NATIONAL STRATEGIC GERMPLASM AND CULTIVAR COLLECTION ASSESSMENT AND UTILIZATION PLAN:

Technical Details, Analyses, and Approaches

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Summary

The 2018 Farm Bill directed the USDA to "develop and implement a national strategic germplasm and cultivar collection assessment and utilization plan that takes into consideration the resources and research necessary to address the significant backlog of characterization and maintenance of existing accessions considered to be critical to preserve the viability of, and public access to, germplasm and cultivars." In response, staff from the USDA/ARS National Plant Germplasm System (NPGS) and USDA/ARS leadership, in consultation with the USDA National Genetic Resources Advisory Council and other scientific experts, formulated a National Strategic Germplasm and Cultivar Collection Assessment and Utilization Plan ("Plan" hereafter) that is described in three documents. The Plan outlines how the plant genetic resources (PGR; synonymous with plant germplasm) held in the NPGS will be maintained, characterized, evaluated, documented, and distributed; and how to reduce the backlogs that could prevent that PGR and associated data from being publicly available.

The present document "National Strategic Germplasm and Cultivar Collection Assessment and Utilization Plan: Technical Details, Analyses, and Approaches" contains technical details, analyses, and approaches for implementing the overall Plan. A companion document entitled "Synopsis of the National Strategic Germplasm and Cultivar Collection Assessment and Utilization Plan" comprises an abridgement for the Plan, presented in more general terms, and focused on strategic elements of the Plan. Another companion document entitled "National Strategic Germplasm and Cultivar Collection Assessment and Utilization Plan: Supplemental Crop and Crop Wild Relative Collections Data" contains extensive, detailed PGR management data for each NPGS genebank unit and the individual crops managed at those genebank units.

This Plan is "data-driven," based on 75,000+ datapoints generated from 75+ quantitative measures. Some of these metrics were developed by the NPGS; many are currently employed by international genebanks to measure PGR management performance. The metrics were applied to the operations of 22 USDA/ARS NPGS genebank units to assess the current status of the NPGS PGR collections and their management (synonymous with "curation") and identify operational backlogs and deficiencies. The NPGS staff and leadership then formulated strategies, priorities, and approaches for addressing those backlogs and strengthening NPGS operations. Beyond reducing the backlogs for characterizing and maintaining PGR, the overall impacts and outcomes of this Plan are to mobilize more effectively those PGR, their valuable traits, and associated descriptive information. This will enable more efficient adaptation of important US crops in response to rapid changes in climate and market demands, to ensure domestic and international food security, and preserve the economic vitality of U.S. agriculture.

In addition to describing the Plan's strategies, priorities, outcomes, and impacts, this document provides extensive technical details, analyses, and approaches that constitute the foundation of the Plan. It is organized according to an Introduction and 13 subsequent sections. The overall strategies and priorities for the Plan are summarized in the Introduction and Component 13 sections, and here in the following paragraphs. The first 12 sections correspond to 12 different Components of PGR management and utilization. Components 1-11 assess the current status and estimate the expanded infrastructure, operational capacities, and research needed to i) reduce or eliminate backlogs, so that NPGS PGR are managed according to national and international

standards; and ii) incorporate leading edge technologies and approaches that enhance the efficiencies of NPGS maintenance, characterization, and evaluation operations and make invaluable PGR and associated information more readily available for utilization now and in the future. Component 12 covers genetic enhancement/pre-breeding, which is not always considered a core responsibility for genebanks. Regardless, this Plan considers genetic enhancement as a critical step for reducing barriers to optimal PGR utilization in crop breeding. The final 13th section of this document outlines interconnected challenges and priorities shared by NPGS genebank units, which are then incorporated into the implementation roadmap presented at the conclusion of this section.

This Plan will be implemented during a 10-year period, with a mid-course assessment at the 5-year point, and an overall retrospective review after 10 years. The specific schedules and sequences for implementing different aspects of the Plan will be determined by the challenges, priorities, and needs of the 22 individual NPGS genebank units and the ca. 200 crops that they manage. Detailed information for the different genebank units and crops is presented in the figures (illustrations) and in Appendix B of the current document and included in the extensive datasets in the companion document "National Strategic Germplasm and Cultivar Collection Assessment and Utilization Plan: Individual Crop and Crop Wild Relative Collections Data."

Implementing the Plan will require substantially greater funding than the current total $38 million net-to-location (NTL) annual recurrent NPGS base budget; Fig. Ia, at the end of the Summary and Component 1 of this document include more budgetary details. *Note: The costs to implement this Plan are estimated and do not constitute a USDA request for funding.* An estimated increase of ca. $17.5 million NTL to the annual recurrent NPGS base budget will be needed to expand PGR maintenance operations and capacities to reduce existing backlogs during the first five (+5) years of this Plan. An additional $12.3 million NTL increase will be needed by ten (+10) years to minimize those backlogs and enable access to more PGR and key genotypic and phenotypic evaluation data. Furthermore, by +5 and +10 years, an additional $25 million NTL increase in the annual recurrent NPGS base budget will be needed for an expanded phenotypic evaluation program for 50-100 crops (Component 11) that will apply leading edge phenomic approaches for phenotyping priority traits; for the development of phenomic analysis protocols; and to support collaborative PGR phenotypic evaluations guided by the 40+ Crop Germplasm Committees (CGCs). An additional $50-$150 million NTL will be required to support new genetic enhancement projects for approximately 100 different crops (Component 12). Finally, a $1.8 million NTL increase in the annual recurrent budget is needed to maintain and deliver data generated by a multi-phase genotypic characterization program (Component 10 and below). If possible, the total $56.5 million NTL addition to the present annual recurrent NPGS base budget of $38 million NTL (Fig. Ia) should proceed incrementally over a decade (+10 years) to enable the additional funds to be efficiently and effectively mobilized to implement the Plan over multiple PGR management cycles and fiscal years.

Upgrades to the NPGS's infrastructure and facilities are integral for the outcomes of reducing or eliminating backlogs; for conducting research to develop superior PGR management methods; and to generate genotypic characterization and phenotypic evaluation data for PGR users. Some

priority facility and infrastructural upgrades are already underway as part of ARS's Capital Investment Strategy (CIS). The estimated costs for expanding or upgrading NPGS infrastructure (buildings, land, etc.) will be incorporated into the CIS as this Plan is implemented. Appendix B of this document discusses the suitability of the current infrastructure and facilities at some NPGS genebank units for effectively managing certain PGR that have been or will be assessed. Ideally, energy-saving green technologies, such as geothermal heat pumps, will be incorporated into infrastructure and facility upgrades and new development to reduce long-term upkeep costs commonly associated with conventionally heated and cooled greenhouses, seed storage areas, growth and vernalization chambers, etc. Based on the assessments, energy-efficient cold-storage facilities (preferably 0˚F, -18˚C temperatures), controlled/protected environment (greenhouse, screenhouse) growing spaces, and field space will be expanded (Fig. Ib and Component 1) or PGR management responsibilities for some crops could be shifted to other NPGS genebank sites.

Currently, 87% of the 569,000+ NPGS PGR "accessions" (distinctly identified genetic type from a single species that was collected/developed at one time and from one location) are available for research, breeding, and education; in an average year, ca. 200,000 samples of those accessions are distributed for those purposes. The origin/provenance for most accessions are documented with data accessible through the NPGS's information management system, GRIN-Global. Genebanks around the world have adopted GRIN-Global and it is considered to be an international standard for PGR information management. Many seed-propagated accessions have been safeguarded in the NPGS's National Laboratory for Genetic Resources Preservation (NLGRP). New cryopreservation methods have been developed for clonally propagated PGR. Additionally, priorities for conserving crop wild relatives (CWR) native to the U.S. have been identified. Therefore, the current NPGS facilities, infrastructure, skilled and experienced staff, and operational capacities furnish an invaluable foundation for implementing this Plan.

Notably, the sizes of most NPGS PGR collections have grown relatively slowly (approximately 1%/year increase in number of accessions) during the last 15 years. The technical and logistical challenges associated with managing unadapted crop varieties, CWR, weedy species, and PGR maintained and propagated as clones have contributed substantially to those backlogs and require significant resources, research, and expertise to address. Thus, the backlogs in PGR maintenance, genotypic characterization, and other NPGS operations described in this Plan have not accumulated directly from rapidly expanding collections but rather, primarily from i) insufficient PGR management capacity at individual genebank units and ii) lack of adequate PGR management methods for some crops and CWR.

Reducing the backlogs in safeguarding PGR from complete loss and making PGR and genotypic characterization and phenotypic evaluation data more readily available will require additional NPGS personnel (Fig. Ib below and Component 1) to support priority PGR and information management operations and to conduct research that reduces or eliminates technical barriers to effective PGR management. Priorities for this Plan are not only to hire such personnel, but to expand substantially the current educational and training programs to serve the next generation of NPGS PGR managers.

It is a priority of this Plan to expand information management capacities at individual genebank units to reduce backlogs in i) digitizing paper documents; ii) incorporating data into GRIN-Global; iii) capturing digital images that document key traits and help maintain genetic integrity of accessions; and iv) safeguarding and disseminating greater volumes of genotypic characterization and phenotypic evaluation data. It is also a priority to expand database and information management capacities so GRIN-Global can handle an expanded volume of data generated (Component 2) to support the outcomes of more effective PGR management and wider PGR utilization in breeding and research.

Expanded PGR management and information management capacities will reduce substantial backlogs in "core" PGR maintenance operations at genebank units (Components 4-7), with the impact of duplicating and backing-up more accessions safely at the NLGRP, according to NPGS and international quality standards for long-term storage. Specifically, increased volumes of seeds and plants from more accessions will be tested for germination, viability, longevity, and the presence of pathogens (especially for those of quarantine importance); such pathogens will be eliminated whenever feasible. Backlogs for regenerating or repropagating PGR are cited by genebank systems throughout the world as some of the most severe challenges to successfully safeguarding PGR ex situ and making them available for research and breeding. Consequently, a priority for this Plan is to regenerate or repropagate more accessions each year when accession health and quality begin to deteriorate or when extensive use reduces accession inventories below minimum thresholds for maintaining genetic integrity and availability for distribution.

Increased PGR management capacities alone cannot reduce the backlogs in PGR maintenance, genotypic characterization, and phenotypic evaluation. In addition, the budget and personnel increases summarized in Figs. Ia, Ib, and Component 1 would address the priorities of strategically expanding the NPGS capacities to conduct applied research to develop new, improved technologies and PGR managerial approaches with the impact of streamlining PGR maintenance operations, particularly for species with complicated biological features. Generating new genotypic characterizations through applied research will guide expanded PGR acquisition and in situ conservation programs (Component 3). More effective methods will be devised for long-term maintenance (ideally, cryopreservation) and back-ups of clonally propagated PGR and those with seeds that cannot be preserved under standard reduced-temperature regimens (Component 4). New testing procedures to predict impending deterioration in seed vigor and viability before such reductions occur can be developed through applied research, with the outcome of identifying endangered accessions without destroying numerous seeds in the process (Component 5). Applied research will also result in the outcome of creating superior approaches for assaying PGR for pathogens and then removing pathogens from accessions (Component 6). The reproductive modes (breeding systems, pollination vectors) for wild species, especially for CWR, of current or potential agricultural importance will be discovered and that knowledge applied to devise more reliable PGR regeneration or repropagation methods (Component 7).

To reduce the "…significant backlog in characterization…" the NPGS will collaborate with public- and private-sector cooperators to conduct a multi-phase 10-year genotypic characterization of NPGS PGR program (hereafter termed "genotypic characterization") for ca. 200 crops. Three initial phases will create the needed knowledge and analytical tools; the subsequent phase will involve genotyping the PGR; and, during the final phase, the NPGS will

store and deliver the resulting data and knowledge through GRIN-Global and other linked sources. Priority applications for the resulting data will include dramatically expanding "…public access to…" volumes of high-quality genotypic data, maintaining PGR accessions pure and true-to-type; identifying unknown, redundant, and misclassified accessions; and pinpointing gaps in the genetic coverage of collections. The overall budget for the five phases of the genotypic characterization program over +10 years would be ca. $16.7 million in one-time costs, and the annual recurrent costs of ca. $1.8 million, mentioned above, to manage and deliver the resulting genotypic characterization data. In addition, optional Whole Genome Sequencing (WGS) of high impact PGR would create a valuable genomic resource that supports crop research and breeding, at a one-time cost of $40.5 million (Fig. Ia and Component 10; *The costs to implement this Plan are estimated and do not constitute a USDA request for funding*).

Reducing the backlogs in PGR management operations and enabling more effective utilization of PGR require comprehensive genetic information generated through systematic genotypic characterizations with leading-edge genomic technologies (Component 10). More accessions will be characterized genotypically during PGR operations, with the outcome of assuring their genetic integrity and generating information for effective PGR management and use. The resulting genotypic characterization data will be applied to rationalize PGR collections; optimize PGR management operations; and reduce the backlog in meeting user demands for those accessions and associated data. New phenomic approaches will be adopted to enlarge substantially the NPGS's current PGR phenotypic evaluation programs, with the impact of delivering to breeders and researchers information regarding horticultural and agronomic traits such as resistance to pathogens and pests; tolerance of abiotic stresses; yield; and new product quality attributes (Component 11).

In some cases, entirely new approaches will be needed to generate priority genotypic characterizations and phenotypic evaluations of PGR (Components 10 and 11). Therefore, this Plan can serve as a unique and timely mechanism for creating innovative ways to produce and analyze genotypic characterization and phenotypic evaluation data via methodological and software "pipelines" that comprise seamless integrations of data generation, storage within GRIN-Global or other information management systems, analysis, interpretation, and visualization. The NPGS is well-situated to generate data for these robust pipelines due to vast genetic diversity captured within the ca. 200 crops and unimproved CWR and 600,000+ accessions in the collection. The pipelines will incorporate tools (e.g., digital imagery, new nucleotide sequencing techniques) that have been developed recently or are currently under development. Applied research will also devise efficient new data management schemes to describe the variability in heterogeneous and heterozygous PGR, information that can serve as valuable guidance for optimal PGR management and use. The impacts of these new pipelines and data management schemes will be to generate and analyze data more rapidly, in volumes that are orders of magnitude greater than what is currently possible, and for much the same costs, once genebank unit facilities and information management capacities are upgraded and personnel have been trained in their use. Combining genotypic characterization and phenotypic evaluation data will enable researchers and breeders to use PGR more effectively to identify genes encoding useful traits, thereby achieving the outcome of extending the capacities for marker-assisted selection and gene editing of these traits.

Reducing backlogs in PGR maintenance and conducting genotypic characterizations and phenotypic evaluations are major priorities for the Plan. Importantly, the Congress requested a "national strategic germplasm and cultivar collection assessment and utilization plan." Effectively exploiting the genetic potential of PGR will require that, at the minimum, NPGS genebank units support breeding and genetic enhancement programs by providing needed genetic raw materials in the form of more available accessions and more thoroughly characterized and evaluated PGR. Where genetic improvement programs lack sufficient capacity to use unimproved PGR, i.e., accessions are too unadapted, too wild/weedy, or crosses to elite material are too difficult, NPGS genebank units could participate more extensively to support, or even provide leadership for, associated collaborative genetic enhancement programs for some crops. Consequently, Component 12 of this Plan includes strategies for the NPGS to support generating new breeding populations or cultivars through genetic enhancement. This role for the NPGS extends beyond widely accepted core genebank responsibilities and capacities. Consequently, increases for that purpose would be needed in the annual recurrent base budgets of affiliated ARS breeding programs or NPGS genebank units in the range of $500,000 to $1.5 million per year per crop or related groups of crops. The approximate annual recurrent funding for implementing such programs for 100 priority U. S. crops concurrently would range from $50 million to $150 million per year (Fig. Ia and Component 12; *The costs to implement this Plan are estimated and do not constitute a USDA request for funding*). Once sufficient budgetary, personnel, and infrastructural capacities become available specifically for the purpose of genetic enhancement, NPGS genebanks could collaborate with other ARS projects and public- and private-sector partners to support, participate in, or even lead, genetic enhancement programs for priority crops that are critical for delivering the intrinsic value of NPGS PGR to U.S. farmers, producers, processors, and consumers.

A schedule to address Plan priorities and minimize or eliminate backlogs through an increased annual volume of regenerations and other associated operations within the 10 years of the Plan is outlined in Component 13. Implementing phased, incremental annual funding increases that are aimed at concurrently funding all aspects (maintenance, characterization, and evaluation) of the Plan is fundamental to "… preserve the viability of, and public access to, germplasm and cultivars…" in the most efficient and effective manner. The priorities outlined here address existing backlogs, use applied research to discover innovative and cost-effective approaches to PGR management, correct infrastructural deficiencies with cost-effective solutions, and deliver a greater volume of more valuable resources and associated data to public- and private- sector users. The development and incorporation of advanced, leading-edge technologies and approaches discovered through applied research outlined in Components 3 to 12 are pivotal to successful implementation of the Plan.

a. NPGS Plant Genetic Resource Management Funding (NTL $)

Time	NPGS Operations and Programs & Applied Research	Additional Funding	Total Annual Recurrent Funding	One-time funding (NTL $)
Now	Overall Operations		$38.01 M	
	Total		***$38.01 M***	
+ 5 Yrs.	Maintenance	$17.45 M	$55.46 M	
	Characterization	$1.80 M	$1.80 M	
	Trait Evaluations	$25.00 M	$25.00 M	
	Sub-Total	***$44.25 M***	***$82.26 M***	
	Genetic Enhancement (HIGH)	$150.00 M	$150.00 M	
	Total	***$194.25 M***	***$232.26 M***	
+10 Yrs.	Maintenance	$12.25 M	$67.71 M	
	Characterization		$1.80 M	
	Trait Evaluations		$25.00 M	
	Sub-Total	***$12.25 M***	***$94.51 M***	
	Genetic Enhancement (HIGH)		$150.00 M	
	Total	***$12.25 M***	***$244.51 M***	
One-Time	Genotypic Characterization	$16.67 M		$16.67 M
	Whole Genome Sequencing*	$40.50 M		$40.50 M
	Sub-Total	***$57.17 M***		***$57.17 M***
	Total	***$57.17 M***		***$57.17 M***

M = Millions

b. NPGS Personnel and Infrastructural Needs

		Now	+ 5 Yrs.	+ 10 Yrs.
Personnel	Personnel Levels (# FTE)	302	444	518
Cold Storage & Growing Space	Field Space (acres)	2,333	2,528	2,719
	Greenhouse & Enclosed Space (ft2)	264,565	365,747	430,207
	Cold storage space (ft3)	380,230	498,154	582,397

Fig. Ia: NPGS Plant Genetic Resource Management Funding (net-to-location, NTL) summarizes in millions (M) the current levels for the annual recurrent funding (NTL) and estimated additional annual recurrent funding and "one-time funding" needed to implement this Plan. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.* The column "Time" identifies particular time points: "Now" is the current time; "+5 Yrs." is five years after the beginning of Plan implementation; "+10 Yrs." is ten years after the beginning of Plan implementation; and "one-time" indicates the support for those operations will not involve annual, recurrent funding but rather expenditures that begin and end within the ten-year Plan period. The column "NPGS Operations & Programs" lists the different general categories of NPGS PGR operations and the applied research that supports those operations. The "HIGH" designation for Genetic Enhancement indicates that the "higher" cost estimate for supporting genetic enhancement operations for 100 crops was included. Consult the Introduction and Components 1-12 of the Plan for details about these categories.

The "Additional Funding" column lists the increases of annual recurrent funding from current levels ("Now") that are needed to expand particular NPGS operations and applied research at specific time points of the Plan. Funding increases needed to support "core" NPGS PGR operations are provided in the Sub-Total rows, shaded in the lighter beige hue. Genetic enhancement is listed separately from other NPGS PGR operations and applied research because of its unique role in enabling PGR utilization (see Component 12). Funding increases for NPGS Operations & Programs have been summarized for each time point in the Total rows, shaded in the darker beige hue.

The "Total Annual Recurrent Funding" column lists the annual recurrent funding levels at present ("Now") and needed at the +5 Yrs. and +10 Yrs. time points to support the three general categories of NPGS PGR operations. Total annual recurrent funding at each time point has been summarized in the Sub-Total and Total rows as described above.

The last column, "One-time Funding (NTL $)", summarizes the expenditures for genotypic characterization that begin and end within the ten-year timeframe for the Plan. The 5 phases of characterization and the optional operation "Whole Genome Sequencing" are explained in Component 10 of the Plan.

Fig. Ib: NPGS Personnel and Infrastructural Needs summarizes the expanded personnel (# FTE) staffing and infrastructural capacities (field space, greenhouse and enclosed space, and cold storage space) needed to implement the Plan. The column "Now" is the current time; "+5 Yrs." is five years after beginning to implement the Plan; "+10 Yrs." is ten years after beginning to implement the Plan. Consult Component 1 of the Plan for additional details.

Acronyms and Abbreviations

AOSA	Association of Official Seed Analysts
ARS	USDA Agricultural Research Service
BRW	Acronym for the genebank unit in BRownWood and College Station, TX, that manages the National Pecan Germplasm Collection
C	Celsius scale for temperature
CGC	Crop Germplasm Committee(s)
CGIAR	Consultative Group for International Agricultural Research, the international organization that operates the international plant genebank system
COR	Acronym for the genebank unit in CORvallis, OR, that manages the national germplasm collection of temperate fruits and nuts
COT	Acronym for the genebank unit in College Station, TX, that manages the National COTton Germplasm Collection
CWR	Crop Wild Relative(s), the ancestor(s) or relative(s) of domesticated crops
DAV	Acronym for the genebank unit in DAVis, CA, that manages the national germplasm collection of fruits and nuts adapted to Mediterranean-type climates
F	Fahrenheit scale for temperature
FAO	Food and Agriculture Organization of the United Nations
FTE	Full Time Equivalent, a measure of personnel staffing
GEN	Acronym for the genebank unit in GENeva, NY, that manages the national germplasm collection of apple, tart cherry, and cold-hardy grapes
GRIN-Global or GG	USDA/ARS Germplasm Resources Information Network-Global, NPGS's information management system
GSOR	Acronym for the Stuttgart, AR, genebank unit that manages the Rice Genetic Stock Collection= "Genetic Stock *ORyza*" (the genus for rice)
GSZE	Acronym for the Urbana, IL, genebank unit that manages the Maize Genetic Stock Collection= "Genetic Stock *ZEa*" (the genus for maize)

H. R.	House of Representatives
HILO	Acronym for the genebank unit in HILO, HI, that manages the national germplasm collection of tropical fruits and nuts for the Pacific Basin region
LN	Liquid nitrogen
MAY	Acronym for the genebank unit in MAYagüez, PR, that manages the national germplasm collection of tropical fruits for the Caribbean region
MIA	Acronym for the genebank unit in MIAmi, FL, that manages the national germplasm collection of subtropical and tropical fruits, ornamentals, and sugarcane
NC7 or NCRPIS	Acronyms for the Ames, IA genebank unit, derived from the North Central Regional Research Project NC7
NCGR	National Clonal Germplasm Repository
NE9	Acronym for Geneva, NY, genebank unit that manages seed-propagated germplasm, derived from the Northeast Regional Research Project NE9
NGRAC	National Genetic Resources Advisory Council
NGRL	Acronym for National Germplasm Resources Laboratory in Beltsville, MD, that manages the GRIN-Global database and Plant Exchange Office
NIFA	USDA National Institute for Food and Agriculture
NLGRP	Acronym for National Laboratory for Genetic Resources Preservation, the genebank unit in Fort Collins, CO, that safeguards duplicates of PGR from other NPGS genebank units, and conducts research on genetic resources preservation
NPGS	USDA/ARS National Plant Germplasm System
NR6	Acronym for Sturgeon Bay, WA, genebank unit that manages the National Potato Germplasm Collection, derived from the National Research Support Project NR6
NSF	National Science Foundation
NSGC	Acronym for the genebank unit in Aberdeen, ID, that manages the National Small Grains Collection

NTL	Net-To-Location, referring to the annual recurrent budgets for NPGS genebanks
PARL	Acronym for the PARLier, CA, genebank unit that manages plant germplasm adapted to arid conditions, and that regenerates accessions for other NPGS genebank sites.
PGR	Plant Genetic Resource(s), synonymous with plant germplasm
P. I. or PI	Plant Introduction, a prefix that, when combined with a serially assigned number, e.g., PI 123456, comprises a permanent, unique identifier for NPGS PGR accessions
RIV	Acronym for the genebank unit in RIVerside, CA, that manages citrus and date germplasm
S9	Acronym for Griffin, GA, genebank unit, derived from the Southern Regional Research Project S9
SAES	State Agricultural Experiment Station(s)
SNP	Single Nucleotide Polymorphism, a type of DNA genetic marker
SOY	Acronym for Urbana, IL, genebank unit that manages the National SOYbean Germplasm Collection.
SSR	Simple Sequence Repeat, a type of DNA genetic marker
UAS	Unoccupied Aerial System
USC	United States Code
USDA	U. S. Department of Agriculture
USFS	U. S. Forest Service
USNA	Acronym for the genebank unit at the U.S. National Arboretum, Washington, DC
W6	Acronym for the Pullman, WA, genebank unit, derived from the Western Regional Research Project W6

Introduction (Figs. A-E)

National Strategic Germplasm and Cultivar Collection Assessment and Utilization Plan

The 2018 Farm Bill (H. R. 2—Agriculture Improvement Act of 2018) contained the following directives (green shaded highlights):

SEC. 7205. NATIONAL STRATEGIC GERMPLASM AND CULTIVAR COLLECTION ASSESSMENT AND UTILIZATION PLAN.

