

Genebanks QMS

Charlotte Lusty, December 2023

Genebanks operations





Information

management

6.11



duplication



Regeneration & characterization



testing



Distribution

Acquisition Characterization Cryopreservation Distribution Germination testing Germplasm health testing Information and data management InVitro subculture **Live Plants** Long-term storage Medium-term storage

Regeneration / Multiplication

Seed processing

Relevant standards



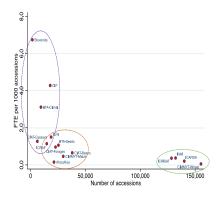


Diverse crops & collections



Collection size

Crop	Category	Crops		
type				
1	Self-pollinated cultivated cereal	Wheat, barley, rice, small millets		
2	Self-pollinated food legume	Beans, cowpea (& other leguminous spp at IITA), chickpea, lentil, pea		
3	Self-pollinated wild cereal	Wild relatives of crop type 1		
4	Cross-pollinated cultivated cereal	Maize, sorghum, pearl millet		
5	Cross-pollinated wild cereal	Wild relatives of crop type 2		
6	Cross-pollinated food legume	Grasspea, faba bean, pigeon pea		
7	Cross-pollinated forages, species that are difficult to manage	Forages, trees, wild potato & sweet potato held as seed at CIP, groundnut		
8	Clonal	Banana, cassava, potato, sweetpotato, yam, Andean roots and tubers		





Performance management system



Backlogs in CGIAR genebanks in 2012

All genebanks (except IRRI) had backlogs

- Of total 708,761 accessions

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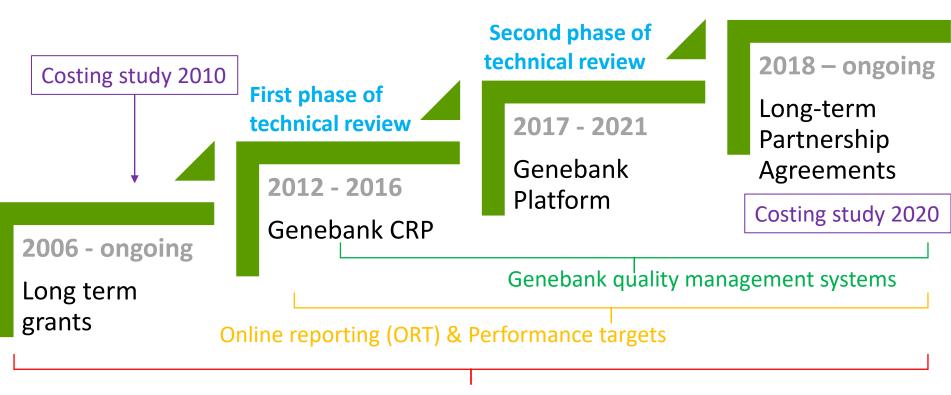
- 34% not physically available without regeneration or cleaning
- 45% not safety duplicated in two locations

Genebanks CRP response

- Performance targets
- Online reporting
- Quality management system
- SOP documentation audit
- External review and validation.

Genebank performance management





Online reporting



Main menu	IRRI Pe	Performance indicators			2016	Anr	Rice	
View Profile	Save as Excel				Δ	ttachments	<u>History</u>	Correspondence
Logout (celusty)	ARS.02 TABLE AS4 - Seed collection accession numbers							
Performance indicators								
Financials	Total number of accessions	Live	LTS	LTS MTS	Total number accessions counting individual accessions only		Summed	
Recommendations	Total number of accessions	plants	plants LIS		once			total
Quality management	In the costed collection	3	122,538	127,678			127,917	250,219
Data triangulation	Legally available within the costed collection	3	117,640	122,782			123,019	240,425
	Genetic stocks within the costed collection	0	3,546	8,916			8,916	6 12,462
Other functions	With health status tested	0	104,473	109,148			109,185	5 213,621
Calendar of events	Health tested in 2016	0	2,851	8,065			8,065	5 10,916
Document repository	With health status clean	0	104,389	109,054			109,093	213,443
Submission schedule	Disease cleaned in 2016	0	4	1,376			1,376	1,380
Center annual report	With known viability		120,330	125,509			126,575	245,839
Grantee dump	Tested for viability in 2016		5,031	18,785			21,570	23,816
News	With acceptable viability		115,350	120,459			124,923	235,809
Reporting Download User Manual	Regenerated (because of low viability) in 2016		437	2,509			2,537	2,946
Download USer Manual	With acceptable seed number		117,968	126,688			127,912	2 244,656
	Subjected to seed increase in 2016		254	3,287			3,291	3,541
	Legally and physically available	3	111,031	120,071			120,074	231,105

Comments The proportion of accessions in LTS is decreasing because we no longer routinely put genetic stocks into LTS.

Few LTS germination tests because we've fully implemented the new efficiency measure not to test samples in LTS if the equivalent sample in MTS has satisfactory germination.

Few MTS germination tests because (1) we are at the low point in the post-GPG1 cycle and (2) as agreed we are not routinely monitoring genetic stocks. Because of the policy on genetic stocks, the number of samples with known viability and acceptable viability in MTS will become a decreasing % of total accessions stored in MTS.

