per year	FAO-WIEWS (2014-2019) ⁴	30,616	
Passport data completeness index : median value in Genesys (Range 0–10)	Genesys (2024)	6	

¹ Some of these metrics were updated after the publication of the strategy

² Twenty-one genebanks completed the 2021–2022 survey on global *Vigna* conservation

³ This figure does not include safety duplicates at Svalbard Global Seed Vault

⁴ As reported in *The Plants that Feed the World* (Khoury et al., 2023).

Crop descriptors

Genebanks have been using independent descriptors for characterization data leading to gaps in trait characterization and discrepancies in how data are recorded. 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.

Human and financial resources

Challenges reported by the survey respondents include untrained staff, and lack of expertise in taxonomy, identification and characterization. Some genebanks reported difficulties in retaining scientific and technical staff long term. Most of the genebanks reported that funding is not stable and that they rely on short-term funding. Uncertainty of long-term funding was listed as one of the primary threats to the collections.

Distribution and obstacles to use

Seventy-three percent of the accessions notified as available in the Multilateral System of the ITPGRFA (MLS) are conserved in international collections, and 50% are *Vigna unguiculata*, another 27% are *V. radiata*, 6% *V. subterranea*, and the remaining is spread among the other *Vigna* species.

Most collections among the surveyed genebanks make materials available to users from one or more genebanks by request. Many of these genebanks reported distributing cowpea and mung bean, while only one genebank reported distributing other minor *Vigna* crop species (such as *V. trilobata*, *V. glabrescens*, *V. luteola* and *V. marina*).

Most of the respondents reported that they have adequate procedures in place for the distribution of accessions to the requestor. Obstacles to distributions reported by the respondents included: the time to process a SMTA within the institute, the costs of phytosanitary certification and for the shipping material, the lack of proper legislation at national level, and the limited availability of seeds because of damage caused by pests and disease.

Recommendations and priorities

- Establish a long-term global funding strategy for the collection, conservation and distribution of *Vigna* genetic resources.
- Establish an International *Vigna* Advisory Group 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 genebanks with large *Vigna* collections and engage with other *Vigna* key collections.

- Support and encourage contracting parties of the ITPGRFA with inclusion (and notification) of their *Vigna* collections in the Multilateral System of the ITPGRFA.
- Conduct training programs for staff involved in *Vigna* conservation in germplasm conservation and management activities.
- Catalog all available *Vigna* accession 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.
- Conduct phenotyping and genotyping of newly collected accessions to identify unique materials.
- Increase the number of core and mini-core collections.
- Develop a standardized and comprehensive list of descriptors across *Vigna* species for consistency of data collection.
- Evaluate *Vigna* germplasm for resistance to biotic and abiotic stresses and for nutritional/health related compounds.
- Collect seed of threatened and endemic wild relatives of *Vigna* crops, which require urgent conservation. Priority should be on rare and/or endangered species, and on species not well represented in genebank collections.
- Monitor and conserve populations of wild *Vigna in situ* in protected areas, and other areas, and engage national conservation programs in collaboration with local communities and national universities to monitor their population.

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