(a) IN GENERAL.—Section 1632(d) of the Food, Agriculture, Conservation, and Trade Act of 1990 (7 U.S.C. 6 5841(d)) is amended—

(1) in paragraph (5), by striking ‘‘and’’ at the end;

(2) by redesignating paragraph (6) as paragraph (7); and

(3) by inserting after paragraph (5) the following:

‘‘(6) develop and implement a national strategic germplasm and cultivar collection assessment and utilization plan that takes into consideration the resources and research necessary to address the significant backlog of characterization and maintenance of existing accessions considered to be critical to preserve the viability of, and public access to, germplasm and cultivars; and’’.

(b) PLAN PUBLICATION.—Section 1633 of the Food, Agriculture, Conservation, and Trade Act of 1990 (723 U.S.C. 5842) is amended by adding at the end the following:

‘(f) PLAN PUBLICATION.—On completion of the development of the plan described in section 1632(d)(6), the Secretary shall make the plan available to the public.’’

Three documents comprise the requested “national strategic germplasm [understood as “plant germplasm”] and cultivar collection assessment and utilization plan.” They were developed by USDA/Agricultural Research Service (ARS) plant genetic resource (PGR—synonymous with “plant germplasm”) management personnel, researchers, and regional and national leadership, with input from other U.S. government experts, academia, the seed/biotechnology industry, and other customers/stakeholders. As stipulated by 7 USC 5843 section (3) (A) (iv), the National Genetic Resources Advisory Council (NGRAC) contributed to the development of the Plan. The Plan records the current status and capacities of the U.S. National Plant Germplasm System (NPGS; the U.S. national strategic plant germplasm and cultivar collection); identifies the future goals and priority needs for reducing or eliminating backlogs in NPGS PGR maintenance, characterization, evaluation and genetic enhancement/pre-breeding; and outlines the steps for implementing the Plan.

The present document “National Strategic Germplasm and Cultivar Collection Assessment and Utilization Plan: Technical Details, Analyses, and Approaches” contains a comprehensive quantitative assessment of the current status and quality of the NPGS PGR collections. Based on

that assessment, strategies, priorities, approaches, and a roadmap for addressing backlogs and strengthening NPGS operations were formulated, and the technical details, analyses, and approaches for implementing the overall Plan are presented. A companion document entitled "National Strategic Germplasm and Cultivar Collection Assessment and Utilization Plan: Supplemental Crop and Crop Wild Relative Collections Data" (hereafter termed "Supplemental Data") contains extensive, detailed PGR management data for each NPGS genebank unit and the individual crops managed at those genebank units. A second companion document entitled "Synopsis of the National Strategic Germplasm and Cultivar Collection Assessment and Utilization Plan" (hereafter termed "Synopsis") comprises an abridgement for the Plan, presented in more general terms, and focused on strategic elements of the Plan.

The U.S. National Plant Germplasm System (NPGS)

The U.S. NPGS comprises 22 genebank and support units at 19 geographical locations (see Figs. A and B—located at the end of this Introduction section) operated primarily by recurrent funding from the USDA/ARS's budget. Many of the NPGS genebank units also receive substantial in-kind recurrent support from Land-Grant Universities on whose campuses they are located. Four of those genebank units (Ames, Geneva, Griffin, Pullman) also receive recurrent funding from "off-the top" USDA/NIFA Regional Capacity Funded projects allocated by the U.S. State Agriculture Experiment Stations (SAES; Byrne et al., 2018). The NPGS also provides logistical support (PGR storage at the NPGS's National Laboratory for Genetic Resources Preservation [NLGRP]; and/or data incorporated into GRIN-Global) for several affiliated PGR collections (Fig. C) that are not managed by the USDA/ARS. These affiliated collections are not addressed by this Plan. The herbaceous ornamental PGR collections of the Ornamental Plant Germplasm Center (OPGC) at The Ohio State University, Columbus are also not covered by this Plan. The unique funding model for this genebank, the current transition in OPGC leadership, and lack of capacity to compile the requisite data precluded consideration of the OPGC's future development at this time. The OPGC represents a special case that could be covered in future analyses.

Plant Genetic Resource (PGR) Management

Plant genetic resource management (also termed "curation") is a complicated, multiphase process that requires comprehensive planning on an extended timescale (FAO, 2014; Byrne et al., 2018; Bretting, 2018). Activities that comprise PGR management include:

- Acquisition—New samples of PGR (termed "accessions" hereafter) are acquired through plant explorations (Williams, 2005), exchanges with other genebanks, or through donation by owners for incorporation into the NPGS collection. Current acquisitions are primarily focused on closing gaps (genetic, taxonomic, ecogeographical, e.g., Ramírez-Villegas et al. 2010; Khoury et al. 2020) in current PGR collections.

- Maintenance—Keeping accessions secure, viable, vigorous, and healthy is the highest priority goal for the NPGS. Accessions of seed-propagated crops are maintained as seeds in 4˚C (41˚F) and/or -18˚C (0˚F) storage, whereas those of clonally propagated crops are maintained as living plants, in vitro tissue cultures, and as pollen, buds, and/or shoot tips in ultra-cold cryopreservation (liquid nitrogen [LN] vapor) conditions (Byrne et al.,

2018). Accessions are periodically monitored/tested for viability, vigor, and presence of selected pathogens. Whenever feasible, duplicate samples of NPGS accessions are safeguarded at the NLGRP, and for seed-propagated crops, also at the Svalbard Global Seed Vault (Fowler, 2016). Maintaining accessions true-to-type genetically is also a primary goal for PGR maintenance (Crossa et al., 1993). When the viability, vigor, health, and/or seed or propagule numbers drop to pre-determined thresholds, accessions must be regenerated or repropagated (also termed "increased"). Regeneration or repropagation can require controlled cultivation, pollination, and/or harvest. It is often the most expensive, labor-intensive, and time-consuming phase of PGR management (Byrne et al., 2018).

- Documentation—The information associated with accessions is critical for optimal PGR management and use (Weise et al. 2020). So-called "passport data" encompass the accession's unique identifier (a "Plant Introduction" or "PI" number for NPGS PGR), scientific and common names, provenance (ideally geospatial data) and date of collection, collector, life form (annual, perennial), and other data (FAO, 2014). Characterization and evaluation data (see below) add significant value to PGR and enhance their utility for research, breeding, and production.

- Distribution—The NPGS is one of the largest distributors of PGR worldwide (Byrne et al., 2018; Bretting, 2018). Distribution embodies the successful culmination of other PGR management operations. The NPGS PGR are distributed free of charge in the form of seeds, plants, pollen, and/or tissue cultures. Distribution provides access to PGR that are key for research and development, food security, and recovery from crop failures.

- Characterization—Also termed "genotyping," PGR characterization involves assaying highly heritable, often simply inherited characteristics (morphological and/or genotypic) that do not vary considerably when measured over time and location. At present, the NPGS characterizes PGR via morphological traits and/or simple-sequence repeat (SSRs) or single nucleotide polymorphisms (SNP) genotypic markers (Byrne et al., 2018).

- Evaluation—Also termed "phenotyping," PGR evaluation involves assaying agronomically and/or horticulturally-important traits (e.g., yield, adaptation, resistance, tolerance, quality) with relatively complicated inheritance, substantial variability over time and location, and genotypic by environment interactions (Byrne et al., 2018).

- Genetic Enhancement—Also termed "pre-breeding," genetic enhancement can involve incorporating key traits from non-adapted, exotic PGR into adapted, elite breeding genepools, or developing diverse genepools, de novo, through long-term selection of genetically-novel populations, genotypes, gene arrays, etc., for adaptation (Falk, 2016; Byrne et al., 2018).

- Applied Research—Research and development at NPGS genebank units generally seek to devise more efficient and effective PGR management approaches/procedures, add value to accessions through characterization and/or evaluation, and/or generate genetically-improved PGR via genetic enhancement/pre-breeding (Byrne et al., 2018).

Uses and Impacts of NPGS PGR

Forecasts of future demands for and utilization of PGR should be informed by current and past uses and impacts of PGR on agriculture, especially on crop genetic improvement. Several publications (e.g., Qualset and Shands, 2005; Kurtz et al. 2016; Byrne et al. 2018; Bretting, 2018) have summarized the key roles of NPGS PGR and their impacts on agriculture in recent years. The NPGS PGR have provided genes and cultivars that have saved farmers billions of dollars of crop losses from virulent diseases and pests, increased product yields and food quality, furnished genetic systems for hybrid crop production, and served as crucial research tools, e.g., for elucidating the genetic control for key crop traits. It has been challenging to estimate the economic value of PGR (Day Rubenstein et al., 2005), but the return on investment has clearly been substantial. For example, yield gains in peanuts during the past 50 years have resulted from introgression of genes and traits from NPGS PGR, including from unadapted CWR, that confer host-plant resistance from disease, nematodes, drought, etc. (Holbrook et al., 2014; Holbrook, 2019). Based on the input from some of the 40+ CGCs (Fig. D) that provide technical input for PGR management in the form of crop vulnerability assessments (e.g., for apple, Volk et al. 2015), the future demands for NPGS PGR and associated information will likely increase (Byrne et al. 2018). This Plan reflects that forecast.

Scope and Approaches for the Plan

For the purpose of this Plan, the "Germplasm and Cultivar Collection" mentioned in the 2018 Farm Bill has been defined to encompass the non-cultivar and cultivar PGR under active management by USDA/ARS NPGS which, at this writing, comprises ca. 569,000 accessions of 13,000+ plant species (Figs. B, 1.1).

The first step for formulating the overall strategy for the Plan was to apply quantitative metrics developed by the NPGS and by international genebanks (Lusty et al., 2022) to assess the current status, strengths and weaknesses, support capacities, and performance of the NPGS's PGR management program and to identify operational backlogs and quality deficiencies. Based on the extensive dataset resulting from that assessment, input from technical experts, recommendations from the National Genetic Resources Advisory Council and the National Plant Germplasm Coordinating Committee, the NPGS staff and leadership then formulated strategies, identified priorities, and developed approaches and 5- and 10- year timelines for attaining the outcomes of reducing current backlogs, avoiding future backlogs, strengthening NPGS operations, improving the overall quality of NPGS PGR collections, and meeting the needs of NPGS customers and stakeholders more comprehensively.

The Plan identifies the needs to be addressed from now to 5 (+5) and 10 (+10) years from the beginning of Plan implementation in order to reduce or eliminate PGR management backlogs; strengthen the NPGS's current PGR management capacities; and to align the NPGS with voluntary international plant genebank standards and the practices of other globally important genebanks (FAO, 2014; Engels and Visser, 2003; Rao et al. 2006; Reed et al. 2004; Lusty et al., 2022). It also forecasts future demands for the NPGS's PGR and associated information, plus goals and aspirations for PGR conservation and sustainable use. The Plan presents "the resources

and research necessary to address the significant backlog of characterization and maintenance of existing accessions considered to be critical to preserve the viability of, and public access to, germplasm and cultivars" (2018 Farm Bill). Although the PGR management operations of characterization and maintenance are emphasized herein, they cannot be considered independently of PGR acquisition, documentation, distribution, evaluation, and genetic enhancement/pre-breeding, so those operations have also been integrated into the Plan.

Data, Variables, and Metrics

Data describing the NPGS, its current research and PGR management capacities, collection qualities, operational performance, and future goals were generated, analyzed, and compiled according to individual NPGS genebank units and their constituent PGR collections. That approach corresponds to the genebank units operating as independent ARS Research Units and/or Research Projects with designated budgets appropriated by Congress under ARS's overall annual budgets. It also recognizes that individual PGR collections at individual genebank units share many resources such as facilities, equipment, and personnel.

The total of 75,000 + datapoints were generated, analyzed, and compiled through MS Excel spreadsheets and workbooks for ca. 200 individual PGR collections, and 22 NPGS genebank units, to collectively describe the NPGS's overall status, collection quality, operational performance, research and PGR management capacities, and projections of needs and goals for the future. Data for individual genebank units and PGR collections were aggregated and summarized to provide a panoramic NPGS-wide perspective. Subsequently, the data were analyzed and visualized pictorially via Tableau software, which also generated all the tabular figures in this Plan.

Data for the metrics or variables defined in Appendix A were collected, projected, approximated and/or estimated and presented in Figures 1-12 and Appendix B of this document, and in Supplemental Figs. S3.1-S10.1 in the companion document "Supplemental Data." These metrics were developed during the last 25+ years by NPGS PGR managers, and also include several variables assessed during a study of the NPGS 20+ years ago (GAO, 1997). Some of these metrics are currently employed by the Global Crop Diversity Trust (Hay et al., 2021; Lusty et al. 2021) to manage and assess operations and performance qualities at genebanks at international agricultural research centers (e.g., International Rice Research Institute, International Center for Maize and Wheat Improvement). The metrics or variables were grouped according to major PGR management functions. For "Current" (also termed "Now") data, averages were calculated over the most recent five years or, if five years of data were unavailable, over the longest recent period for which data exist. Estimates for the status, needs, and future goals of the NPGS at +5 years and +10 years from the beginning of Plan implementation were based on trends from past years; data for the "Current" status; decades of experience of NPGS PGR managers; and the needs for PGR and associated information forecast by NPGS PGR managers and CGCs.

Organization of the Plan and this document

As mentioned earlier in the Summary, this Plan is segmented into three separate, interconnected documents. The current document, entitled "National Strategic Germplasm and Cultivar

Collection Assessment and Utilization Plan: Technical Details, Analyses, and Approaches" (hereafter termed "Technical Details") provides extensive background information, data, strategies, priorities, implementation timetables, and supporting information for how PGR held in the NPGS will be maintained, characterized, evaluated, documented, genetically enhanced, and distributed; and how to reduce and avoid the backlogs that could prevent that PGR and associated data from being publicly available. A companion document "National Strategic Germplasm and Cultivar Collection Assessment and Utilization Plan: Supplemental Crop and Crop Wild Relative Collections Data" (hereafter termed "Supplemental Data") provides supplemental detailed information and data for specific crops and CWR in support of the plans and conclusions from the present document. Finally, the document "Synopsis of the National Strategic Germplasm and Cultivar Collection Assessment and Utilization Plan" (hereafter termed "Synopsis") represents an abridgement of the two other documents, and focuses on the main points, strategies, and implementation timetable for the Plan that are summarized from the current document.

This document is organized primarily according to 12 major PGR management Components. The "current" data presented in Components 1-12 and their accompanying figures, Appendix B, and the companion document "Supplemental Data," collectively describe the current NPGS PGR management and research operations, capacities, and the resources available to support those operations and capacities. That information comprises an assessment of the NPGS's status at this writing, including its operational backlogs, and strengths and weaknesses. Component 13 outlines an implementation schedule.

The "+5 years" and "+10 years" data presented herein collectively serve to identify and forecast strategic goals, priorities, actions, capacities, and resources needed for the NPGS to reduce or eliminate operational backlogs and meet the demands for PGR and associated information forecast for five and 10 years from the beginning of Plan implementation. Those data and analyses focus on ascertaining the actions and goals "critical to preserve the viability of, and public access to, germplasm and cultivars" (2018 Farm Bill) for the near term and the future. The "+5 years" and "+10 years" data are presented in the figures and discussed collectively in narrative text under the overall headings of "Needs" and "Implementation" for each of the Components of the Plan. The Supplemental Data document contains additional information for these Components.

The data for Components 1-2, which document the current, proposed or forecast NPGS budgets, personnel, facilities, infrastructure, and information management capacities, were generated and analyzed according to the 22 different genebank units, rather than by those genebank units' constituent PGR collections, because the individual management operations for different PGR at an individual genebank unit often share facilities, equipment, personnel, and information management capacities. In addition to information in Components 1-2, Appendix B, located with Appendices A and C and the end of this document, includes more details about the challenges, goals, priorities, approaches, and proposed actions for implementing this Plan at specific NPGS genebank units and the PGR collections they manage.

The data in Components 3-12 were mainly generated, analyzed, and compiled initially according to individual PGR collections at NPGS genebank units. Next, the individual PGR collection data

for each metric were aggregated for each genebank unit, and for the NPGS overall. Data for current status, forecast or proposed future conditions, and goals for individual PGR collections were generated, analyzed, and compiled. They describe in greater detail the NPGS's strengths, weaknesses, and overall status for its current research and PGR management efforts. That information is accompanied by forecasts for future status or conditions, and the strategies, priorities, and actions needed to reduce PGR management backlogs and support future improvements to NPGS PGR management. When aggregated and summarized in Components 3-12, Figs. 3-12, and Appendix B of this document, plus Supplemental Figs. S3.1-S10.1 in the companion document, the data for the individual PGR collections constitute a "snapshot" for the status of the genebank units at this writing. When aggregated and summarized across all the genebank units, those data and narrative text depict the NPGS's overall current status. They also form the foundation for the "assessment and utilization plan that takes into consideration the resources and research necessary to address the significant backlog of characterization and maintenance of existing accessions" (2018 Farm Bill).

Following the assessment of the overall NPGS operational capacities in Component 1 of this Plan, subsequent Components are considered according to the two broad PGR management elements of maintenance and characterization. Components 2-8 describe and assess the operations that contribute to the ongoing and future maintenance of NPGS PGR and associated data/information, and the actions, strategies, priorities, goals, and resources needed for reducing backlogs in PGR and data/information management. Component 2 focuses on the current status and future needs for maintenance of the data/information associated with NPGS PGR, primarily in reference to the content and management capacity of GRIN-Global. Component 3 describes plans for expanding the NPGS's PGR collection through targeted acquisitions based on gaps in the collection and the needs of PGR users, and for expanding the NPGS's role for in situ PGR conservation.

Components 4 through 7 cover the current status, future needs, and proposed actions and goals for reducing backlogs in what might be considered the "core operations" for PGR maintenance: Component 4 Safeguarding PGR through Long-Term Storage; Component 5 Germination, Viability, and Longevity Testing of NPGS PGR Accessions; Component 6 Pathogen Testing and Clean-up; and Component 7 PGR Regeneration/Repropagation (Fig. E). Although conducted separately, the progress and success for any of those operations depend on the other operations, and also on information from genotypic characterizations (discussed below). For example, without PGR regenerations/repropagations that yield sufficient high-quality seeds or propagules, PGR cannot be successfully duplicated or backed-up. Without germination, viability, longevity testing, and genotypic characterization data, priorities for regenerations/repropagations to maintain collection diversity cannot be efficiently identified.

These PGR maintenance operations are cyclical, i.e., involving recurrent actions often according to a defined time schedule, with intervals determined based on biological features and effects of the production environment. For example, seeds of some PGR are tested for viability every 20 years; greenhouse-grown plants of other PGR are tested for the presence of specific pathogens every month; and field plantings for other crops are repropagated every 15 years. Because some of those cycles are asynchronous with the +5 year and +10 year timeframes of this Plan, the values for some seemingly interdependent metrics (e.g., "number of accessions requiring

pathogen testing" and "average number of accessions tested annually for pathogens") in Components 4-7 can appear unrelated. Nonetheless, those apparent discordances are usually artifacts caused by the preceding asynchrony among actual PGR maintenance cycles and the +5 and +10 year timeframes in this Plan.

Component 8 PGR Availability and Distribution can be considered a "capstone" for the PGR maintenance portion of the Plan. Availability of PGR from NPGS collections represents a gauge for the success of PGR maintenance operations in enabling accessions to be distributed for research, breeding, education, production, and other uses. The volume of accessions distributed annually depends on availability of PGR and associated data, and also represents an overall measure for the value of those PGR to users.

Components 9-11 describe the current status and plans for addressing the backlog in NPGS PGR documentation, characterization, and evaluation, operations that are crucial for efficient and effective PGR maintenance and for use of PGR in research and breeding. Unlike the mainly cyclical operations comprising PGR maintenance described above, many aspects of documentation, characterization and evaluation can be performed according to a "closed-end" schedule. Component 9 Documentation assesses the quality of and needs for augmenting what PGR managers term "passport information," such as the accession's provenance, history of genetic improvement, if any; the circumstances of its acquisition; documentation of its geographical origin; and its identification and assignment to a scientific species. Component 10 PGR Genotypic Characterization examines the extent to which NPGS PGR have been characterized genotypically, to the level of locus/allele or even nucleotide sequence content. It presents an extensive multi-phase, multi-year comprehensive plan including strategies, priorities, and approaches for genotypic characterization of the entire NPGS collection through leading edge DNA analytical technologies. Component 11 PGR Phenotypic Evaluation and Digital Imaging examines the extent to which NPGS PGR have been evaluated for traits that collectively determine their relative agronomic, horticultural, or compositional merits and utility. As with Component 10, it presents comprehensive plans for strategically evaluating NPGS's PGR via leading edge technical approaches that are tailored to the biological features of PGR and the needs of PGR users. The priorities for phenotypic evaluations will be partially determined by the genetic profiles and interrelationships among accessions that have been documented by genotypic characterizations and digital images.

This Plan addresses both assessment and utilization of NPGS PGR. As mentioned earlier, successful PGR management results in the availability of PGR and descriptive information that researchers, breeders, and producers can use to attain their specific objectives. For some crops, successful utilization of PGR requires incorporating genes and traits from those PGR into genetic backgrounds that facilitate that use. In those instances, NPGS genebank units could expand their responsibilities beyond PGR maintenance, characterization, and evaluation to participate in or support genetic enhancement/pre-breeding operations, serving as centers of innovation for crop genetic improvement. Notably, reducing backlogs in PGR maintenance and characterization is the primary goal of the Plan; NPGS genebank units would only participate in genetic enhancement/pre-breeding programs once the backlogs in PGR maintenance, characterization, etc. were successfully reduced, and sufficient budgetary, personnel, and infrastructural capacities

become available specifically for the purpose of genetic enhancement/pre-breeding, which is covered in Component 12 of this document.

Component 13, Cross-Cutting Strategies and Roadmap for Plan Implementation, follows the 12 PGR Management Components. It integrates all the goals, actions, approaches for PGR management presented in the prior Components into a comprehensive implementation strategy with overall sequences and timelines/schedules for executing the overall Plan.