Genebanks QMS (rather than ISO)



- Based on FAO genebank standards rather than generic standards
- Holistic: acquisition to distribution rather than selected procedures or processes
- Internally driven with collective and individual goals
- Efficient in terms of the amount of paperwork
- Allows integration of topical issues and emerging risks
- Easily tailored to the unique situation of each genebank
- Suitable for a network with templates and shareable elements across countries, crops and conservation systems

Genebanks QMS



Phased assessment of written SOPs for key processes:

- Conservation (viability testing, processing, storage)
- Regeneration & characterization
- Acquisition
- Distribution
- Safety duplication
- Information management

Same template, but individual genebank's SOP

Document SOPs

Audit for compliance with standards

Other QMS elements

- Restricted access
- Staff succession
- Barcoding
- Data management system
- Equipment calibration



External validation

GOAL workshops & QMS intensives





Benefits of Genebank QMS



- More meaningful technical reviews and useful recommendations
- Strengthened staff succession and emphasis on *long-termism*
- Staff empowerment, clarity of responsibility and motivation
- Opportunities for capacity building and alignment between institutes
- Effective prioritization and pipeline for research & optimization
- Basis for costing and cost savings (USD 3 million/yr)
- Strengthened collective thinking
- 350+ drafted SOPs

es QMS strongly endorsed in 2017 IEA & 2023 IAES reviews

QMS Harmonization

Persisting issues:

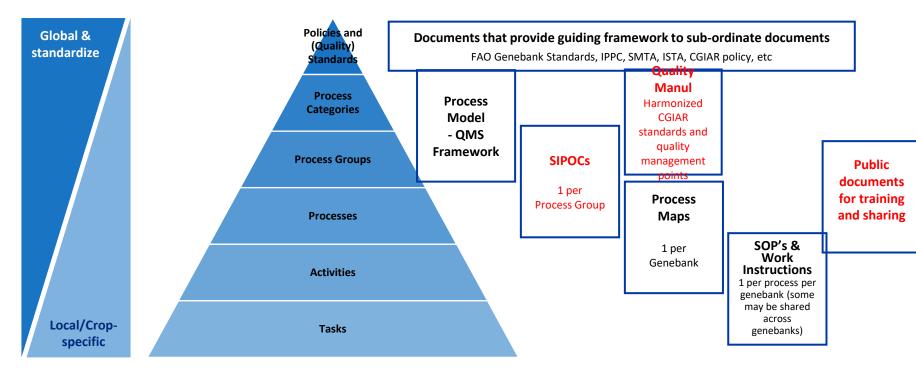
- Switching comprehensively to one data management system
- Parity in costs and standards (esp phytosanitary)
- Evolving beyond mandate crops to a more regionalized approach
- Continuous workflow efficiency
- Expensive crops (e.g. forages, clonal crops)
- How to sustain auditing & updating on top of System, Centre and Crop Trust-commissioned evaluations





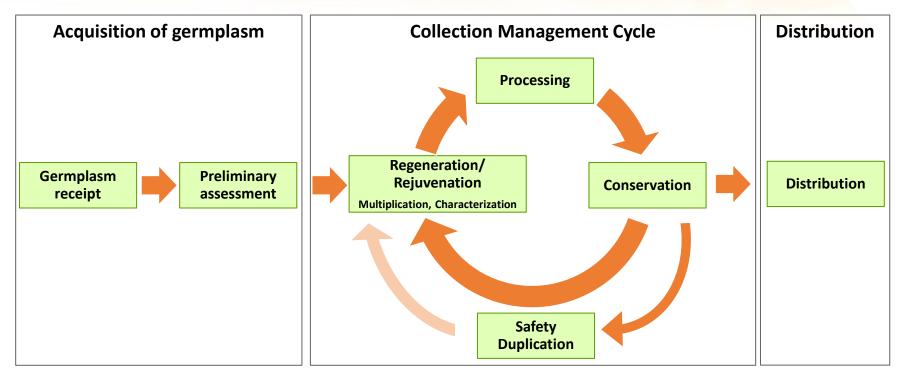
Structure and documentation of the CGIAR Genebank Process Model (BPM)





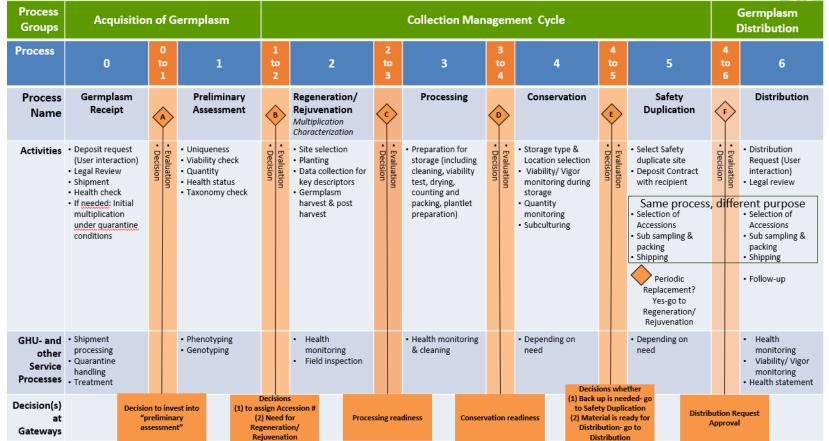
CGIAR

Genebank's Process Model



Overall Process Map for Genebanks Process





Genebank harmonization – Dec 2023





- Processes are different for good reasons
- Chose carefully areas for harmonization vs standardization (e.g. user management, germplasm distribution, phytosanitary health, critical decision & quality points).
- Move from CoPs into selfsustaining cross-Centre teams
- Basis for data management system

Thank you