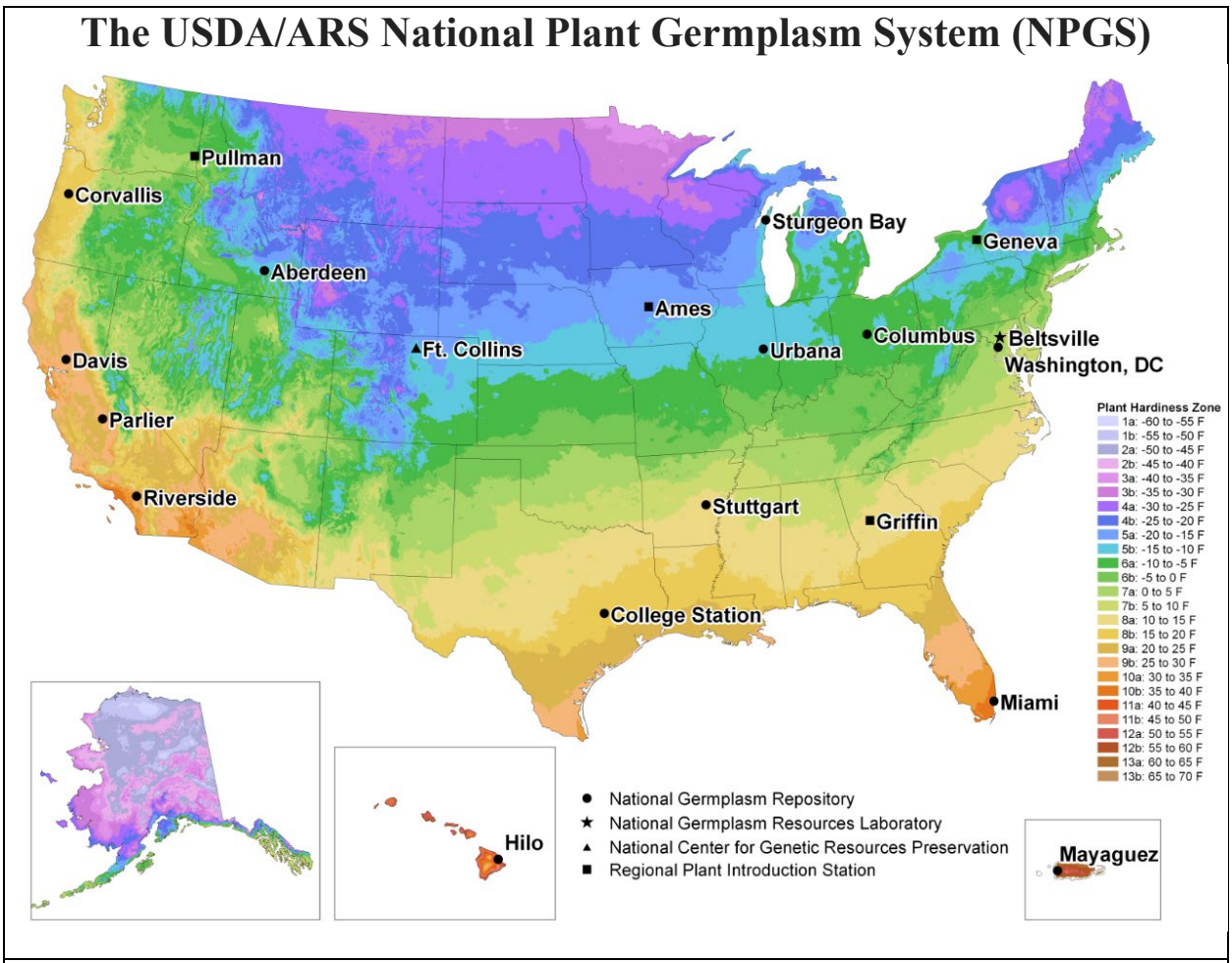


Fig. A: The USDA/ARS National Plant Germplasm System (NPGS). The locations of individual NPGS genebank units are projected on the USDA/ARS Plant Hardiness Zone Map. The College Station, Geneva, and Urbana locations each host two separate genebank units.

National Plant Germplasm System (NPGS): Genebank Units, Annual Recurrent Funding (NTL $), and Sizes of Collections

Primary Type of Germplasm	NPGS Genebank Unit	Recurrent Funding (NTL $)	Accessions (#)	Funding (NTL $) per Accessions	Crops (#)	Funding (NTL $) per crop
Managed as Seeds	Aberdeen, ID (NSGC)	1,401,700	136,667	10	10	140,170
	Ames, IA (NC7)	2,905,618	53,705	54	25	116,225
	College Station, TX (COT)	893,147	9,813	91	1	893,147
	Geneva, NY (NE9)	1,594,890	12,707	126	13	122,684
	Griffin, GA (S9)	2,911,541	100,181	29	28	103,984
	Pullman, WA (W6)	3,240,845	100,158	32	24	135,035
	Sturgeon Bay, WI (NR6)	799,900	5,834	137	1	799,900
	Stuttgart, AR (GSOR)	397,000	38,375	10	1	397,000
	Urbana, IL (GSZE)	576,529	42,411	14	1	576,529
	Urbana, IL (SOY)	1,347,848	22,497	60	2	673,924
Managed as Both	Parlier, CA (PARL)	576,860	1,178	490	7	82,409
Managed as Clones	College Station, TX (BRW)	183,000	4,108	45	1	183,000
	Corvallis, OR (COR)	1,684,082	13,105	129	17	99,064
	Davis, CA (DAV)	1,339,130	7,064	190	10	133,913
	Geneva, NY (GEN)	1,292,514	7,618	170	5	258,503
	Hilo, HI (HILO)	2,154,000	949	2,270	16	134,625
	Mayaguez, PR (MAY)	2,066,292	1,114	1,855	9	229,588
	Miami, FL (MIA)	2,153,598	1,334	1,614	7	307,657
	Riverside, CA (RIV)	1,754,370	1,687	1,040	2	877,185
	Washington, DC (USNA)	1,389,029	8,368	166	1	1,389,029
	Genebank Units Total	**30,661,893**	**568,873**	**54**	**181**	**169,403**
NPGS-wide Responsibilites	Beltsville, MD (NGRL)	2,301,400	0			
	Ft. Collins, CO (NLGRP)	5,047,000	436,519	12	181	27,884
NPGS-wide	**NPGS Total**	**38,010,293**	**568,873**	**67**	**181**	**210,002**

Fig. B: National Plant Germplasm System (NPGS): Genebank Units, Funding (NTL $), and Sizes of Collections. The USDA/ARS National Plant Germplasm System (NPGS). The NPGS genebank units are listed alphabetically by their geographical locations. The three- to five-letter acronyms used in GRIN-Global to identify each genebank unit follows the location name. Those genebank units that manage plant genetic resources (PGR) primarily in the form of seeds are listed first, then the Parlier (PARL) genebank unit that manages an equivalent number of PGR accessions in the form of seeds and clones is listed, followed by genebank units that manage PGR primarily in the form of clones. Finally, two genebank units with NPGS system-wide responsibilities are listed. The annual recurrent, Net-to-Location (NTL) base-funded budgets for overall genebank operations are listed for each genebank unit, summed across all genebank units that distribute PGR, and then the preceding two units' budgets are added to calculate a sum for the budgets for operations of all those NPGS genebank units covered by this Plan. The numbers of PGR accessions and crops (as defined by PGR managers) managed by each genebank unit are listed and summed for NPGS totals. Note that the Beltsville (NGRL) genebank unit manages no accessions, and the Ft. Collins (NLGRP) genebank unit manages duplicates of accessions managed elsewhere, so its holdings are not included in the overall accession sum. The budgets for each genebank unit were divided by the number of accessions managed to calculate the funding $ per accession, and similarly divided by the number of crops managed to calculate the funding $ per crop.

PGR Collections Affiliated with the NPGS	
C. M. Rick Tomato Genetics Resource Center	Davis, CA
Desert Legume Program	Tuscon, AZ
Forest Service National Seed Laboratory	Dry Branch, GA
Ornamental Plant Germplasm Center	Columbus, OH
Plant Germplasm Quarantine Program	Beltsville, MD
U.S. Nicotiana Germplasm Collection	Raleigh, NC

Fig. C: PGR collections affiliated with the NPGS but not covered by this Plan are listed alphabetically by the names of the individual genebanks, and their geographical locations are provided.

The 40+ Crop Germplasm Committees (CGCs)	
Alfalfa	Peanut
Apple	Phaseolus
Barley	Potato
Carya	Prunus
Citrus	Pyrus
Clover & Special Purpose Legume	Rice
Coffee and Cacao	Root and Bulb
Cotton	Small Fruits
Crucifer	Sorghum and Millets
Cucurbit	Soybean
Date Palm	Specialty Nuts
Food Legume	Sugarbeet
Forage and Turfgrass	Sugarcane
Grape	Sunflower
Herbaceous Ornamental	Sweet Potato
Juglans	Tobacco
Leafy Vegetable	Tomato
Maize	Tropical Fruit and Nut
Medicinal	Vigna
New Crops	Wheat
Oats	Woody Landscape Plant
Pea	

Fig. D: The 40+ Crop Germplasm Committees (CGCs) are listed alphabetically. The CGCs provide technical input for PGR management in the form of crop vulnerability assessments, recommendations for optimal management practices, and contributions to establishing priorities for PGR acquisition and evaluation.

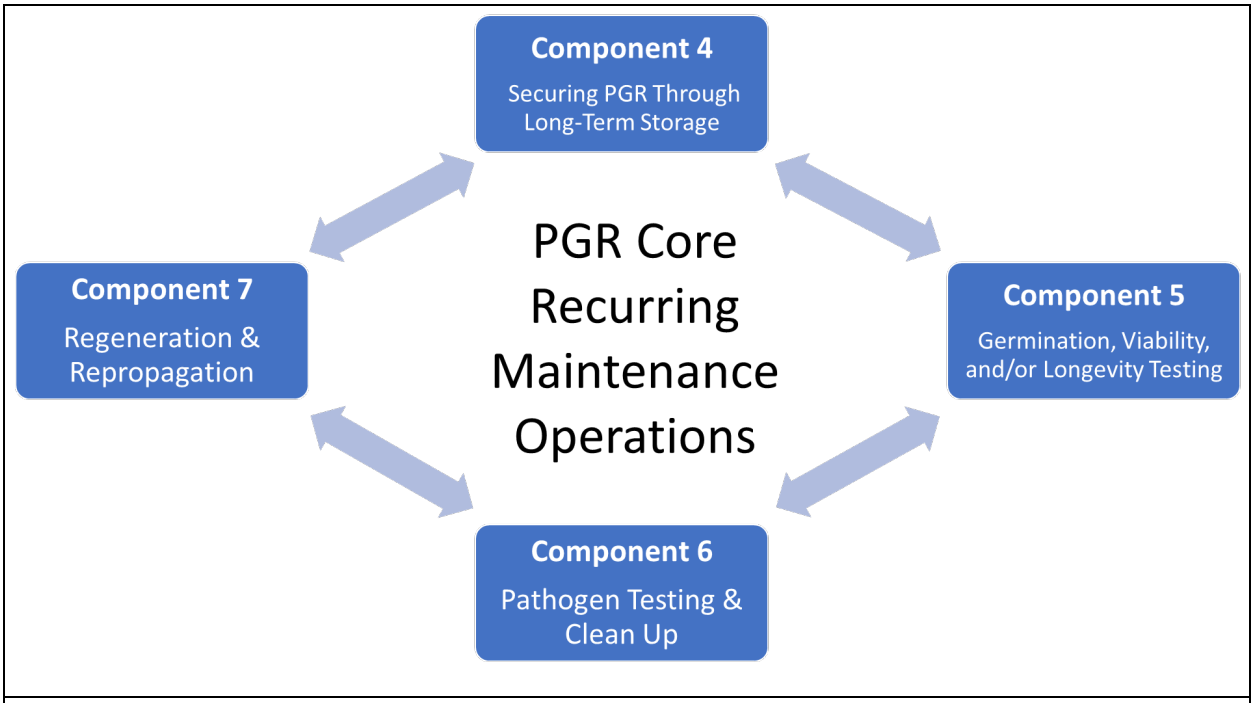


Fig. E: PGR "Core" Recurring Maintenance Operations. Components 4 through 7 of this Plan cover the current status, future needs, and proposed actions and goals for reducing backlogs in the core operations for NPGS PGR maintenance. As depicted by the double-headed arrows in this figure, these PGR maintenance operations in the blue boxes are interdependent and cyclical, i.e., involving recurrent actions often according to a time schedule.

Plan Components 1-8: PGR Maintenance

Component 1: Strategically Expanding Infrastructure, Capacity, and Support for PGR and Information Management and Research (Figs. 1.1-1.7)

Current Status

Overall, the 22 different NPGS genebank units covered by this Plan currently manage PGR of ca. 200 crops in the form of ca. 569,000 accessions of 13,000+ species (Fig. 1.1). Most of the accessions belong to ca. 100 or so crops of national and/or global food security and/or economic importance. The NPGS is notable among national PGR genebank systems because of its substantial collections of another ca.100 crops with more local, regional, and "niche" importance; these are sometimes covered under the category "Other crops" in this Plan.

Figure 1.1 depicts the substantial variability in the size and taxonomic complexity of the PGR collections managed at different NPGS genebank units. For example, genebank units for small grains (Aberdeen), cotton (College Station) and soybean (Urbana) manage PGR of one or several major crops comprising relatively few plant taxa (a term for taxonomic categories such as species and subspecies), but many thousands of accessions for those taxa and crops. In contrast, genebank units in Ames, Griffin, and Pullman (all Plant Introduction Stations) manage many accessions of many crops and taxa. Genebank units for primarily clonally propagated tropical (Hilo, Mayagüez, and Miami) and temperate (Corvallis, Washington, DC) PGR manage a great diversity of different plant taxa and crops, but relatively few accessions per taxon or crop.

The current overall annual USDA/ARS budget that supports primarily PGR maintenance operations in the NPGS genebank units covered by this Plan is ca. $38.0 million (net-to-location; equivalent to ca. $42 million gross appropriated funds) for FY 2020 (Fig. B, Fig. 1.2). That sum encompasses the costs of all personnel (salaries and benefits), equipment, utilities, supplies, travel, and other operations. Approximately 300+ FTE (ca. 248 permanent, 55 temporary) USDA/ARS and land-grant university personnel support NPGS operations and/or conduct research focused on PGR topics (Fig. 1.3). Salaries and benefits constitute the largest recurrent expense for the NPGS. Figure 1.2a depicts the substantial variability in the budgets appropriated to different NPGS genebank units. The different funding levels across genebank units correspond roughly to the sizes and complexity of the PGR collections, the differential costs per accession of managing different crops, plus numerous historical, genebank unit-specific, and crop-specific factors. Additional details for individual genebank units are included in Appendix B, and in a subsequent discussion of cross-cutting issues in the section Overall Implementation of the NPGS Plan, which appears later in this document, and in the companion document Synopsis of the National Strategic Germplasm and Cultivar Collection Assessment and Utilization Plan (termed "Synopsis" hereafter).

The facilities currently available to the NPGS for PGR management and associated research include ca. 380,000+ cubic feet of cold storage space (crucial for PGR maintenance); ca.144,000+ square feet of greenhouse space and ca. 120,000+ square feet of screenhouse and other enclosed space; and ca. 2,300+ acres of field space (Fig.1.2b). The preceding facilities comprise a mixture of Federal (USDA/ARS), land-grant university, and SAES properties. Access

to land-grant university and SAES properties has been crucial to overall NPGS operations. Office and laboratory space occupied by the NPGS is not recorded here, because this Plan focuses on key metrics for PGR management, rather than more generic measures appropriate for less-specialized research and development operations. Figure 1.2b depicts the substantial ranges in the size and diversity of growing space available at different genebank units. That variability also corresponds roughly to substantial ranges in the sizes and complexity of the PGR collections, differential operational requirements for different crops, plus numerous historical, genebank unit-specific, and other crop-specific factors.

The information associated with PGR is almost as valuable as the PGR itself (Weise et al. 2020); consequently, maintaining and delivering it is an NPGS priority. Quantitatively measuring the NPGS's information management/information technology capacities proved challenging. Ultimately, the strategy of assessing several metrics such as volumes of records and bytes in GRIN-Global, personnel skilled in GRIN-Global use and the complexity and impact of NPGS information management/information technology operations was applied to gauge the extent and quality of information management conducted at genebank units (Figs.1.3, 1.4, 2.1).

As of this writing, 143+ NPGS staff use the GRIN-Global Curator Tool for an average of 2.3 hours/day/user (Fig. 1.4), and there are 89+ "advanced" (i.e., users with advanced capabilities) GRIN-Global data entry accounts. Figure 1.4 depicts the substantial variability in the information management/information technology capacities at different genebank units. Those different capacities also correspond roughly to the sizes and complexity of the PGR collections, the overall size of a genebank unit's staff and budgets, plus numerous historical, genebank unit-specific, and crop-specific factors. Notably, some genebank units invested early and strategically in information management/information technology capacities, whereas others did not, necessitating additional investments for the latter units.

The NPGS depends strongly on USDA/ARS's external research and PGR management collaborations with USDA/NIFA, land-grant universities, SAES, the private sector, other domestic organizations, and international institutions as a primary strategy for supporting PGR management operations and associated research. The annual average number of external (with cooperating institutions outside of ARS) research collaborations (Fig. 1.5) can serve as one index for NPGS technology transfer. As a genebank system, the NPGS currently participates annually in an average of 340+ such external collaborations (Fig. 1.5). Most of those collaborations are bilateral with specific U.S. public and private sector organizations and institutions, but some involve international organizations, e.g., PROCINORTE NORGEN Taskforce for Genetic Resources composed of USDA/ARS, Agriculture and Agri-Food Canada, and the Instituto Nacional de Investigaciones Forestales, Agrícolas, y Pecuarias (INIFAP) in Mexico (PROCINORTE, 2018); and the Crop Trust and the Centro Internacional de Mejoramiento de Maíz y Trigo (CIMMYT) for developing the GRIN-Global PGR information management system (https://www.grin-global.org/). These numerous collaborations indicate the importance of partnerships for attaining the Plan's objectives. They also document the NPGS genebank units' crucial roles as centers of innovation that furnish PGR, associated information, knowledge, research tools, other technology, and experience to underpin U.S. and global crop research and development.

Strategies and Implementation

As introduced earlier under Scope and Approaches, the Strategies and Implementation sections of the Plan outline the goals and actions proposed for meeting key current and future NPGS needs and challenges. Discussions of Implementation especially focus on "the resources and research necessary to address the significant backlog of characterization and maintenance of existing accessions considered to be critical to preserve the viability of, and public access to, germplasm and cultivars" (2018 Farm Bill). The strategies, goals and actions that constitute the overall NPGS Strategic Plan were formulated by analyzing and synthesizing information from individual genebank units documented herein in Components 1-12, the section Overall Implementation of the NPGS Plan, Appendix B. As described later in this document and the Synopsis, some of the actions should be implemented concurrently, and others sequentially according to chronological and/or developmental factors. The resources and research required for implementation were estimated according to current and forecast requirements and costs.

The preceding analyses have also documented current trends, across PGR collections and genebank units, for increased demand for PGR and associated information and forecasts for +5 and +10 years from the beginning of Plan implementation. Thus, the Strategies and Implementation sections also consider how to meet those future demands. If the forecast demands for PGR and associated information cannot be adequately fulfilled, then backlogs in PGR characterization, maintenance, and other operations will not be sufficiently reduced or could re-emerge. Many PGR management activities, especially the "core maintenance operations" described in Components 4-7 (Fig. E), are extensively integrated and operationally interconnected. Consequently, addressing the current operational backlogs in the NPGS will require a coordinated sequence of actions, some of which are applicable NPGS-wide, and others tailored to the specific conditions at individual genebank units and their constituent PGR collections (see Appendix B for more information).

Strategically Expanding the NPGS's PGR Operational Capacities to Reduce or Eliminate Backlogs in PGR Maintenance and Manage Expanded NPGS PGR Collections

Expanded NPGS collection size: The volume of PGR accessions, taxa, and crops managed at a genebank unit are among the most important determinants for the level of infrastructure, operational capacity, and budgetary resources required for adequate PGR management according to international standards (FAO, 2014; Lusty et al., 2021). The NPGS collection is forecast to expand to ca. 636,000+ accessions at +10 years, or ca. 12% larger than its current size (Fig. 1.1; details in Component 3 PGR Acquisition and In Situ Conservation). Collectively, those new accessions will represent an estimated 1,000+ additional taxa and ca. 25 additional crops.

Expanded NPGS budgetary support: Considering the projected future growth of the NPGS collections discussed above, and the current maintenance, characterization, evaluation, and genetic enhancement/pre-breeding backlogs described in subsequent Components of this Plan, successfully implementing the NPGS Plan will require expanded budgetary support. Estimates for the NPGS's overall future needs for implementing the Plan have been projected in Figs. 1.2, 1.3, 1.4, 1.6, 1.7, and Appendix B for individual genebank units based on past trends, current

status, and decades of practical experience of NPGS PGR managers and CGCs (*The costs to implement this Plan are estimated and do not constitute a USDA request for funding)*.

Strategies for meeting future needs for PGR maintenance include increasing the NPGS's present overall recurrent operating "base" budget for the 22 genebank units covered by this Plan from an estimated $38.0 million NTL at present to approximately $55.5 million NTL at +5 years and to approximately $67 million NTL at +10 years from now (Figs. 1.2, 1.6, 1.7). If possible, the base budget would be increased incrementally over 10 fiscal years (FYs), rather than during 1 or 2 FYs to enable most efficient mobilization of the additional fiscal resources. The increased annual budgetary support would be devoted strategically to the priority goals and actions, described especially in Components 2-8, which will reduce maintenance backlogs, and make more high-quality NPGS accessions and associated information available for distribution and use.

The preceding increases in recurrent budgets would also partially support expanded capacities needed for implementing the strategies described in Components 9-12, which would reduce backlogs in PGR characterization, evaluation, genetic enhancement, and make more high-quality accessions and associated information available for distribution and use. Implementing over +10 years the genotypic characterization program described under Component 10 will require ca. $17 million to support "one-time costs," and annual recurrent costs of ca. $300,000 for quality assurance genotyping. An optional Whole Genome Sequencing (WGS) analysis to create a research resource applicable to most of the NPGS PGR would necessitate an additional one-time cost of $40.5 million+ (Fig. 1.7).

As explained in Component 11, reducing the current backlogs in phenotypic evaluations requires a novel phenomics approach incorporating additional equipment and information management capacities costing <$100,000 every five years for individual genebank units that evaluate PGR. An estimated annual recurrent increase of $25 million would fund collaborative NPGS-cooperator phenotypic evaluations guided by the 40+ CGCs and support the personnel needed to develop the analytical protocols and conduct phenomic trait evaluations at NPGS genebank units (Fig. 1.7).

Finally, Component 12 describes the expanded capacities needed to implement and sustain new genetic enhancement programs for specific crops or related groups of crops. Those programs, conducted mainly by genetic enhancement and/or breeding projects in collaboration with genebank units, would require recurrent base funding increases in the range of $500,000 to $1.5 million per year, per crop. Implementing such programs for 100 crops of economic importance to the United States would necessitate an estimated recurrent cost of $50 million to $150 million annually (Fig. 1.7), above and beyond the budgetary support described above for reducing or eliminating operational backlogs in PGR maintenance, characterization, and evaluation.

Expanded NPGS staffing: Insufficient permanent and temporary technical and research staff represents a major cause for the backlogs in PGR maintenance. Consequently, more personnel (total of 444 FTE at +5 years; total of 518 FTE at +10 years; Figs.1.3, 1.6, Appendix B) will be hired strategically to attain the primary goals of this Plan: reducing backlogs in PGR maintenance, characterization, evaluation, and genetic enhancement. In the future, the information associated with PGR will become ever more valuable, especially that generated by the greatly expanded genotypic characterizations and phenotypic evaluations described in

Components 10 and 11. Consequently, the preceding personnel increases, together with training, would require additional (218 users at +5 years; 247 users at +10 years) skilled GRIN-Global users within the NPGS staff as a strategy for managing the increased volume of information generated (Fig. 1.4, Appendix B).

Hiring additional scientific and technical personnel is a strategy not only to help reduce such backlogs, but also enable applied research to be conducted. Research and development will enable gains in specific high priority areas, such as developing and applying advances in information management, artificial intelligence, cryopreservation (long-term storage of seeds and vegetative propagules in ultracold conditions), optimal controlled pollination and propagation described in Components 3-9, and the expanded genotypic characterization and phenotypic evaluation efforts described in Components 10 and 11. That applied research, discussed under each subsequent Component, is a key strategic element for developing more efficient and effective PGR management approaches critical for reducing operational backlogs and ensuring that they do not recur.

Training NPGS personnel and students: The substantial needs for increased NPGS staffing and for dealing with numerous upcoming NPGS staff retirements (ca. 1/3 will have retired at +5 years from now) represent major organizational and operational challenges. Currently, no formal, comprehensive program exists in the United States or internationally for training new PGR managers. Consequently, the NPGS and its university cooperators have implemented a training program for PGR management to be delivered primarily through distance learning. Educational and training priorities already have been identified through an extensive survey (Volk et al. 2019), and online instructional materials are under development; an example can be accessed at https://colostate.pressbooks.pub/cropwildrelatives/. Supported by a USDA/NIFA Higher Education Challenge grant and USDA/ARS funds, development of this educational/training program will extend at least +5 years. Online training and educational materials will be maintained and delivered from the GRIN-Global information system for the foreseeable future through the dedicated website https://grin-u.org/ . During the next +5 to +10 years, this training and education program will be expanded strategically to reach more personnel (particularly from underrepresented minority groups), to encompass additional aspects of PGR management, and to incorporate novel PGR management approaches and genetic, biological, and information technologies as they evolve in the future.

Expanded and upgraded cold-storage facilities and controlled/protected environment (greenhouse, screenhouse) and field space for NPGS operations: As mentioned earlier, maintaining accessions at least two geographically separate sites is a key standard for PGR management (Engels et al., 2003; FAO, 2014; Reed et al., 2004; Lusty et al., 2021). Such maintenance requires adequate cold-storage space. Based on aggregated data from NPGS genebanks, the volume and quality of cold-storage facilities (focusing on 0˚F, -18˚C) at numerous genebank units must be expanded, for an overall NPGS-wide increase from 380,000+ cubic ft. to ca. 498,000+ cubic feet at +5 years and 582,000 + cubic feet at +10 years (Figs. 1.2, 1.6; Appendix B). More detailed information for strategies tailored to individual genebank units can be found in the summaries in Appendix B. Storing as many NPGS accessions as possible at lower temperatures (0˚F, -18˚C; or cryogenic temperatures) can attain the crucial outcome of extending PGR viability and the time between accession regenerations and viability testing, thereby reducing the backlogs for those key PGR management operations. As an initial priority,

NPGS genebank units that require more cold-storage space will confer with ARS Buildings and Facilities Division to formulate the optimal mix of retrofitting current cold-storage space and constructing new storage space, tailored to the specific requirements and parameters of each genebank unit. Based on those consultations, solutions applicable to multiple genebank units might emerge. Such generic approaches could reduce per unit PGT management expenses strategically. Estimates for overall costs of this effort must await the preceding consultations and analyses. In the interim, ongoing planning for expanding and upgrading the cold-storage space for genebank units at Ames, Griffin, and Pullman should be completed and implemented. The unique challenges posed by maintaining the Ft. Collins NLGRP facilities are discussed in detail in Appendix B, as are challenges presented by facilities at other genebank units. Some of these expansions could warrant inclusion in USDA/ARS's Capital Investment Strategy.

The aggregated data from NPGS genebanks indicate that to reduce maintenance backlogs, controlled/protected environment space should also be expanded NPGS-wide for greenhouses from ca. 144,000 sq. ft. to ca. 264,000 sq. ft. at +10 years, and screenhouse space from ca. 120,000 sq. ft. to ca. 165,000 sq. ft. at +10 years (Figs. 1.2, 1.6). Strategies for individual genebank units can be found in the summaries in Appendix B. Access to controlled/protected environment space is strategically important for attaining the outcome of reducing PGR maintenance backlogs and increasing the availability of accessions, such as some CWR, which are problematic to regenerate, propagate, or evaluate under standard field conditions. As with expanding cold room facilities, individual genebank units will confer with ARS Buildings and Facilities Division to identify the optimal designs and configurations for those structures, tailored to local climatic conditions and the specific requirements for each genebank site. Based on those consultations, strategies, solutions, and/or recommended vendors that are applicable to multiple genebank units might emerge. Such generic approaches could reduce per unit construction expenses. Estimates for overall costs of this effort must await the preceding consultations and analyses. Some of these expansions could be of a size to warrant inclusion in USDA/ARS's Capital Investment Strategy. In the interim, ongoing greenhouse renovations at the Corvallis genebank unit will be completed, and the protected screenhouse area at the Riverside genebank unit will be expanded.

The available field space for PGR maintenance is adequate for some genebank units but is inadequate at others. Across the NPGS a total of ca. 2,700 acres of field space will be needed at +10 years to support expanded PGR management operations (Figs. 1.2, 1.6). As reported in Appendix B, genebank units focused on maintaining clonally propagated PGR in orchards or vineyards, such as at Davis and Hilo, require additional field space. The genebank unit in Pullman, WA, also requires more field space for managing the expanded collection size projected. Importantly, many if not most genebank units have long (70+ years in some cases) relied on the strategy leasing land, sometimes annually, sometimes for decades, from land-grant university and SAES partners. Some of these partners recently have reduced or eliminated the land area available for genebank unit operations because of campus expansion or changing institutional priorities. In some cases, rental charges have increased substantially, and duration of land leases have been reduced significantly, e.g., proposed duration of leases for orchard plantings as short as 5 years. Accordingly, these partners must be consulted at the inception of this Plan and frequently during its implementation to secure long-term leases requisite for expanded NPGS operations. If needed land is unavailable under acceptable conditions, then

USDA/ARS must strategically identify other land to lease, perhaps commercially, or even to purchase. In some cases, if land is insufficient for genebank operations, then the genebank unit and its collections might require relocation.

Expanded collaborations: To implement the numerous Components of this Plan, additional and more extensive strategic collaborations (400+ collaborations at +5 years; 430+ collaborations at +10 years; Fig. 1.5) with domestic and international organizations will be established. Information about such collaborations appear under the individual Components, and under the summaries for individual genebank units in Appendix B. Projected future outcomes include expanded partnerships with land-grant universities, international genebank organizations, commodity groups, and private-sector partners mentioned above. New collaborations will likely include consortia such as the current USDA/ARS-Cornell University Breeding Insight Project (see Component 10).

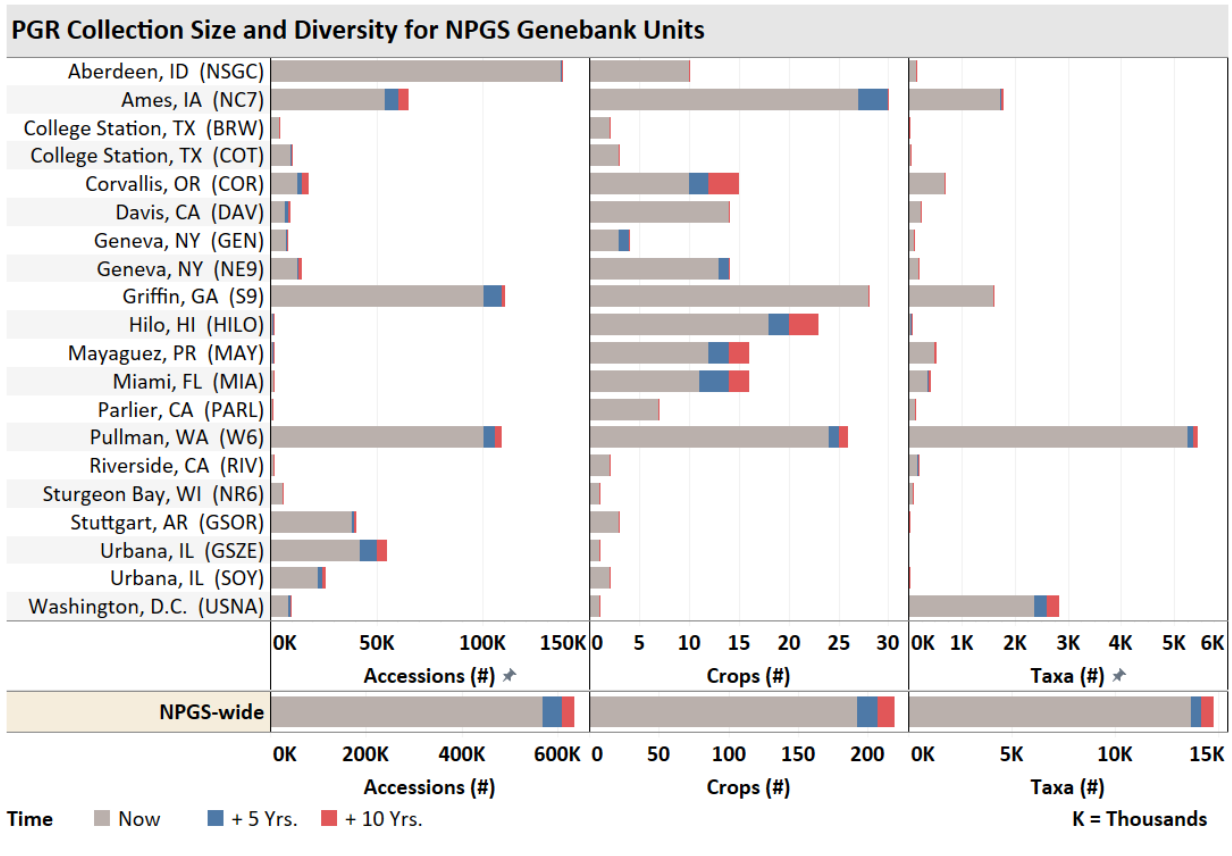


Fig. 1.1: PGR Collection Size and Diversity for NPGS Genebank Units. For individual genebank units, listed by their geographical locations; the current numbers of PGR accessions managed; numbers of crops (as defined by PGR managers) corresponding to those accessions; and numbers of taxa (e.g., species, subspecies, varieties) corresponding to those accessions are shown by gray bars. The estimated increases at +5 years are shown by blue bars, and at +10 years by rust red bars. The total NPGS values for the preceding metrics are shown in the bottom row of the figure.

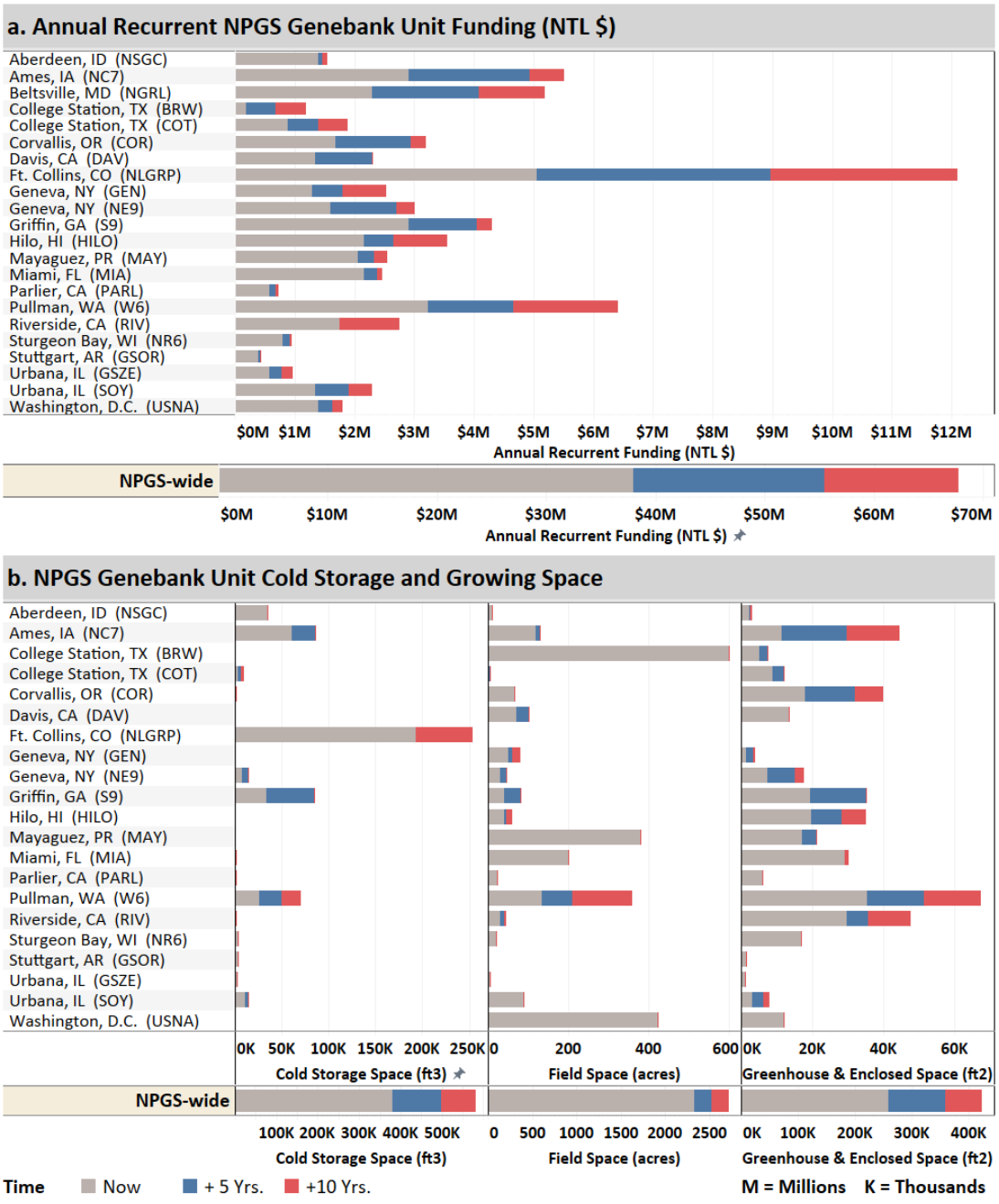


Fig. 1.2a: Annual Recurrent NPGS Genebank Unit Funding (NTL $). The current values for the annual recurrent funding (Net-to-Location, NTL) for overall operations at the NPGS individual genebank units, listed alphabetically by their geographical locations, are shown by gray bars. The estimated increases needed to attain the PGR maintenance and applied research goals of the Plan at +5 years are shown by blue bars, and at +10 years by the rust red bars. An NPGS summary is included at the bottom. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*

Fig. 1.2b: NPGS Genebank Unit Cold Storage and Growing Space. The current volumes for the NPGS cold storage space (in ft3) used by NPGS operations at individual genebank units, listed alphabetically, are shown by gray bars. The estimated increases in space needed to attain the goals of the Plan at +5 years are shown by blue bars, and at +10 years by rust red bars. The current areas for the NPGS field space (in acres) used by NPGS operations are shown by the gray bars. The estimated increases for field space needed to attain the goals of the Plan at +5 years are shown by blue bars, and at +10 years by rust red bars. The current areas for the NPGS greenhouse and enclosed space (e.g., screenhouses; in ft2) used by NPGS operations are shown by gray bars. The estimated increases needed to attain the goals of the Plan at +5 years are shown by blue bars, and for +10 years by rust red bars. The total NPGS values for the preceding metrics are shown in the bottom row of the figure.

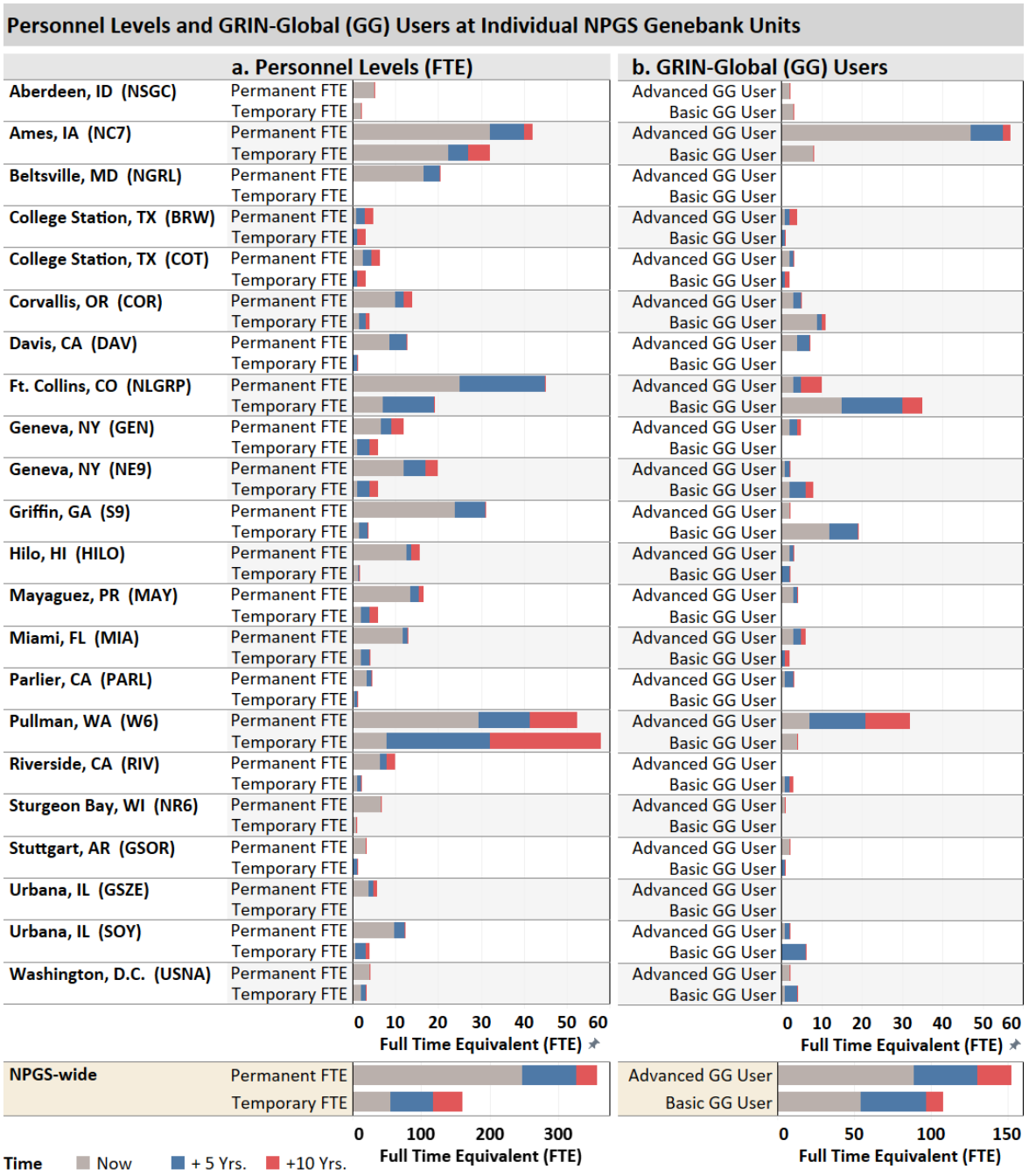


Fig. 1.3: Personnel levels and GRIN-Global (GG) Users at Individual NPGS Genebank Units

Fig. 1.3a For individual genebank units, listed alphabetically by their geographical locations, the current numbers of permanent and temporary staff members (full-time equivalents, FTEs) are shown in 1.3a by gray bar, goals for +5 years by blue bars, and for +10 years by rust red bars. The total NPGS values for the preceding metrics are shown in the bottom rows of the figure.

Fig. 1.3b The numbers of advanced and basic users of the NPGS's information management system GRIN-Global (GG) Curator Tool are shown in 1.3b by gray bars, goals for +5 years by blue bars, and for +10 years by rust red bars. The total NPGS values for the preceding metrics are shown in the bottom rows of the figure.

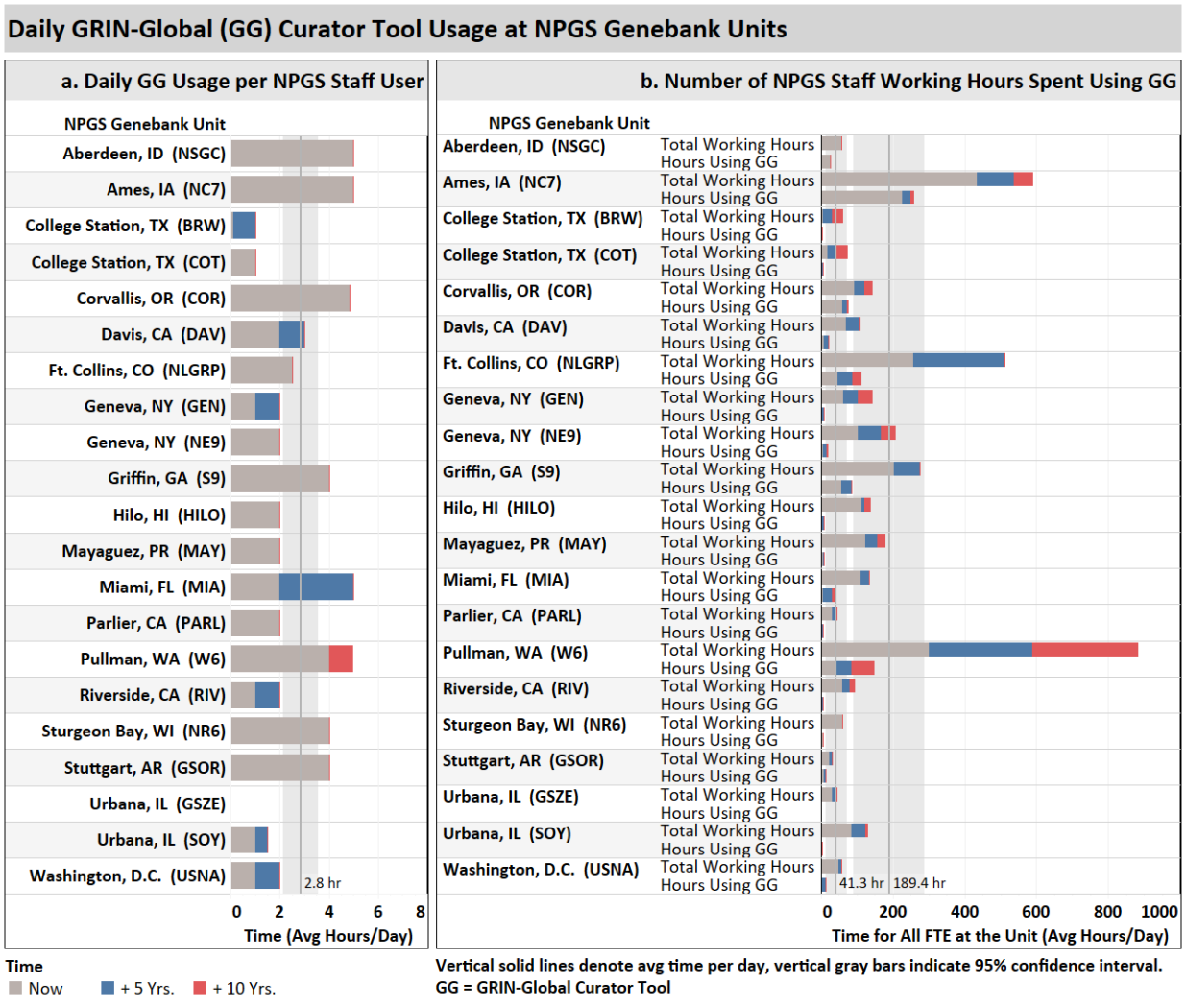


Fig. 1.4: Daily GRIN-Global (GG) Curator Tool Usage at NPGS Genebank Units.

Fig. 1.4a: For individual genebank units, listed alphabetically by their geographical locations, the current average numbers of hours per day, per NPGS staff user, spent using NPGS information management system GG Curator Tool are shown by gray bars. The goals for +5 years are shown by blue bars, and for +10 years by rust red bars. The current average hours per day across all NPGS genebank units in total are shown by the vertical line, and the 95% confidence interval for this average is shown by the vertical gray band.

1.4b: For individual genebank units, listed alphabetically, the current numbers of total working hours and numbers of working hours for all FTE spent using the NPGS information management system GG Curator Tool are shown by gray bars. The goals for +5 years are shown by blue bars and for +10 years by rust red bars. The average across all NPGS genebank units for hours per day using GRIN-Global and for total working hours per day, respectively, are shown by the vertical lines and the 95% confidence intervals for those averages are shown by the vertical light gray bands.

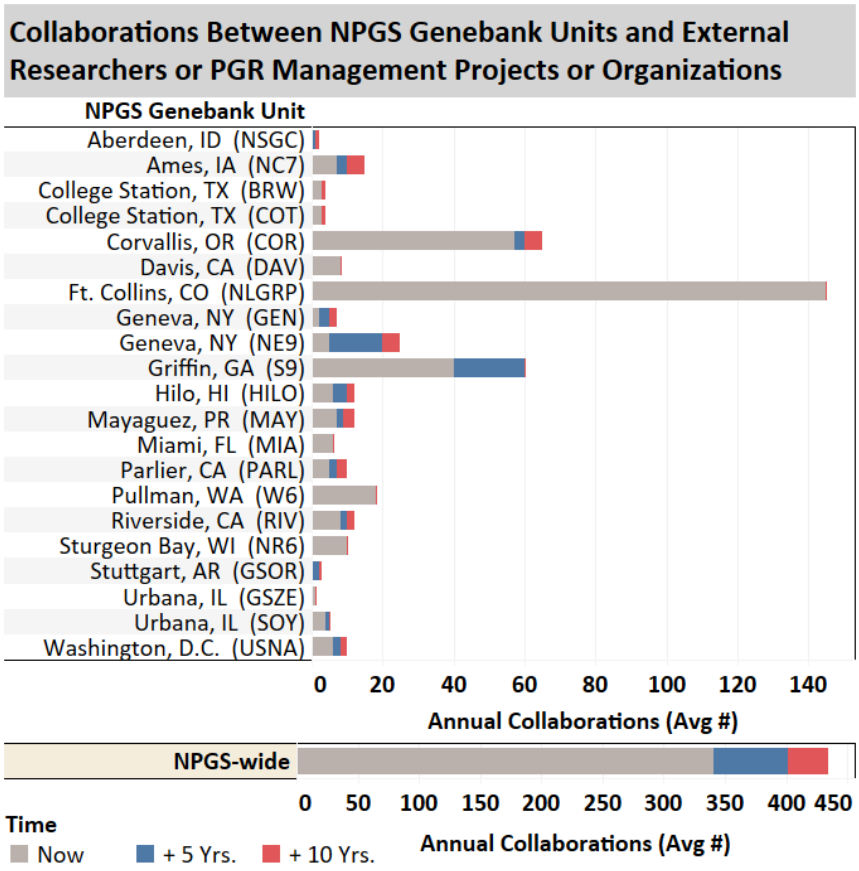


Fig. 1.5: Collaborations Between NPGS Genebank Units and External Researchers and PGR Management Projects or Organizations. For individual genebank units, listed alphabetically by their geographical locations, the current average annual numbers of formal research and PGR management collaborations with external research and PGR management projects or organizations are shown by gray bars. The goals for +5 years are shown by blue bars and for +10 years by rust red bars. The total NPGS collaborations are shown in the bottom row of the figure.

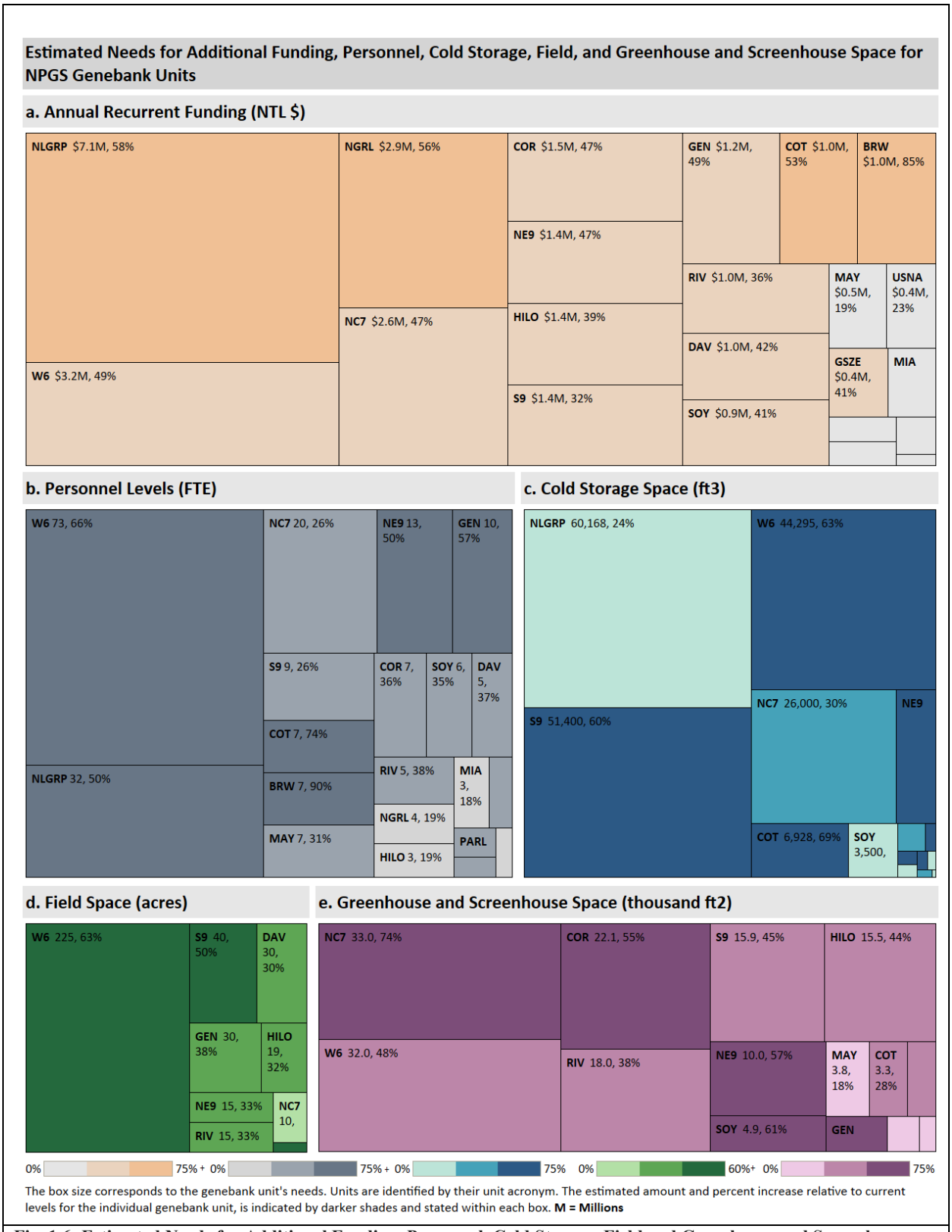


Fig. 1.6: Estimated Needs for Additional Funding, Personnel, Cold Storage, Field and Greenhouse and Screenhouse Space for NPGS Genebank Units. Figure 1.6 depicts estimates for increased funding (NTL $), personnel (FTEs), cold storage space (ft3), field space (acres), and greenhouse and screenhouse space (ft2) needed to attain the NPGS Plan goals for +10 years. The larger the box, the more funding, personnel, cold storage, field, and greenhouse and screenhouse space are

needed by individual NPGS genebank units, as identified by their acronyms. The colors of the individual boxes depict the percentage increases above the current levels needed for individual genebank units. The amounts of funds, personnel, cold storage, field, and greenhouse and screenhouse space and the percentage increases above current levels are listed after the acronyms within the boxes, as the format permits. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*

Fig. 1.6a: at the top depicts the amount and percentage increases in annual recurrent funding (NTL $) for PGR maintenance and applied research that is needed by individual genebank units to attain Plan goals at +10 years. Orange boxes represent percentage increases of ca. 50% or more; light orange boxes percentage increases between ca. 25% and 50%; and light gray boxes percentage increases of less than ca. 25%. Due to format limitations, information for increases less than ca. $300,000 is sometimes omitted. The individual genebank summaries in Appendix B provide that information.

Fig. 1.6b: at the middle left depicts the amount and percentage increases in personnel needed by individual genebank units to attain Plan goals at +10 years. Dark gray boxes represent percentage increases of ca. 50% or more; gray boxes percentages between ca. 25% and 50%; and pale gray boxes percentages less than 25%. Due to format limitations, information for increases less than 2 FTE is sometimes omitted. The individual genebank summaries in Appendix B provide that information.

Fig. 1.6c: at the middle right depicts the amount and percentage increases in cold storage space needed by individual genebank units to attain the Plan goals at +10 years. Dark blue boxes represent percentage increases of ca. 50% or more; blue boxes percentages between ca. 25% and 50%; and light blue boxes percentages of less than ca. 25%. Due to format limitations, information for increases less than 7,000 ft3 is sometimes omitted. The individual genebank summaries in Appendix B provide that information.

Fig. 1.6d: at the bottom left depicts the amount and percentage increases in field space needed by individual genebank units to attain the Plan goals at +10 years. The dark green boxes represent percentages of ca. 40% or more; green boxes percentages between ca. 20% and 40%; and light green boxes percentages of less than ca. 20%. Due to format limitations, information for increases less than ca. 2 acres is sometimes omitted. The individual genebank summaries in Appendix B provide that information.

Fig. 1.6e: at the bottom right depicts the amount and percentage increases in greenhouse and screenhouse space needed by individual genebank units to attain the Plan goals at +10 years. The dark purple boxes represent percentage increases of ca. 50% or more; purple boxes percentages between ca. 25% and 50%; and light purple boxes percentages of less than ca. 25%. Due to format limitations, information for increases less than ca. 2,000 ft2 is sometimes omitted. The individual genebank summaries in Appendix B provide that information.

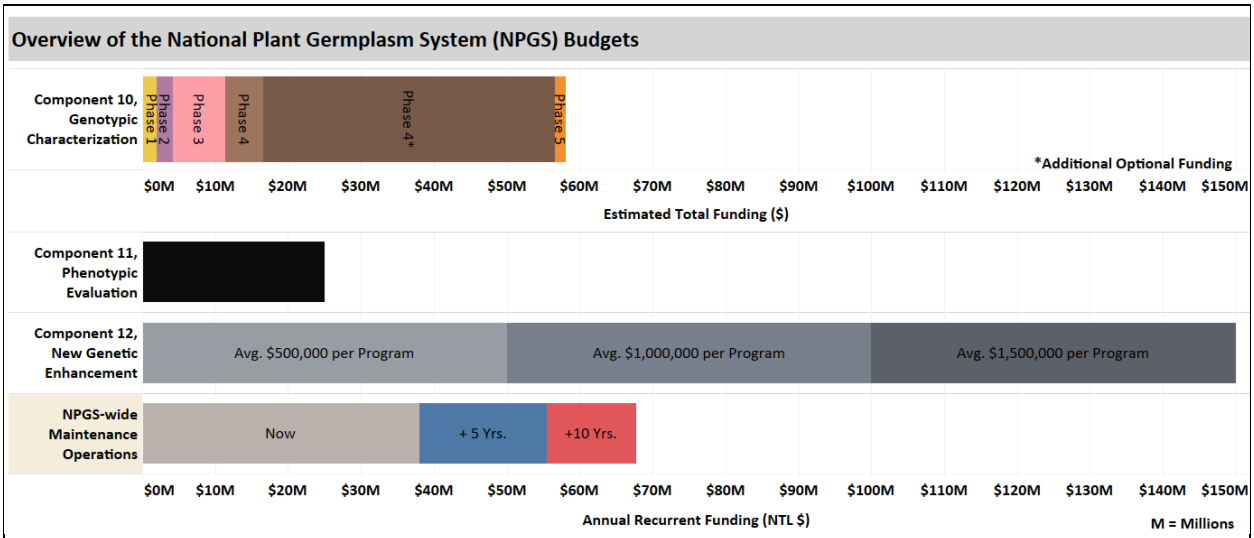


Fig. 1.7: Overview of the National Plant Germplasm System (NPGS) Budgets. The first row of Fig. 1.7 depicts the estimated additional funding ("one-time" $ rather than recurrent funding) needed to conduct the five Phases of the comprehensive genotypic characterization of NPGS PGR as described in Component 10 of this Plan. The one-time funding needed for Phase 1 is depicted by the yellow bar, Phase 2 by the purple bar, Phase 3 by the pink bar, Phase 4 by the light brown bar, the optional (denoted by the *) segment of Phase 4 by the dark brown bar, and Phase 5 by the orange bar. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*

The second row depicts by the black bar the estimated additional annual recurrent NPGS funding needed to conduct the comprehensive phenotypic evaluation of NPGS PGR described in Component 11 of this Plan.

The third row depicts the range for estimated increases in annual recurrent NPGS funding needed to conduct the comprehensive genetic enhancement programs for 100 U.S. crops, as described in Component 12 of this Plan. Based on prior experience, the annual recurrent base funding needed to conduct a single genetic enhancement/pre-breeding program ranges from ca. $500,000 to ca. $1.5 million, depending on the crop, existing knowledge and infrastructure, and other factors. The gray bar has been segmented to depict the estimated minimum ($50 million; light gray), average ($50 million-$100 million; gray), and maximum ($100 million-$150 million; dark gray) annual recurrent base funding for new genetic enhancement /pre-breeding programs for 100 crops.

For comparative purposes, the fourth row depicts the total annual recurrent NPGS funding (NTL $): the gray bar shows the FY19 funding level for overall genebank operations. The estimated funding increase needed to attain the overall PGR maintenance and applied research goals for Components 3-9 at +5 years is shown by the blue bar, and for +10 years by the rust red bar.

Component 2: PGR Information Management (Figs. 2.1-2.3)

GRIN-Global Data Volume and Usage (Fig. 2.1)

Current Status

Safeguarding and communicating the information associated with NPGS PGR comprise key priorities for effectively maintaining and facilitating the use of that PGR. Since the mid-1980s, the National Germplasm Resources Laboratory (NGRL) has spearheaded the development of information management/information technology for the NPGS. It hosts and maintains GRIN-Global, the NPGS's system-wide information management/information technology "backbone", that has played a primary role in developing and updating this crucially important information management tool.

As of this writing, GRIN-Global contains more than 50,700,000 records and more than 18.6 GB in the GRIN-Global database per se, with an additional 422 GB in attachments (Fig. 2.1a). Digital images of PGR account for much of the total volume of bytes currently comprising GRIN-Global data. Researchers, breeders, and other users of NPGS PGR and associated information access GRIN-Global online through the public website at https://www.ars-grin.gov/. In 2019, a total of 212,000+ users accessed the GRIN-Global public website during 405,000+ access sessions, which generated a total of 3.3 million+ individual "page views" (Fig. 2.1b). This extensive GRIN-Global usage is possible because it is operational essentially 24/7/365, functioning 99+% of the time during 2019.

Strategies and Implementation

The current trends to incorporate more digital images of PGR, digitized documents (see below), and many more genotypic and phenotypic data (Components 10 and 11) into GRIN-Global are forecast to continue. Consequently, the overall information management capacity in the NPGS must expand strategically. Precise forecasts for future information management needs are difficult to formulate because information management technology is evolving rapidly and unpredictably. Nonetheless, strategies for supporting the NPGS's overall operations can be formulated by extrapolating from the current status, reference to recent trends, and the plans for strategically expanding genotypic characterizations and phenotypic evaluations.

In the future, GRIN-Global could expand in +5 years to contain approximately 128,700,000+ information records, increasing to 210,500,000+ at +10 years; and 94.9+ GB in the database per se with 2,172 GB in attachments at +5 years, increasing to 178+ GB in the database per se with 3,781+ GB in attachments at +10 years (Fig. 2.1a). By +5 years, a total of approximately 250,000+ users are forecast to access the GRIN-Global public website annually during 477,000+ access sessions, which could generate annually a total of 3,800,000+ individual "page views." Usage is forecast to increase at +10 years to approximately 304,000+ users accessing the GRIN-Global public website annually during 579,000+ access sessions, which could generate a conservative estimate of 4,700,000+ total annual individual "page views" (Fig. 2.1b).

As a strategy for meeting the increased demand for and reducing the current backlogs in data management, additional information management personnel, content specialists (e.g., for nomenclature and taxonomy), and data technicians at individual genebank units will be hired. They will implement technical innovations developed by NPGS bioinformatics and information management research to automate data capture and processing. Those information management specialists and additional computer programmers (permanent and contract personnel) would be hired at the NGRL, NLGRP, and Ames genebank units (Appendix B) to expand the capacity of the GRIN-Global information system to handle the projected substantial increase in demand for information technology support (Fig. 1.5a).

Document Digitization and Uploading to GRIN-Global (Fig. 2.2)

Current Status

At present, 456,000+ documents, mostly paper and many that contain critical historical information about NPGS PGR, require digitization and uploading to GRIN-Global (Fig. 2.2). Not surprisingly, some of the larger and older NPGS genebank units (e.g., Ames, Geneva, Pullman, Urbana) maintain the most documents requiring digitization (Fig. 2.2). An average of 36,000+ (16%) of such documents are currently digitized annually. This annual rate of document digitization does not meet current needs: consequently, a backlog has accumulated for this important task of safeguarding these irreplaceable documents.

Genebank units currently manage, in local databases and data storage devices, 88,000+ digital records for PGR maintenance actions, and genotypic characterization and phenotypic evaluation data that have not yet been uploaded into GRIN-Global for safeguarding and facilitating access by the wider scientific community (Fig. 2.2). Each year an increasingly larger volume of such data are generated. An average of 68,000+ (78%; data not shown) of such records are uploaded annually to GRIN-Global, a rate that does not meet the current needs, and consequently has generated a backlog for this important operation.

Strategies and Implementation

As additional valuable paper documents in genebank units are digitized each year, the total volume of such documents remaining to be processed should steadily decrease (Fig. 2.2), mainly because ever fewer paper documents should be generated in the future. This Plan's strategy is to provide adequate personnel, equipment, and resources (Figs. 1.1, 1.2, 1.4, Appendix B) for the task of digitization to approach completion at +10 years, at a rate dependent on the current backlog, and the available processing capacities. Once complete, the personnel, equipment, and financial resources devoted to document digitization can be strategically redirected to other PGR and information management priorities. In contrast to the non-digital documents discussed above, an increasing volume of local digital records could be generated in the future, especially if expanded PGR genotypic characterization and phenotypic evaluation programs generate an increased volume of digital images and nucleotide sequence data (see Components 10 and 11). Without automated uploading procedures, and personnel, equipment, and resources sufficient for

timely uploading of such digital records to GRIN-Global, the current backlogs could expand. Consequently, it is a priority to develop such methods and expand capacities to implement them.

Data in GRIN-Global Taxonomy (Fig. 2.3)

Current Status

A stable system of scientific plant nomenclature is critical not only for plant research and breeding, but also for optimal PGR management. If incorrect scientific names are attached to PGR accessions, those errors can propagate as the accessions are widely distributed and used. Consequently, during 30+ years the NPGS has invested substantial resources in building and maintaining an information system to communicate the correct scientific names for thousands of plants of economic importance. GRIN-Global Taxonomy, the taxonomic portion of GRIN-Global, provides the classification and nomenclature for the PGR in the NPGS and other genebanks, and for many other economic plants on a worldwide basis. The information included in GRIN-Global Taxonomy has been instrumental for enabling critical research, e.g., underpinning assessments of the conservation status for CWR indigenous to the United States (Khoury et al., 2013; Khoury et al., 2020), and serves as an indispensable reference for governmental regulations and commercial communications.

Currently, GRIN-Global Taxonomy includes scientific names for 27,000+ plant genera (14,000+ accepted), 1,400+ infragenera (1,300+ accepted), and 120,000+ species or infraspecies (Fig. 2.3; 66,000+ accepted), plus common names, geographical distributions of taxa, literature references, and information regarding economic importance. Generally recognized standards for abbreviating authors' names and botanical literature have been adopted in GRIN-Global. The scientific names are verified, in accordance with the international rules of botanical nomenclature, by taxonomists of the NGRL through available taxonomic literature and consultations with taxonomic specialists. Included in GRIN-Global Taxonomy are data for federal- and state-regulated noxious weeds and federally and internationally-listed threatened and endangered plants (GRIN-Global, 2020) https://npgsweb.ars-grin.gov/gringlobal/taxon/abouttaxonomy?chapter=summ.

At present, GRIN-Global Taxonomy incorporates an average of 2,900 new species records annually (Fig. 2.3). About 7% of those records currently have protologue links, which encompass valuable information associated with a name in its valid publication, such as description or diagnosis, illustrations, references, synonymy, geographical data, citation of specimens, etc. About 70% of the names in GRIN-Global Taxonomy are not accompanied by geographical data (Fig. 2.3) and about 2,800 nomenclatural records are missing or unverified. As of this writing, only three horticultural crops, all of them ornamentals, have been evaluated for geographical data for CWR.

Strategies and Implementation

As Fig. 1.1 indicates, the numbers of accessions and taxa in the NPGS are forecast to increase during the next decade. Consequently, the number of records of species in GRIN-Global

Taxonomy is forecast to increase to 161,000+ at +10 years, necessitating that number of new species records created annually to ca. 5,800 per year (Fig. 2.3). The NGRL will adopt a strategy that by +10 years, will increase to 30% the species records with protologue links; reduce to 35% (Fig. 2.3) the number of names in GRIN-Global Taxonomy with missing geographical data; and reduce to about 300 the nomenclatural records that are missing or unverified. The strategy is to have evaluated about 50 ornamental crops for CWR data at +10 years (Fig. 2.3). The preceding strategic approach will enable GRIN-Global Taxonomy to continue to deliver accurate, up-to-date scientific names and associated information to users throughout the world.

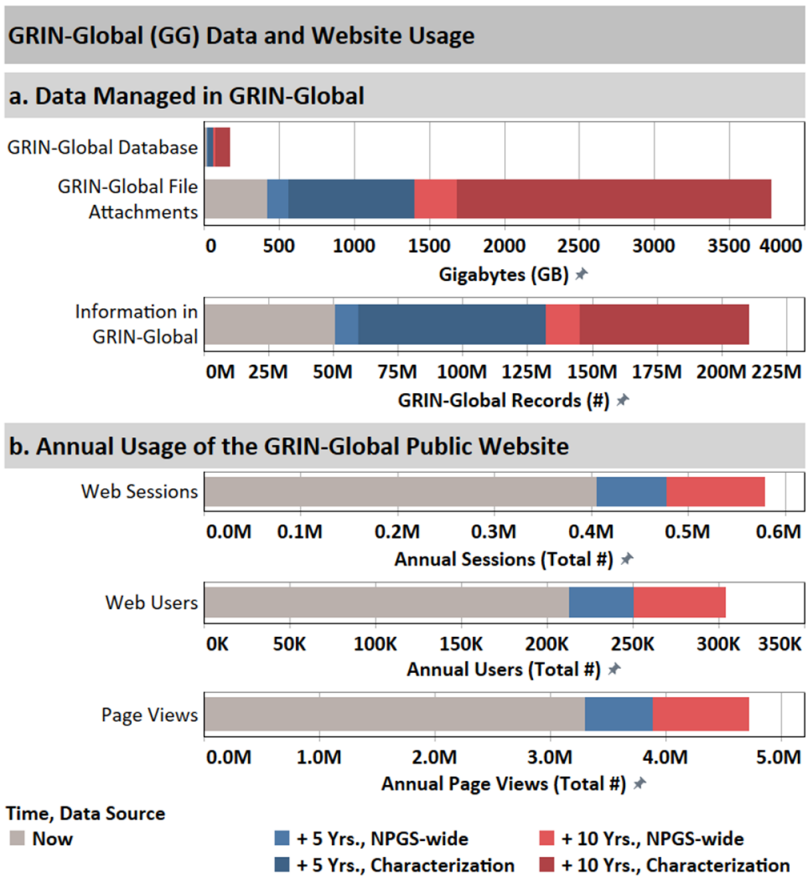


Fig. 2.1: GRIN-Global (GG) Data and Website Usage.

Fig 2.1a: GRIN-Global (GG) is the information management system for the NPGS. The current numbers of gigabytes (GB) in the GG database and in GG file attachments are shown by gray bars. The estimated increases for those standard PGR maintenance and evaluation data at +5 years are shown by light blue bars and at +10 years by light rust red bars. The estimated increases for genotypic characterization (see Component 10) data at +5 years are shown by dark blue bars, and at +10 years by dark rust red bars. The current number of records in GG is shown by the gray bar. The estimated increases for number of records at +5 years is shown by the light blue bar and at +10 years by the light rust red bar. The estimated increases for number of records for genotypic characterization (see Component 10) at +5 years is shown by the dark blue bar and at +10 years by the dark rust red bar.

Fig. 2.1b: The current total annual number of web sessions for the GRIN-Global (GG) public website is shown by the gray bar. The estimated increase at +5 years is shown by the blue bar and at +10 years by the rust red bar. The current total annual number of users for the GG public website is shown by the gray bar. The estimated increase at +5 years is shown by the blue bar, and at +10 years by the rust red bar. The current total annual number of page views for the GG public website is shown by the light gray bar. The estimated increase at +5 years is shown by the blue bar, and at +10 years by the rust red bar.

NPGS Legacy Documentation

Primary Type of Germplasm	NPGS Genebank Unit	a. Paper Records to Digitize: Now	a: + 5 Yrs.	a: + 10 Yrs.	b. Uploaded to GRIN-Global: Now	b: + 5 Yrs.	b: + 10 Yrs.	c. Digitized Annually: Now	c: + 5 Yrs.	c: + 10 Yrs.
	NPGS-Wide	456,411	240,240	24,290	88,277	136,985	173,384	36,661	65,190	46,890
Managed as Seeds	Ames, IA (NC7)	250,000	90,000	10,000	6,000	7,500	10,000	32,000	32,000	32,000
	College Station, TX (COT)	20	0	0	4,800	6,000	12,000	0	0	0
	Geneva, NY (NE9)	84,425	80,500	5,500	159	343	386	0	15,000	5,500
	Parlier, CA (PARL)	2,350	1,850	0	500	0	0	0	100	400
	Pullman, WA (W6)	50,000	25,000	5,000	50,000	99,912	123,618	0	5,000	5,000
	Urbana, IL (SOY)	20,000	15,000	1,000	5,000	10,000	15,000	100	5,000	1,000
Managed as Clones	College Station, TX (BRW)	20,000	15,000	0	1,000	2,750	1,000	1,000	5,000	0
	Corvallis, OR (COR)	10,000	5,000	1,000	10,000	1,000	1,000	1,000	1,000	1,000
	Davis, CA (DAV)	2,000	1,500	1,000	190	100	100	8	100	100
	Geneva, NY (GEN)	10,000	5,000	0	5,000	7,500	7,500	0	1,000	1,000
	Hilo, HI (HILO)	500	600	0	500	100	0	0	100	0
	Miami, FL (MIA)	0	0	0	276	1,000	2,000	0	0	0
	Riverside, CA (RIV)	0	0	0	0	0	0	1,000	100	100
	Washington, D.C. (USNA)	3,816	490	490	4,552	480	480	1,253	490	490
	Fort Collins, CO (NLGRP)	3,300	300	300	300	300	300	300	300	300

GSOR, GSZE, MAY, NGRL, NR6, NSGC, and S9 have no backlog of legacy documentation.

0 20,000+ 0 10,000+ 0 10,000+

Fig. 2.2: NPGS Legacy Documentation. The top row of Fig. 2.2a, shaded light beige, depicts the total number of paper records at all the NPGS genebank units that must be digitized, and goals for reducing the digitization backlog for +5 and +10 years. The same information is then provided for individual NPGS genebank units, listed alphabetically by their geographical locations, in two groups. The top group encompasses genebank units that primarily manage seed-propagated crops, and the lower group encompasses genebank units that primarily manage clonally-propagated crops. The darker the blue hue, the more paper records from individual genebank units that need to be digitized.

The top row of Fig. 2.2b, shaded light beige, depicts the total number of digital records uploaded to GRIN-Global from all the NPGS genebank units, and goals for increasing the numbers uploaded at +5 and +10 years. The same information is then provided for individual NPGS genebank units, listed alphabetically by their geographical locations, in two groups. The top group encompasses genebank units that primarily manage seed-propagated crops, and the lower group encompasses genebank units that primarily manage clonally-propagated crops. The darker the green hue, the more digital records from individual genebank units that will be uploaded to GRIN-Global.

The top row of Fig. 2.2c, shaded light beige, depicts the total number of paper records digitized annually for all the NPGS genebank units, and goals for increasing the numbers of paper records digitized annually at +5 and +10 years. The same information is then provided for individual NPGS genebank units, listed alphabetically by their geographical locations, in two groups. The top group encompasses genebank units that primarily manage seed-propagated crops, and the lower group encompasses genebank units that primarily manage clonally-propagated crops. The darker the lavender hue, the more paper records from individual genebank units that will be digitized annually.

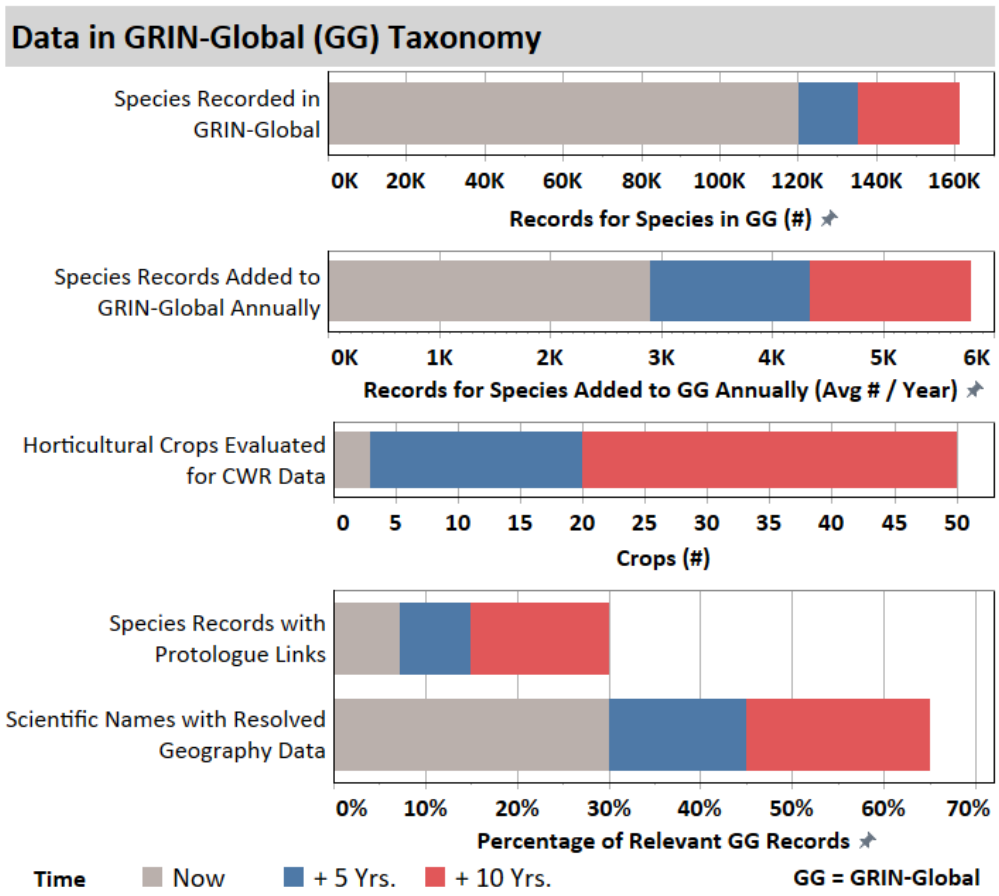


Fig. 2.3: Data in GRIN-Global (GG) Taxonomy. In the first row, the current number of records for species in GRIN-Global Taxonomy is shown by the gray bar. In the second row, the current average number of records for species added annually to GRIN-Global Taxonomy is shown by the gray bar. The estimated increases at +5 years are shown by blue bars, and at +10 years by rust red bars.

In the third row, the current number of horticultural crops evaluated for crop wild relative (CWR) data is shown by the gray bar. In the fourth row, the current percentage of taxonomy records with protologue links in GRIN-Global Taxonomy is shown by the gray bar. In the fifth row, the current percentage of taxonomic names with resolved geography data in GRIN-Global Taxonomy is shown by the gray bar. The goals for +5 years are shown by blue bars and for +10 years by rust red bars.

Component 3: PGR Acquisition and In Situ Conservation (Figs. 3.1-3.2)

Current Status

Currently, the entire NPGS PGR collection is growing at an average rate of ca.1-1.5% per year, adding an average total of ca. 8,400+ new accessions/year (Fig. 3.1, Fig. S3.1; Note that Figs. S3.1-S12 are found in the companion document "Supplementary Data"). The growth rate varies substantially across crops, with relatively high average increase rates for collections of genetic stocks (e.g., for maize in the Urbana genebank unit), horticultural/specialty crops (e.g., in the Miami and Mayagüez genebank units), certain field crops (e.g., sorghum in the Griffin genebank unit), formerly proprietary cultivars for which Plant Variety Protection has expired (Kurtz et al., 2016), and crop wild relatives and wild species indigenous to the US, acquired through the multi-Federal agency Seeds of Success (SOS) program (Haidet and Olwell, 2015) and maintained at the Pullman genebank unit (Fig. 3.1). Notably, genetic stocks, clonally propagated plants, and crop wild relatives are among the most complicated types of PGR to manage in genebanks, with predictably high per accession management costs (see Component 7 and the section Outline for NPGS Plan Implementation**)**.

By virtue of its mandate, the NPGS has emphasized PGR management ex situ, rather than in situ conservation through protected land reserves. The USDA/ARS is not a land management agency but does currently partner with other agencies and institutions (e.g., the U.S. Forest Service (USFS) and USDA/ARS, 2014) that manage lands where several in situ conservation projects for the PGR of U.S. CWR are located, such as for chile peppers (Khoury et al. 2019) and cranberries (Khoury et al. 2020). A total of ca. 10 species and populations are currently encompassed by land management agency plans (Fig. 3.2) that include current and future commitments to conserving these taxa in situ.

Strategies and Implementation

Much of the planned expansion of the NPGS collection during the next +10 years will encompass targeted acquisitions to fill genetic gaps (often identified through crop vulnerability assessments, e.g., Volk et al., 2015); cultivars whose intellectual property rights have expired; genetic stocks generated by genomic and biotechnology research; exchanges with other genebank systems and botanical gardens; and donations from discontinued research and breeding programs that add genetic diversity currently unrepresented in the NPGS collections. Overall, it is forecasted that the NPGS collection will continue to grow at an average rate of ca. 1-1.5% per year, adding a total of 70,000+ accessions during the next +10 years (Fig. 3.1). The growth rate will likely continue to be highest for collections with currently rapid growth rates.

Regrettably, many historical accessions of vegetable PGR at the Geneva genebank unit were lost decades ago; consequently, collections for crops such as *Apium* (celery), *Asparagus, Fagopyrum* (buckwheat), and *Raphanus* (radish) must be expanded or re-established through targeted acquisitions. Furthermore, new collections will be established for several important crops to meet the needs of U.S. agriculture. For example, in FY 19 Congress directed the NPGS to establish new collections for coffee (*Coffea*) at the Hilo genebank unit and hemp (*Cannabis sativa*) at the Geneva genebank unit. Because of biological factors (and also legal/regulatory factors for hemp),

the PGR for both of these crops will be relatively complicated and expensive to manage per accession. Substantial research and development must be conducted to devise the most efficient and effective approaches for PGR management of these crops. Expansion of collections for those crops in particular could potentially generate new PGR maintenance backlogs or exacerbate current backlogs (Appendix B). Consequently, when information about accession origin and genotypic characterization data (Component 10) identify redundant accessions, those will be removed from active management and archived.

Acquisition of additional accessions for the NPGS collection will be strategic and guided by the knowledge and experience of PGR managers and CGCs (Fig. D), and information generated by the genotypic characterization program described later in Component 10. Detailed knowledge of the genetic profiles of accessions currently managed in NPGS collections will reveal gaps in the overall coverage of the genetic diversity that represent priorities for acquisition. At present, gaps in genetic coverage exist especially for tropical/subtropical crops, e.g., *Carica* (Hilo genebank unit), *Citrus* (Riverside), *Macadamia* (Hilo), *Mangifera* (Miami), *Musa* (Mayagüez), *Persea* (Miami), and *Theobroma* (Mayagüez). Conversely those genotypic characterization data can provide evidence of genetically redundant accessions to be removed from the collections. For example, genebank units at Miami, Mayagüez, and Hilo will follow the strategy of applying genotypic characterization data to reconcile duplicate PGR holdings and determine which genebank unit would have the lead responsibility for accessions in legacy PGR collections.

Public-sector genomic and genetic engineering research programs will continue to generate genetic stocks, primarily according to available grant funding and research community priorities. These will be incorporated strategically into the NPGS collections in consultation with the PGR developers, funding agencies (NIFA and NSF), and research communities. The Plant Variety Protection Certificates of an estimated 3,200+ cultivars will expire during the next +10 years (unpublished information from the Plant Variety Protection Office). Those cultivars, many from crops such as cotton, maize, soybean, wheat, potatoes, vegetables, and forage and turfgrasses, will then be incorporated into the NPGS PGR collection. The high frequency with which NPGS accessions of these cultivars are currently distributed reflects their importance to researchers, breeders, and producers. Consequently, they are priorities for incorporation into NPGS PGR collections.

During the next +10 years, the Seeds of Success program operated by the U.S. Department of the Interior, Bureau of Land Management, will collect an estimated 5,000+ samples of indigenous U.S. plant species for research, development, conservation, and ecosystem restoration, with the ultimate goals of increasing the quality and quantity of native plant materials available for restoring and supporting resilient ecosystems (Haidet and Olwell, 2015). Applying the methods outlined above and aligning with the U.S. CWR priorities presented below, NPGS PGR managers will acquire strategically those samples that would fill genetic, taxonomic, or ecogeographical gaps in the collections.

Acquisition through nationally coordinated plant explorations--When gaps in the collections are identified, potential new crops are developed, new uses for established crops evolve, and new threats (diseases, pests) emerge, the NPGS will attempt to collect PGR from the field. These explorations will continue to try to meet current and future demands, especially for CWR native

to the United States. Because of complications with securing permits and logistical planning, especially for international efforts, the NGRL coordinates and financially supports most of the field collections for the NPGS. Currently, such field collections yield an average of 500 new accessions/year (0.08% of the total current size of the NPGS PGR collection; Fig. 3.1). Based on current knowledge of gaps in the NPGS collections and the needs of researchers and breeders, the volume of field collections of PGR should be doubled between now and +5 years (ca. 1000 new accessions/year, 0.16% of the total current number of accessions expected then; Fig. 3.1), and then should increase slightly slower thereafter (ca. 600+ new accessions/year, 0.11% of the total current number of accessions at +10 years; Fig. 3.1). These field collections, primarily of CWR indigenous to the United States (see below) will add an estimated 7,500+ new accessions to the overall NPGS collection (Fig. 3.1) with the outcome of filling priority gaps in the NPGS holdings during the 10-year Plan.

Numerous species native to the United States are CWR of important crops (Greene et al. 2018, 2019). Identifying the priorities for U.S. CWR to be acquired by the NPGS during the next +10 years is based on an updated analysis by Khoury et al., 2020. The highest priority (Priority 1A) for ex situ and in situ conservation was assigned to 253 taxa that are the closest relatives of globally important crops or important wild utilized food plants. A lower priority (Priority 1B) was assigned to188 taxa that are more distantly related to these crops. All of these taxa are currently underrepresented in NPGS collections, and many are missing entirely. During the next +10 years, the NPGS plans to obtain accessions of all these taxa. The first +5 years will concentrate on the Priority 1A taxa, collecting 10 accessions of 20% of those taxa each year (506 per year). The second five years will concentrate on collecting 5 accessions of 20% of the Priority 1B taxa each year (188 accessions per year).

Complementary in situ, dynamic PGR conservation--Whenever feasible, the preceding CWR indigenous to the United States should also be safeguarded in situ through dynamic, in situ conservation in land reserves, according to the strategies described below. Weighing their combined ex situ and in situ conservation status, Khoury et al. (2020) determined that 349 U.S. CWR taxa (58.8%) were urgent priorities for further action; 220 (37%) were high priority; and 25 (4.2%) were medium priority, with none currently considered low priority. Of the U.S. CWR most closely related to crops and therefore of greatest potential for crop genetic improvement, Khoury et al. (2020) identified 135 (53.4%) that warrant urgent priority for further combined ex situ and in situ conservation, 101 (39.9%) as high priority; and 17 (6.7%) as medium priority.

U.S. CWR of cereal, fruit, fiber, pulse, nut, root and tuber, sugar, spice, and vegetable crops collectively generate over $116 billion in annual U.S. agricultural production value (Khoury et al. 2020; USDA National Agricultural Statistics Service, 2020), and thus encompass the greatest proportions of taxa that warrant urgent priority for conservation (Khoury et al. 2020). Specifically, U.S. CWR for avocado (*Persea*), chestnut (*Castanea*), *Citrus*, melon (*Cucumis)*, pecan (*Carya*), potato bean (*Apios*), sugar maple (*Acer*), sugarcane (*Saccharum*), *Vanilla*, and wild rice (*Zizania*) represent the most urgent priorities on average across taxa, whereas U.S. CWR of beans (*Phaseolus*), cherimoya (*Annona*), *Echinacea*, sunflower (*Helianthus*), and squashes (*Cucurbita*) are of lesser concern at present (Khoury et al. 2020).

Many U.S. CWR occur on public lands managed by Federal or state agencies in the United States that could facilitate in situ, dynamic conservation (Bretting and Duvick, 1997). Successful in situ conservation can increase the amount of genetic diversity conserved and eliminate some of the costs and technical difficulties of maintaining CWR in genebanks. Nonetheless, USDA/ARS is not a land management agency. Public lands in the United States are administered by many different agencies with different procedures for establishing and managing protected areas. Consequently, establishing and managing the capacities for in situ conservation involve interagency arrangements that are often complicated and time-consuming to develop. Some NPGS PGR managers and CGCs have identified crops with CWR in the United States (e.g., grape (*Vitis*), apple (*Malus*), and cranberry/blueberry (*Vaccinium*) that could be conserved in situ (Fig. 3.2), but they lack the expertise or resources for establishing such interagency arrangements. Therefore, a coordinated NPGS program to establish and maintain agreements with public land management agencies for in situ conservation of U.S. CWR is planned, and would build on current expertise at the NGRL, augmented by expanded overall NPGS personnel and budgetary resources (Fig. 1.1).

The planned program for in situ conservation of U.S. CWR focuses strategically on the 253 Priority 1A taxa that Khoury et al. (2020) identified but would expand as new species and opportunities were identified. Specific sites for in situ conservation of CWR would be designated for half of these taxa during the next +10 years, at a rate of 13 (5%) per year. Incorporating these taxa into the management plans of land management agencies is a long process dependent on the existence of established procedures, especially for monitoring species and populations of particular interest. It is projected that, in collaboration with these agencies, approximately half of the total sites designated for conservation each year could be included in these agencies' land management plans. Because of its inherent complexities, the process of establishing agreements with land management agencies for in situ conservation of U.S. CWR will extend beyond the 10-year period covered by this Plan. This process will include further field exploration to validate data, fill information gaps about current status, and facilitate access to CWR (Khoury et al. 2020).

Agreements with land management agencies for complementary ex situ/in situ CWR conservation are needed particularly for CWR of crops such as apple (*Malus*), cotton (*Gossypium*), small fruits, sunflower (*Helianthus*), and woody landscape plants (Fig. 3.2). The College Station genebank unit has already established such agreements with state and Federal land management agencies for ca. 1,000 populations of pecan (*Carya*). Based on current discussions and information, the NPGS will seek to incorporate additional species/populations into agencies' land management plans, to conserve in situ those species/populations at +10 years from now (Fig. 3.2). Current U.S. protected areas that safeguard the highest concentration of CWR include the Patuxent Research Refuge and Grand Canyon, Kings Canyon, Olympic, Mount Rainier, Indiana Dunes, Gulf Islands, Yellowstone, Rocky Mountain, and other national parks, shores, and wilderness areas (Khoury et al., 2020). Those protected areas would be priority targets for establishing cooperative agreements for complementary in situ/ex situ conservation. Additional complementary ex situ/in situ CWR conservation programs will require expanded infrastructure, PGR management capacity, and budgetary resources, as noted above, plus addressing applied research needs described below.

Applied Research for Determining Priorities for PGR Acquisitions, In Situ Conservation and NPGS PGR Collection Sizes

The extensive operations described in this Component 3 will be guided by data from the expanded genotypic characterization and genetic diversity assessment program described in Component 10. These data should be combined with information about ecogeographical distributions and genetic profiles of accessions to identify gaps in the NPGS collections' coverage of crop genepools. Genotypic characterization data would also be applied to identify evidence of genetically redundant accessions to be removed from the overall NPGS collection. This research will also refine the priorities for PGR acquisition and in situ CWR conservation goals outlined in this Component. Additional field explorations would be conducted to validate ecogeographical distribution data for CWR in the United States fill information gaps about current CWR status in nature, and extend the current knowledge accumulated by Khoury et al. (2020), with the outcome of facilitate access to these CWR in situ, and from NPGS collections.

Expansion of the NPGS PGR Collection

Primary Type of Germplasm	NPGS Genebank Unit	NPGS Collection Size			Annual New Acquisitions (Avg # Accessions)			Annual Growth Rate		
		Now	+ 5 Yrs.	+ 10 Yrs.	Now	+ 5 Yrs.	+ 10 Yrs.	Now	+ 5 Yrs.	+ 10 Yrs.
	NPGS-wide	**569,197**	**608,384**	**640,414**	**7,934**	**7,840**	**6,408**	**1.4%**	**1.3%**	**1.0%**
	PGR specialization	**523,526**	**557,267**	**583,934**	**7,184**	**6,749**	**5,335**	**1.4%**	**1.2%**	**0.9%**
Managed as Seeds	Aberdeen, ID (NSGC)	136,667	136,932	137,197	206	53	53	0.2%	0.0%	0.0%
Managed as Seeds	Ames, IA (NC7)	53,705	60,580	65,297	323	1,376	945	0.6%	2.3%	1.4%
Managed as Seeds	College Station, TX (COT)	9,813	10,070	10,370	51	51	60	0.5%	0.5%	0.6%
Managed as Seeds	Geneva, NY (NE9)	12,707	13,292	14,032	4	117	148	0.0%	0.9%	1.1%
Managed as Seeds	Griffin, GA (S9)	100,181	109,044	118,030	1,714	1,773	1,797	1.7%	1.6%	1.5%
Managed as Seeds	Parlier, CA (PARL)	1,178	1,278	1,509	1	20	46	0.1%	1.6%	3.1%
Managed as Seeds	Pullman, WA (W6)	100,158	106,299	109,892	1,527	1,228	719	1.5%	1.2%	0.7%
Managed as Seeds	Sturgeon Bay, WI (NR6)	5,834	5,984	6,134	30	30	30	0.5%	0.5%	0.5%
Managed as Seeds	Stuttgart, AR (GSOR)	38,375	39,425	40,460	208	210	207	0.5%	0.5%	0.5%
Managed as Seeds	Urbana, IL (GSZE)	42,411	50,000	55,000	3,000	1,518	1,000	7.1%	3.0%	1.8%
Managed as Seeds	Urbana, IL (SOY)	22,497	24,363	26,013	120	373	330	0.5%	1.5%	1.3%
	PGR specialization	**45,671**	**51,117**	**56,480**	**751**	**1,091**	**1,073**	**1.6%**	**2.1%**	**1.9%**
Managed as Clones	College Station, TX (BRW)	4,108	4,300	4,500	38	38	40	0.9%	0.9%	0.9%
Managed as Clones	Corvallis, OR (COR)	12,855	13,754	14,689	179	180	187	1.4%	1.3%	1.3%
Managed as Clones	Davis, CA (DAV)	7,064	8,494	9,854	77	286	272	1.1%	3.4%	2.8%
Managed as Clones	Geneva, NY (GEN)	7,618	7,924	8,248	43	61	65	0.6%	0.8%	0.8%
Managed as Clones	Hilo, HI (HILO)	1,197	2,295	3,384	37	222	218	3.1%	9.7%	6.4%
Managed as Clones	Mayaguez, PR (MAY)	1,229	1,391	1,516	51	32	25	4.1%	2.3%	1.6%
Managed as Clones	Miami, FL (MIA)	1,545	1,812	2,082	63	53	54	4.1%	2.9%	2.6%
Managed as Clones	Riverside, CA (RIV)	1,687	1,747	1,807	12	12	12	0.7%	0.7%	0.7%
Managed as Clones	Washington, D.C. (USNA)	8,368	9,400	10,400	250	206	200	3.0%	2.2%	1.9%
	Beltsville, MD (NGRL)	0	0	0	500	1,006	688	0.0%		3.0%+

Fig. 3.1: Expansion of the NPGS PGR Collection. The top row of the figure, shaded light beige, depicts the expansion of the total NPGS collection by the current numbers of accessions, and estimates for +5 years and for +10 years; the average numbers of accessions currently acquired annually, and estimates for +5 years and for +10 years; and the current annual rate (percentage) growth for the total collection and estimates for +5 years and for +10 years. The same information is then estimated for individual NPGS genebank units, listed alphabetically by their geographical locations, in two groups. The top group encompasses genebank units that primarily manage seed-propagated crops, and the lower group encompasses genebank units that primarily manage clonally-propagated crops. The higher the annual growth rate the darker the lavender hue, with 3% growth rate the darkest. Totals values for each of the two groups are listed in the first row, shaded light beige, for those groups. The bottom-most row lists the average numbers of accessions collected annually through the plant exploration program operated by the NGRL.

NPGS Support of In Situ PGR Conservation

NPGS Genebank Unit	Crop	Conserved In Situ (# Species/Populations)			Land Management Agency Plans (# Species/Populations)		
		Now	+ 5 Yrs.	+ 10 Yrs.	Now	+ 5 Yrs.	+ 10 Yrs.
	NPGS-wide	**1,108**	**1,175**	**1,214**	**9**	**94**	**193**
Ames, IA (NC7)	Brassicaceae	1	1	1	1	1	1
	Pseudocereals	1	1	1	1	1	1
	Sunflower	3	3	3	3	3	3
Beltsville, MD (NGRL)	Numerous Crops	2	13	13	2	7	7
College Station, TX (BRW)	Pecan	1,000	1,000	1,000	1	10	20
College Station, TX (COT)	Cotton	100	100	100	0	50	100
Corvallis, OR (COR)	Hazelnuts CWR	0	0	5	0	0	5
	Hops CWR	0	0	5	0	0	5
	Mint CWR	0	0	3	0	0	3
	Ribes CWR	0	0	5	0	0	5
	Rubus CWR	0	0	5	0	0	5
	Strawberry CWR	0	0	5	0	0	5
	Vaccinium CWR	0	0	5	0	0	5
Geneva, NY (GEN)	Apple CWR	0	2	4	0	2	4
	Grape CWR	0	3	5	0	3	5
Griffin, GA (S9)	Pepper	1	1	1	1	1	1
Parlier, CA (PARL)	Parthenium	0	0	1	0	0	1
Pullman, WA (W6)	Allium CWR	0	0	1	0	0	1
Washington, D.C. (USNA)	Woody Landscape	0	51	51	0	16	16

Fig. 3.2: NPGS Support of In Situ PGR Conservation. In addition to conserving PGR in its genebank units, the NPGS also supports in situ PGR conservation primarily in partnership with land management agencies. The top row of the figure table, shaded beige, estimates the total number of individual populations or species for which the NPGS currently provides such support, and goals for +5 years and for +10 years. The total number of individual populations or species currently included in land management agency plans, and goals for +5 years and +10 years are also provided. The same information is then estimated for individual NPGS genebank units that provide such support and the specific crops, groups of crops, or CWR, listed alphabetically, for species or populations conserved in situ.

Component 4: Safeguarding PGR Through Long-Term Storage (Figs. 4.1-4.5).

Current Status

The PGR managed as seeds at NPGS genebank units are stored in moisture-controlled, medium-term refrigerated (41˚F, 5˚C) or long-term freezer (0˚F, -18˚C) facilities. The PGR managed as clones are maintained as plantings in the field, greenhouse, screenhouse, or as in vitro plantlets in laboratories. Plant genetic resources maintained at a single site can be vulnerable to natural disasters, equipment failures, and human error. To minimize the risk of losing valuable PGR, duplicate samples of each NPGS accession should be secured in at least two geographically separated locations (FAO, 2014; Engels et al., 2003).

The National Laboratory for Genetic Resources Preservation (NLGRP) serves as the NPGS's high-security, long-term storage facility for this purpose. It applies resident cryobiological expertise to preserve the viability of duplicate accessions in the smallest possible space for the longest possible time. The NLGRP has the capacity to store 2.5 million samples and currently houses more than 1.2 million (i.e., its cold storage vaults are half full). Of the NPGS's current 514,000+ accessions covered by this Plan, 410,000+ (80%) are duplicated at the NLGRP (Figs. 4.1, 4.2, 4.3). An additional 47,000+ accessions of maize and rice genetic stocks, of which ca. 18% are duplicated at NLGRP, are also part of the NPGS collection, but duplication data from those genebank units are analyzed separately as explained below. The NLGRP also provides essential storage for duplicate samples of non-NPGS PGR collected by universities, other Agencies, foreign countries, the CGIAR, and conservation groups within the United States.

The safety provided by duplication is enhanced when samples meet additional quality and quantity criteria that minimize the risks of losing viability or genetic identity (FAO, 2014; Engels et al., 2013). Samples meeting these criteria are considered "backed-up." Currently, 19% of the NPGS accessions meet the applicable technical criteria for back-up (Figs. 4.1, 4.3). The following back-up criteria differ for seeds and clonal propagules (e.g., shoot tips or dormant buds) because there are different risks for genetic shifts that can accompany the back-up process (Volk and Walters, 2004; Walters et al., 2018):

- A seed sample having 2,000+ seeds with 85+% viability in a test conducted within 15 years (i.e., a recent test; modified slightly from FAO, 2014).

- A clonally-propagated sample having 60+ viable propagules with 40+% normal regrowth following cryoexposure (Volk et al., 2017a; Panis and Nagel, 2020).

About 86% of the accessions from NPGS genebank units that manage predominantly seed-propagated crops currently are duplicated and ca. 20% are backed-up (Figs. 4.1, 4.3). In contrast, ca. 14% of the accession at genebank units managing predominantly clonally propagated crops are duplicated and ca. 8% are backed-up. The extensive biological diversity of the PGR managed by NPGS is the root cause of the variation in duplication and back-up proportions among PGR from different genebank units and crops. Accessions of crops such as cereals and pseudocereals are almost fully duplicated (98 - 100%, Fig. S4.3a) because the species typically produce many highly vigorous seeds that mature simultaneously. Fewer viable seeds are produced by other

crops, depending on pollen availability or seed developmental patterns. Crop wild relatives (CWR) often yield fewer seeds with lower germination capacity as compared to their domesticated counterparts. Among PGR maintained as seeds, low rates of back-up also result from the back-up quality criteria, namely 85% viability and 15-year monitoring intervals. Initial low viability is sometimes a challenge for backing-up CWR. For all PGR, viability can decrease as time in storage increases, requiring detection by monitor testing (discussed later in Component 5).

Genetic stocks of grain crops comprise some of the NPGS collections with the lowest (near 0%) proportion of duplicated or backed-up accessions, as a result of numerous factors. Genetic stocks are produced under specific methodological conditions that yield small sample sizes and genetically true-to-type stocks generally cannot be recreated. Furthermore, some genetic stocks serve as research tools that will become less relevant through time as they are superseded by newer genetic stocks and once the original seed supplies are depleted.

Biological barriers to long-term storage are pronounced for PGR of clonally propagated crops because the propagules are highly sensitive to preservation conditions and must undergo extensive cryoprotection prior to long-term storage (Panis and Nagel, 2020). Of the 47,000+ accessions at genebank units managing predominantly clonal PGR, 7,000+ (14% of total) accessions are duplicated at the NLGRP (Figs. 4.1, 4.3). The relatively high duplication rates of apple, strawberry, and citrus (Fig. S4.3a) illustrate the potential for developing technologies to preserve clonal PGR, as well as concerted efforts to duplicate PGR from CWR of those crops in the form of seeds (Volk and Walters, 2004; Volk et al., 2017b; Walters et al., 2018). Duplication and back-up of PGR from genebank units that manage tropical crops present the most formidable challenges because both seeds and clonal propagules for those crops are often highly sensitive to the cold or dry conditions required for long-term storage (Walters et al., 2013). For some of those difficult-to-store PGR of tropical crops, the high risk of loss is mitigated by cultivating duplicate plantings of the same accessions at two locations (e.g., accessions of avocado (*Persea*) planted at the Miami and Hilo genebank units), although this tactic can be quite costly and insecure as compared to long-term storage. Clonally-propagated accessions of other crops (e.g., sweet potato (*Ipomoea*), and banana and plantain (*Musa*) are duplicated in vitro (i.e., tissue culture), which is labor-intensive.

The NLGRP operates two storage platforms to preserve the viability of the NPGS's seeds, pollen, and clonal propagules. Conventional storage in regular freezers maintains 88% of NLGRP's holdings as seeds, which have an innate ability to survive at freezer temperatures (-18˚C, 0˚F) if dried properly (Figs. 4.2b, 4.4; Walters et al., 2005; FAO, 2014). The remaining 12% of the NPGS accessions at the NLGRP are safeguarded in cryogenic storage, which takes advantage of the low temperature and availability of liquid nitrogen (LN, ~ -196˚C, -321˚F). Liquid nitrogen storage of most crop seeds is an optional method (Walters et al., 2004). In contrast, storage at the temperature of LN is mandatory for preserving the viability of clonal propagules, pollen and seeds that do not survive in the freezer (Panis and Nagel, 2020; Volk et al., 2012; Tanner et al., 2020). These physiological differences among propagule types are reflected by the extent to which conventional and cryogenic storage are enlisted to preserve viability: 89% of the accessions from genebank units that manage predominantly PGR as seeds

are stored in the NLGRP freezer, whereas 73% of the accessions from genebank units managing PGR primarily as clones are stored cryogenically at the NLGRP (Figs. 4.2b, 4.4).

The NLGRP receives 4,000+ samples from other NPGS genebank units each year, leading to a duplication rate for the overall NPGS collection of about 0.8% per year (Fig. 4.3c; 514,000 x 0.008 = 4112 accessions). Most of these samples originate from genebank units managing PGR primarily as seeds. Approximately 300 samples per year originate from genebank units managing PGR primarily as clones. Based on the current rates of sample submission to the NLGRP, the accessions from genebank units that manage PGR primarily as seeds can be 95% duplicated and 80% backed-up in ca. 14 and 22 years, respectively (estimates for duplications based on data shown in Figs. 4.5 and S4.5 and internal NLGRP data for back-ups; Figs. S4.3a, b, and c provide additional data). In contrast, based on the current annual rate (0.6% of total number of accessions) that genebank units managing PGR primarily as clones send duplicate samples to the NLGRP, 95% duplication and 80% back-up levels are anticipated in ca. 56 and 85 years, respectively (estimates for duplications based on data shown in Fig. 4.5 and internal NLGRP data for back-ups; Figs. S4.3a, b, and c provide additional data).

Duplicate samples from 139,000+ NPGS accessions are currently stored as seeds in the Svalbard Global Seed Vault ("Svalbard" hereafter; Fowler, 2016), representing nearly 27% of NPGS's total collection. Submissions to Svalbard have occurred every other year since 2008 at a rate of 4.5% per every 2 years. Svalbard maintains PGR in conventional freezer storage (-18˚C, 0˚F), which is suitable for many seed-propagated crops, but not suitable for shoot tips, dormant buds, pollen, or seeds from most nut or tropical fruit crops. The extent of future duplication of NPGS PGR at Svalbard is not described in this Plan; nonetheless, this process is envisioned to continue as a byproduct of regenerating seed-propagated PGR, with aliquots of samples surpassing the NPGS back-up criterion of 2,000 seeds to be sent to Svalbard for safekeeping.

Strategies and Implementation

This Plan has the goal of increasing the total proportion of NPGS accessions safeguarded by duplication at the NLGRP at an overall rate of ca. 0.8% per year from the current level of 80% to 82% at +5 and 83% at +10 years (Figs. 4.1, 4.3). These percentage changes might seem modest, but when translated into numbers are equivalent to ca. 17,000 more accessions that are safeguarded by duplication. These figures were estimated according to current projections for growth of the NPGS collection, resource availability, PGR managerial capacity, and available long-term storage and regeneration technologies (see Components 1 and 3; Fig. 4.1). For genebank units managing clonal crops, recently completed research for cryopreserving clonal propagules, as well as seeds and pollen of CWR, will be implemented to increase the rate of duplication incrementally from the current rate of 0.6% per year to about 1% per year (Fig. 4.3c) and increase safety duplication of accessions at genebank units specializing in clonally-propagated PGR from the current level of 14% (Fig. 4.3a) to 18% and 21% at +5 and +10 years (Figs. 4.3a, 4.1a). These goals for clonally-propagated crops are very ambitious. Attaining these outcomes successfully will depend on both expanded PGR management and research capacities (Component 1) and the impact of research to develop new clonal preservation methods.

The choice of conventional or cryogenic storage for accessions stored as seeds will continue to be considered strategically in terms of the added costs of LN storage and the benefits gained in terms of shelf-life. As an overall strategy, fewer accessions of seeds that store well in conventional freezers will be placed in cryogenic storage in the future. The use of cryogenic storage will increase to accommodate the growing number of clonal propagules that can be cryopreserved, as well as the seeds from accessions of taxa known to store poorly under conventional conditions (Figs. 4.2, 4.4).

The strategy described in the prior paragraphs increases the proportion of NPGS accessions duplicated in long-term storage, but about 17% (97,000) of the total NPGS PGR covered by this Plan would still require duplication at +10 years. Should technical advances (see Applied Research below) occur, and additional resources become available, the NPGS would seek to safeguard 84% of the total number of accessions in duplicate storage at the NLGRP at +5 years and 87% at +10 years. To attain these ambitious goals, an additional 46,000 and 41,000 samples of accessions would need to be duplicated at the NLGRP at +5 years and +10 years, respectively, for a total of 87,000 more accessions than at present. Increasing the number of the most vulnerable clonally-propagated accessions that are duplicated at the NLGRP from the projected level of 21% at +10 years (following the strategy described in the prior paragraph, Fig. 4.1a) to 30% at +10 years would require that 10,000 of the total 87,000 accessions originate from genebank units that specialize in clonally-propagated, tropical or woody landscape crops. This ambitious +10-year goal would require an increase of accessions transmitted from those genebank units to the NLGRP from ca. 300 annually to 1,300 annually. Successfully placing an additional 1,000 samples per year (~400 as clonal propagules and ~600 as seeds and pollen from CWR) in cryostorage at the NLGRP will require not only substantial additional cryobiological expertise and capacity at the NLGRP mentioned earlier, but also increased resources for regenerating more accessions at other genebank units (Component 7).

Applying back-up quality criteria is an important strategy for mitigating the risk that accessions placed in long-term storage die without detection of their deteriorating condition. Such a strategy can also help ensure that the propagules in storage remain sufficiently vigorous to regenerate the accessions. Currently, just 19% of the NPGS accessions are backed-up according to FAO criteria (Figs. 4.1a, 4.3b), with projected back-up percentages of 28% and 35% at +5 and +10 years (Figs. 4.1a, 4.3b). At present, about 0.2% of the accessions in the NPGS collection are successfully backed-up each year, a proportion predominantly determined by the FAO criteria for backing-up PGR as seeds. The back-up rate is projected to increase to 1.5% per year (Fig. 4.1b) according to this Plan, based on increased capacity of genebank units to regenerate accessions and increased capacity of the NLGRP to test the viability of accessions at prescribed frequencies. Furthermore, the genebank units will strive to provide the NLGRP with more seeds per sample, to satisfy the FAO criterion of 1,500-2,000 seeds per back-up sample (FAO, 2014).

Currently, 76% of NPGS PGR (312,000+ samples) duplicated at the NLGRP do <u>not</u> meet FAO standards for back-up that attain the outcome of ensuring security against losses from aging during storage and loss of genetic integrity during regeneration (Fig. 4.1c). Changed procedures (prior paragraph) will have the impact of reducing this percentage to 58% (273,000+ samples at NLGRP) in +10 years (Fig. 4.1c). A highly ambitious goal to reduce the percentages of NPGS accessions <u>not</u> backed up to 50% and 30% within +5 and +10 years, respectively, will require

that an additional 73,000+ accessions, and then another 58,000+ accessions, meet back-up criteria, respectively. A multi-pronged strategy is needed to meet an increased processing rate of 12,000 to 18,000 samples per year at the NLGRP. More than half of this outcome can be achieved through the strategy of adopting more sensitive monitoring technologies that reduce the risk of PGR dying during storage (see Component 5). About 30% of the goal can be achieved through increasing the number of accessions regenerated (see Component 7) to address the priority of providing new seeds to replace those that have aged during storage. Another 20% of the outcome can be achieved by strategically reducing the sample sizes needed for conserving PGR (Component 5) and increasing genebank units' capacity to produce the needed volume of seeds during regenerations (Component 7). Consequently, securing and implementing additional financial resources to expand the NPGS's PGR maintenance and research capacities (Fig. 1.1, Appendix B) and to devise novel long-term PGR preservation methods (see subsequent section) are high priorities for this Plan.

Applied PGR Preservation Research

The broad array of biologically diverse PGR managed in the NPGS requires a range of strategies for long-term storage (Walters et al., 2018). Applied research is needed to identify the conditions that prolong PGR lifespans; that information can be applied to devise cost-effective storage conditions to deliver viable PGR to users indefinitely. Such research addresses several major bottlenecks to progress with PGR duplication and back-up, such as slow processing of PGR for storage and unsuccessful recovery of PGR from reduced temperatures. Related research on the long-term survival of PGR in storage is discussed in Component 5. More comprehensive knowledge of the reproductive biology of PGR (Component 7) and of the genetic composition of PGR collections (Component 10) is vital for devising regeneration/repropagation methods that yield the goal of generating sufficient quantities of viable, genetically representative PGR to safely preserve in long-term storage at the NLGRP.

Difficult-to-store propagules are the primary reason for low rates of duplicating PGR at the NLGRP. Superior cryobiotechnologies would provide essential tools for attaining the goal of increasing survival, recovery, and processing speed of propagules that are difficult-to-store (Pence et al., 2020; Walters and Pence, 2020). Research will be conducted to devise more effective general cryoprotection methodology (Reed, 2008); develop strategies that obviate time-consuming in vitro processing steps (Volk et al., 2012; Ellis et al., 2006); improve recovery of propagules from low-temperature storage through microculture (O'Brien et al., 2020; Walters et al., 2013); and formulate approaches that exploit the natural abilities of plants from temperate climates to acclimate to intense cold (Tanner et al., 2020).

The PGR from some tropical crops, such as lychee (*Litchi*), avocado (*Persea*), and mango (*Mangifera*), continue to present challenges for maintenance in vitro and survival after cryoexposure. Developing alternative low-temperature storage approaches that consider metabolic responses of tropical compared to temperate plants following stress, wounding, and repair (Pammenter and Berjak, 2014) could prevent hyper-oxidative reactions that lead to morbidity and create bottlenecks to preserving PGR from genebank units at Hilo, Mayagüez, and Miami.

Plant endophytes (the microbiome) are implicated in the reduced survival of PGR when resuscitated following cryo-exposure (Wang et al., 2009). Endophytes can also be a transmission route for emerging diseases among distributed accessions. Research must be conducted to develop more effective methods for indexing and identifying endophytes and understanding the positive and negative roles they play in plant phenotypes. As part of this strategy, the capacity of cryotherapies to rid pathogens from PGR and to enhance survival of PGR during long-term storage will also be assessed (Wang et al. 2009).

Major bottlenecks to PGR inventory control can arise from the process of assessing seed quality and quantity. Automated, nondestructive imaging and sensor systems could provide solutions to current methods that are labor-intensive and consume valuable seeds. The automated systems also can generate detailed evaluation data to assess seed traits, growth requirements and responses to stress challenges (Colmer et al., 2020; Watt et al., 2020). Within +5 years, a priority of the NLGRP is to implement multispectral scanning and machine learning technologies to confirm taxonomic identifications; obtain seed size information; generate insights related to seed composition; count out seeds for viability testing; and even assay for biochemical markers that detect the earliest stages of PGR aging. In +10 years, automated systems for measuring seed germination could be available for assessment and implementation.

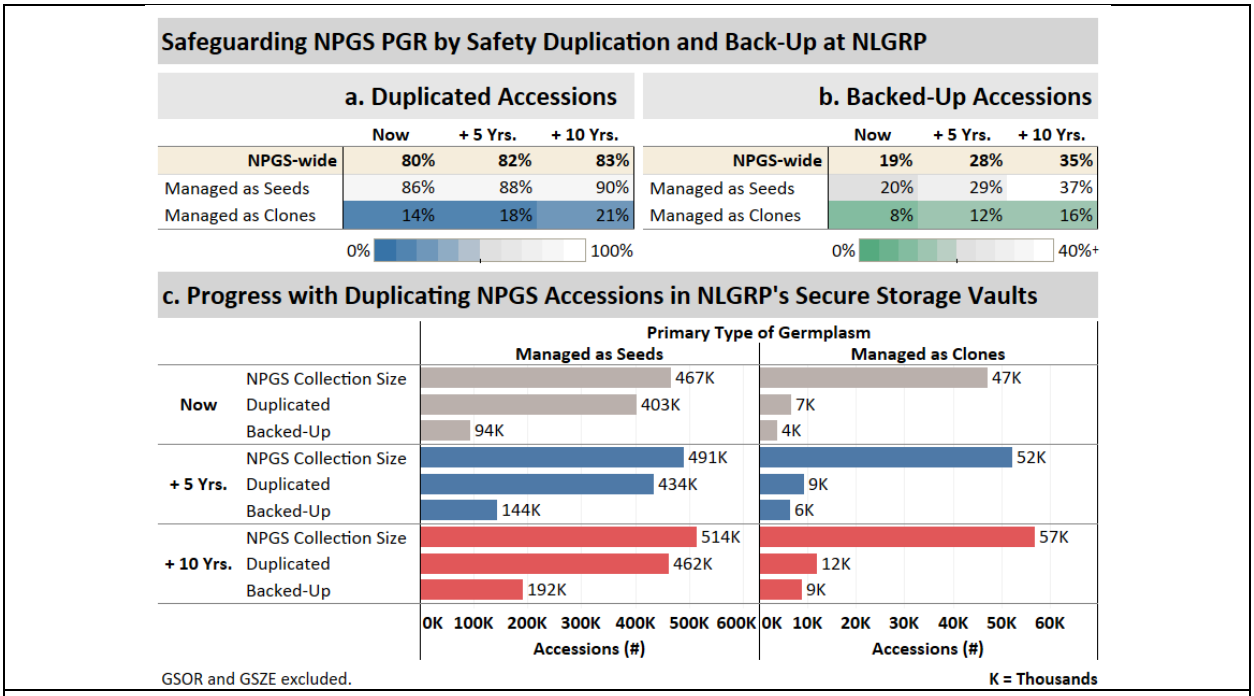


Fig. 4.1: Safeguarding NPGS PGR by Safety Duplication and Back-Up at NLGRP. The top panels compare current and future (+5 years and +10 years) safety duplication (4.1a) and back-up (4.1b) percentages for the NPGS collections overall (top row shaded light beige) and among genebank units that primarily manage accessions in the form of seeds or as clones. The percentage of accession duplication from genebank units primarily managing accessions as clones currently is extremely low (0% duplication the darkest blue hue), increasing at about 2% per year at +5 years and +10 years, assuming current PGR management capacities. The percentages of accessions backed-up from genebank units primarily managing accessions both in the form of seed and clonally currently are very low (0% duplication the darkest green hue), with incremental increases at +5 and +10 years, assuming current PGR management capacities.
The bottom panel Fig 4.1c describes the numbers of accessions from NPGS genebank units primarily managing accessions in the form of seeds (left) or clonally (right) that are currently duplicated at the NLGRP (gray bars) as well as future (blue bars for +5 years, rust red bars for +10 years) goals for duplication based on current PGR management capacities.
Accessions at GSOR and GSZE are excluded because they are genetic stocks; see text.

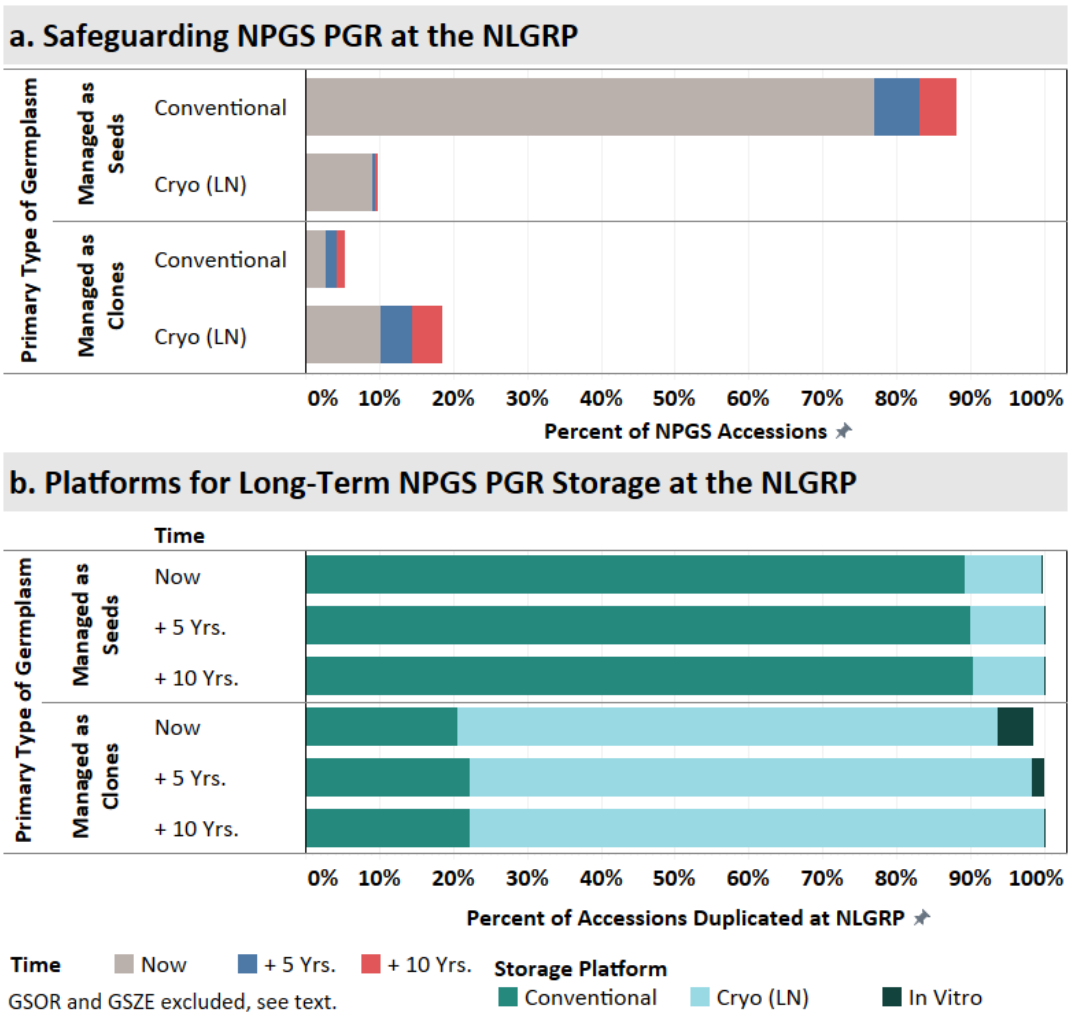


Fig. 4.2: Safeguarding NPGS PGR at NLGRP.

Fig. 4.2a depicts the current numbers of NPGS accessions (gray bar) duplicated at the NLGRP and future goals (blue bars +5 years, rust red bars +10 years) for duplication by conventional storage (in freezers, -18˚C, 0˚F) and cryogenically (liquid nitrogen at -196˚C, -321˚F) for genebank units that primarily manage accessions in the form of seed or as clones. Most of the accessions managed in the form of seeds are placed in conventional storage because that is a cost-effective platform to achieve a shelf-life of at least 50 years (Walters et al., 2005), and the benefits of seed cryopreservation currently remain unestablished (Walters et al., 2004). In contrast, most of the accessions managed primarily as clones are necessarily cryopreserved in LN (Panis and Nagel, 2020), with the smaller proportion of accessions managed as seeds from CWR of clonally-propagated PGR sometimes placed in freezer storage.

Fig. 4.2b describes the goals for increases in +5 and +10 years for the numbers of NPGS accessions primarily managed in the form of seeds and primarily managed as clones that are duplicated in conventional (green bars) and cryogenic (aqua) storage at the NLGRP. The minimal use of in vitro cultures to maintain accessions also is illustrated (dark green). The small gap between the total percentage of accessions duplicated and 100% in the 'Now' bar for primarily clonally-propagated accessions arises from idiosyncrasies of preserving seeds from plants that usually are managed clonally. The proportions of accessions from individual genebank units that are stored either conventionally or cryogenically are detailed in Fig 4.4.

Accessions at GSOR and GSZE are excluded because they are genetic stocks; see text.

Safety Duplication, Back-Up, and Annual Growth Rate in Duplication of the NPGS PGR Collections at NLGRP

Primary Type of Germplasm	NPGS Genebank Unit	a. Duplicated Now	a. Duplicated + 5 Yrs.	a. Duplicated + 10 Yrs.	b. Backed-Up Now	b. Backed-Up + 5 Yrs.	b. Backed-Up + 10 Yrs.	c. Annual Growth Now	c. Annual Growth + 5 Yrs.	c. Annual Growth + 10 Yrs.
	NPGS-wide	**80%**	**82%**	**83%**	**19%**	**28%**	**35%**	**0.8%**	**1.7%**	**1.6%**
	PGR specialization	**86%**	**88%**	**90%**	**20%**	**29%**	**37%**	**0.9%**	**1.7%**	**1.7%**
Managed as Seeds	Aberdeen, ID (NSGC)	95%	95%	96%	25%	30%	34%	0.1%	0.1%	0.1%
Managed as Seeds	Ames, IA (NC7)	81%	84%	87%	21%	31%	41%	1.1%	2.9%	2.6%
Managed as Seeds	College Station, TX (COT)	59%	59%	59%	6%	11%	15%	0.5%	1.0%	0.9%
Managed as Seeds	Geneva, NY (NE9)	73%	79%	82%	27%	41%	51%	1.9%	4.2%	4.3%
Managed as Seeds	Griffin, GA (S9)	89%	90%	92%	15%	24%	33%	0.4%	1.6%	1.5%
Managed as Seeds	Parlier, CA (PARL)	36%	34%	35%	8%	10%	12%	0.1%	2.1%	2.7%
Managed as Seeds	Pullman, WA (W6)	77%	81%	83%	20%	33%	44%	1.8%	2.6%	2.5%
Managed as Seeds	Sturgeon Bay, WI (NR6)	84%	90%	92%	25%	40%	53%	2.5%	2.3%	2.2%
Managed as Seeds	Urbana, IL (SOY)	98%	100%	100%	16%	30%	43%	2.3%	4.6%	4.8%
	PGR specialization	**14%**	**18%**	**21%**	**8%**	**12%**	**16%**	**0.6%**	**1.1%**	**1.0%**
Managed as Clones	College Station, TX (BRW)	1%	4%	7%	0%	2%	4%	0.0%	0.8%	0.7%
Managed as Clones	Corvallis, OR (COR)	16%	22%	26%	8%	14%	18%	0.7%	1.4%	1.3%
Managed as Clones	Davis, CA (DAV)	1%	5%	9%	0%	5%	9%	0.0%	1.1%	1.0%
Managed as Clones	Geneva, NY (GEN)	47%	53%	57%	36%	41%	45%	2.1%	2.1%	1.9%
Managed as Clones	Hilo, HI (HILO)	1%	17%	25%	0%	17%	31%	0.0%	4.0%	3.6%
Managed as Clones	Mayaguez, PR (MAY)	14%	23%	30%	6%	16%	24%	0.7%	2.4%	2.2%
Managed as Clones	Miami, FL (MIA)	8%	8%	8%	1%	1%	1%	0.1%	0.1%	0.1%
Managed as Clones	Riverside, CA (RIV)	15%	23%	30%	14%	22%	29%	0.7%	1.9%	1.8%
Managed as Clones	Washington, D.C. (USNA)	5%	6%	6%	1%	1%	2%	0.1%	0.1%	0.1%

GSOR and GSZE excluded.

0% 100% 0% 40%+ 0.0% 2.0%+

Fig. 4.3: Safety Duplication, Back-Up, and Annual Growth Rate in Duplication of the NPGS PGR Collections at NLGRP. The data represent the proportion of PGR that are placed in the NLGRP (duplicated) and meet FAO standards for quantity and quality (backed-up), as well as the annual rate of increase in the number of accessions duplicated at the NLGRP.

The top row of Fig. 4.3a, shaded light beige, reports the percentages of the accessions in the total NPGS collection that currently are safeguarded by duplication at the NLGRP and the goals for safety duplication at +5 years and at +10 years. The NPGS genebank units are listed below by their geographical locations. Genebank units managing predominantly seed-propagated and clonally-propagated crops are listed in the upper and lower portions of the figure, respectively. The lower the percentage of accessions of the individual genebank unit collections that are duplicated at the NLGRP, the darker the blue hue, with 0% duplication the darkest.

The top row of Fig. 4.3b, shaded light beige, reports the percentages of the accessions in the total NPGS collection that currently are safeguarded by back-up at the NLGRP and the goals for back-up at +5 years and at +10 years. The NPGS genebank units are listed below according to their geographical locations. Genebank units managing predominantly seed-propagated and clonally-propagated crops are listed in the upper and lower portions of the figure, respectively. The lower the percentage of accessions of the individual genebank unit collections that are backed-up at the NLGRP, the darker the green hue, with 0% duplication the darkest.

The top row of Fig. 4.3c, shaded light beige, reports the average annual rates (percentages) whereby the accessions in the total NPGS collection currently are duplicated in the NLGRP and the goals for the annual duplication rates at +5 years and at +10 years. The NPGS genebank units are listed below according to their geographical locations. Genebank units managing predominantly seed-propagated and clonally-propagated crops are listed in the upper and lower portions of the figure, respectively. The lower the average annual rate (percentage) of accessions at individual genebank unit collections that are duplicated at the NLGRP, the darker the lavender hue, with 0% average annual rate of duplication the darkest.

Accessions at GSOR and GSZE are excluded because they are genetic stocks; see text. Transfers of accessions to the NLGRP and the annual growth in the number of accessions in the NLGRP collections are approximated for +5 and +10 years based on current NPGS PGR managerial capacities.

Percentages of Duplicated NPGS PGR Maintained Under Two Storage Conditions at the NLGRP

Primary Type of Germplasm	NPGS Genebank Unit	a. Conventional Freezer: Now	a. Conventional Freezer: + 5 Yrs.	a. Conventional Freezer: + 10 Yrs.	b. Cryo (LN): Now	b. Cryo (LN): + 5 Yrs.	b. Cryo (LN): + 10 Yrs.
	NPGS-wide	**88%**	**88%**	**88%**	**12%**	**12%**	**12%**
Managed as Seeds	**PGR specialization**	**89%**	**90%**	**90%**	**11%**	**10%**	**10%**
Managed as Seeds	Aberdeen, ID (NSGC)	92%	92%	93%	8%	8%	7%
Managed as Seeds	Ames, IA (NC7)	83%	85%	86%	16%	15%	14%
Managed as Seeds	College Station, TX (COT)	100%	100%	100%	0%	0%	0%
Managed as Seeds	Geneva, NY (NE9)	72%	77%	79%	26%	23%	21%
Managed as Seeds	Griffin, GA (S9)	90%	90%	90%	10%	10%	10%
Managed as Seeds	Parlier, CA (PARL)	70%	70%	70%	30%	30%	30%
Managed as Seeds	Pullman, WA (W6)	88%	89%	90%	12%	11%	10%
Managed as Seeds	Sturgeon Bay, WI (NR6)	36%	44%	46%	60%	56%	54%
Managed as Seeds	Urbana, IL (SOY)	100%	100%	100%	0%	0%	0%
Managed as Clones	**PGR specialization**	**21%**	**22%**	**22%**	**73%**	**76%**	**78%**
Managed as Clones	College Station, TX (BRW)	0%	0%	0%	100%	100%	100%
Managed as Clones	Corvallis, OR (COR)	29%	33%	34%	55%	63%	66%
Managed as Clones	Davis, CA (DAV)	5%	2%	0%	95%	99%	100%
Managed as Clones	Geneva, NY (GEN)	0%	6%	9%	100%	94%	91%
Managed as Clones	Hilo, HI (HILO)	0%	1%	0%	0%	99%	99%
Managed as Clones	Mayaguez, PR (MAY)	0%	0%	0%	44%	86%	100%
Managed as Clones	Miami, FL (MIA)	0%	0%	0%	100%	100%	100%
Managed as Clones	Riverside, CA (RIV)	0%	0%	0%	100%	100%	100%
Managed as Clones	Washington, D.C. (USNA)	99%	92%	87%	1%	8%	13%

GSOR and GSZE excluded. 0% 100% 0% 50%+

Fig. 4.4: Percentages of Duplicated NPGS PGR Maintained Under Two Storage Conditions at the NLGRP. The top row of Fig. 4.4a, shaded light beige, reports the percentages of the accessions in the total NPGS collection that currently are duplicated under conventional freezer conditions at the NLGRP and the goals for such safety duplication at +5 years and at +10 years. The NPGS genebank units are listed below by their geographical locations. Genebank units managing predominantly seed-propagated and clonally-propagated crops are listed in the upper and lower portions of the figure, respectively. The lower the percentage of accessions of the individual genebank unit collections duplicated under conventional freezer conditions at the NLGRP, the darker the teal hue, with 0% duplication the darkest.

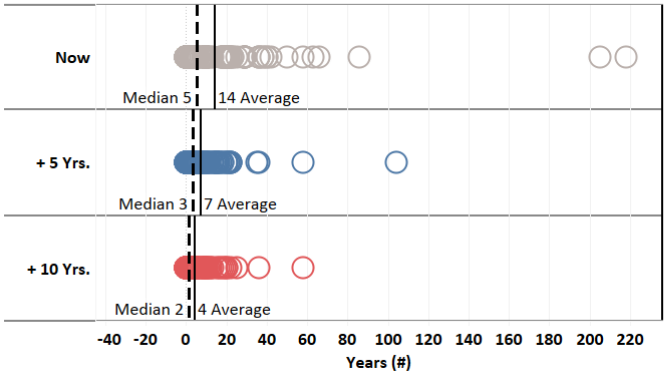
The top row of Fig. 4.4b, shaded light beige, reports the percentages of the accessions in the total NPGS collection that currently are duplicated under cryogenic conditions at the NLGRP and the goals for back-up at +5 years and at +10 years. The NPGS genebank units are listed below according to their geographical locations. Genebank units managing predominantly seed-propagated and clonally-propagated crops are listed in the upper and lower portions of the figure, respectively. The lower the percentage of accessions of the individual genebank unit collections duplicated under cryogenic conditions at the NLGRP, the darker the aqua hue, with 0% duplication the darkest.

Accessions at GSOR and GSZE are excluded because they are genetic stocks; see text. Transfers of accessions to the NLGRP from NPGS genebank units are approximated for +5 and +10 years based on current NPGS PGR managerial capacities.

a. Time Needed to Reduce the Backlogs in NPGS PGR Safety Duplication at the NLGRP

Primary Type of Germplasm Managed	NPGS Genebank Unit	Now MIN (Years)	Now Avg. of Medians	Now MAX (Years)	+5 Yrs. MIN (Years)	+5 Yrs. Avg. of Medians	+5 Yrs. MAX (Years)	+10 Yrs. MIN (Years)	+10 Yrs. Avg. of Medians	+10 Yrs. MAX (Years)
	NPGS-wide	**0**	**14**	**395**	**0**	**7**	**60**	**0**	**4**	**60**
Managed as Seeds	Aberdeen, ID (NSGC)	1	1	2	1	1	1	1	1	1
	Ames, IA (NC7)	0	24	395	1	15	60	1	9	60
	College Station, TX (COT)	20	20	20	10	10	10	5	5	5
	Geneva, NY (NE9)	1	15	50	1	7	17	1	5	14
	Griffin, GA (S9)	0	2	18	0	1	5	0	1	3
	Parlier, CA (PARL)	10	16	20	5	11	15	1	6	10
	Pullman, WA (W6)	0	23	84	1	6	16	1	2	5
	Sturgeon Bay, WI (NR6)	5	5	5	5	5	5	5	5	5
	Urbana, IL (SOY)	1	3	5	1	3	5	1	3	5
Managed as Clones	College Station, TX (BRW)	205	205	205	35	35	35	16	16	16
	Corvallis, OR (COR)	6	20	66	2	9	20	1	3	12
	Davis, CA (DAV)	20	20	20						
	Geneva, NY (GEN)	2		10	2		10	2		5
	Hilo, HI (HILO)	0	0	0	0	11	20	4	12	20
	Mayaguez, PR (MAY)	1	5	5	1	3	5	1	2	5
	Miami, FL (MIA)	0	0	0	11	1	11	8	1	8
	Riverside, CA (RIV)	19	24	28	15	19	22	11	15	19
	Washington, D.C. (USNA)	1	5	30	1	5	30	1	5	30

b. Median Years Needed to Reduce the Backlogs



Years 0 20+

Estimates assume resources documented in Component 1. The darkest hue indicates an estimated 20+ years are needed to reduce the backlog. Blank fields indicate the data could not be estimated.

Bottom graph depicts the median of each crop aggregated by time point. Vertical dashed line represents median of medians and vertical solid line reflects average of medians.

GSOR and GSZE excluded.

Fig. 4.5: Time Needed to Reduce the Backlogs in NPGS PGR Safety Duplication at the NLGRP. Time estimated by PGR managers to remove duplication backlogs (i.e., accessions that need to be duplicated). PGR managers estimated times based on numerous factors including current rates of submissions to the NLGRP, regeneration plans, anticipated resources, and strategies to duplicate at other NPGS genebank units or botanical garden partners.

The top row of Fig. 4.5a, shaded light beige, reports for the total NPGS collection the current extreme minima, extreme maxima, and the average median number of years needed to reduce the backlogs, as much as is feasible, for the safety duplication of accessions at the NLGRP, and goals for reducing the backlog for +5 years and +10 years. The range and median number of years needed to reduce the backlog of PGR back-up at individual NPGS genebank units, according to the best estimates of the PGR managers, then are listed below by the genebank units' geographical locations. The genebank units that primarily manage seed-propagated PGR are in the top portion of the figure, and those that primarily manage clonally-propagated PGR are below them. The more time needed to reduce the backlogs for the individual genebank unit collections, the darker the aqua hue. The darkest hue indicates an estimated 20+ years are needed to reduce the backlog. Many of the longest backlogs result from a current lack of effective means for duplicating the PGR, which will be the focus of applied research in this Plan. Blank fields indicate that data could not be estimated.

Figure 4.5b depicts the current medians, for all the NPGS PGR, for the numbers of years needed to reduce the backlogs for duplicating NPGS accessions at the NLGRP, and the goals for reducing the backlogs at +5 years and +10 years. The current median numbers of years needed to reduce the backlogs in duplicating individual crops and CWR are denoted by light gray circles, the goals for reducing the backlogs at +5 years by blue circles, and the goals for +10 years by rust red circles. The medians of medians for the numbers of years, across all PGR, needed to reduce backlogs are depicted by dashed vertical lines, and averages of medians for the number of years, across all PGR, needed to reduce backlogs are depicted as solid vertical lines.

Accessions at GSOR and GSZE are excluded because they are genetic stocks; see text. Transfers of accessions to the NLGRP from NPGS genebank units are approximated for +5 and +10 years based on current NPGS PGR managerial capacities.

Component 5: Germination, Viability, and Longevity Testing of PGR Accessions (Figs. 5.1-5.3)

Current Status

The NPGS's diverse PGR must retain the capacity to grow and reproduce after years or decades of storage. Thus, it is a priority to detect deteriorating health in storage expeditiously to ensure that the propagules can be regenerated before dying. Viability and vigor are not readily apparent in stored PGR, therefore small subsets of each sample must be periodically retrieved from storage and grown to confirm viability and availability. Consequently, viability tests for stored PGR comprise a critical component of PGR maintenance programs (FAO, 2014; Fu, 2017; Hay and Sershen, 2020) and require substantial investment in personnel and, in some cases, contracts with service testing laboratories.

Collectively, the NPGS conducts 30,000+ viability tests annually (Fig 5.1a). Testing at genebank units comprise about 76% of these viability assessments, with about 3% of the total number of accessions tested for viability each year (Fig 5.2a). Most of these viability tests comprise seed germination assays conducted for accessions of small grains, maize, sorghum, and wild relatives of potatoes (Fig. S5.2a). Several genebank units currently lack seed testing capacity (e.g., Brownwood, Davis, Mayagüez, Miami, and Genetic Stocks Centers; Fig 5.2) whereas the capacity at other genebank units (e.g., Pullman) has diminished from past levels.

Seed viability tests conducted at genebank units evaluate initial seed quality (10,000+ tests per year) or monitor quality during storage (12,000+ tests per year). Initial tests evaluate seed lot quality after harvest to ensure seeds are adequately filled (pollination occurred); free of disease or insect damage; harvested at optimal maturity; and threshed, dried, and cleaned without causing mechanical damage. Seeds are then stored, usually in medium-term refrigerators (5˚C, 41˚F) (Component 4), and distributed to fulfill user requests at a current average rate of ca. 200,000 samples/year (Component 8). Recurrent monitoring tests track the progress of aging to ensure the availability of high-quality seeds for distribution and regeneration. If kept dry in the refrigerator, seeds can survive 8 to 30 years, depending on seed quality factors (Walters et al., 2005, Nagel et al., 2009; Hay et al., 2015). For genebank units with viability testing capacity, seeds stored at 41˚F, 5˚C are tested usually according to 5 to 10-year cycles, depending on the species. PGR managers estimate that 49% of the total number of accessions have been tested recently for germination, viability, and/or vigor, with "recent" being defined by the PGR managers based on technical considerations (Figs. 5.1b, 5.2b, Fig. S5.2b).

The NLGRP serves as the long-term storage facility for the NPGS, where samples are duplicated and stored under conventional freezer conditions or cryogenic conditions in liquid nitrogen (Component 4). About 25% of the NPGS's total volume of viability testing is conducted at the NLGRP (7,000 to 13,000 tests per year) to monitor changes in seed quality during long-term storage (Fig 5.1a, 5.2a--near bottom). Viability tests conducted for research purposes at the NLGRP are not included in this accounting, but are fundamental for developing cryopreservation methods for seeds, pollen, and clonal propagules; predicting and detecting aging rates during storage; and determining germination requirements (i.e., breaking seed dormancy) for crop wild relatives (CWR; see Applied Research below). On receipt of samples of diverse PGR from genebank units (see Component 4), the NLGRP tests the viability of ca. 5,000+ samples per year

under carefully controlled assay conditions, applying expert evaluations to provide baseline information for detecting damage from cryoexposure or aging (AOSA, 2014; Panis and Nagel, 2020; Pence et al., 2020; Tanner et al., 2020). Typically, about 1.7% and 3.6% of NLGRP accessions from genebank units managing seed or clonal crops, respectively, are tested annually (Fig 5.2a--near bottom).

The NLGRP conducts between 2,500 and 4,500 tests per year (Fig. 5.1a) to monitor viability of the 410,000+ NPGS accessions safeguarded there in long-term storage (Component 4). About 46% (187,000+) of these accessions have been tested recently, according to FAO's definition, which recommends a 10- to 20-year monitoring frequency for seeds in freezer storage to ensure against loss or genetic shifts (Component 4; FAO, 2014; Hay et al., 2015; Fu, 2017; Hay and Sershen, 2020; Fig. 5.2b--near bottom). Currently, there are no monitoring standards for cryopreserved clonal propagules.

The Congress specifically requested an assessment of the "backlog of…maintenance of existing accessions." At NPGS genebank units, including the NLGRP, roughly half of stored accessions have not received a recent viability test, amounting to an overall backlog comprising hundreds of thousands of accessions (Figs 5.1c, 5.2c; Fig. S5.2c). The total number and proportion of samples that require testing vary across crops and genebank units (Fig. 5.2c; Fig. S5.2c). Backlogs effectively extend the monitoring interval, increasing the risk that viability declines between testing dates and is not detected. For example, the backlog of 223,000+ samples at the NLGRP that require testing, in combination with a current rate of 3,000 monitoring tests (of the total of 7,000 tests; Fig. 5.2a) per year, translates to a monitoring interval of 70 + years, which is longer than the life expectancy of seeds for nearly 100 of the NPGS's 200 crops (data not shown). Inadequate testing capacity is the primary cause for current backlogs, although testing is also precluded whenever the samples include too few seeds (fewer than 250 to 500 seeds, depending on the species).

For most of the genebank units, PGR managers estimate that a median of 5 years is needed to reduce the backlog of testing samples that currently require testing (Fig. 5.3b; Fig. S5.3b). In contrast, at the NLGRP, a median period of 62 years (Fig. 5.3b; Fig. S5.3b) is estimated across all crops (62 and 156 years for PGR from genebank units that manage primarily seed or clonal crops, respectively; data not shown) for reducing the backlogs of testing samples that currently require testing. During that period, some samples must be regenerated to provide sufficient quantities of seeds to the NLGRP for that viability testing.

Strategies and Implementation

Viability tests should reliably predict the success of reviving a sample that has been exposed to the stress of LN storage or stored for years under conventional low temperature conditions. The Association of Official Seed Analysts (AOSA) seed germination guidelines, which apply defined conditions and distinguish normal and abnormal seedlings, are the industry standards for correlating laboratory assessments with field performance (AOSA, 2014). Nonetheless, guidelines rarely exist for seeds of CWR, which often germinate slowly and asynchronously (De Vitis et al., 2020; Pedrini and Dixon, 2020; White et al., 2018). The NLGRP frequently used proxies, such as vital staining with tetrazolium chloride (i.e., TZ tests), to accelerate testing for

CWR. Nevertheless, slower, more labor-intensive methods that measure germination can more reliably predict the capacity of seeds to produce "normal" plants, especially after long-term storage. Consequently, viability testing methods will be adjusted during the next 5 years, returning to traditional seed testing methods until there are better options. It is a priority to develop additional or improved seed testing protocols. These will be generated as a part of an expanded program for viability testing of CWR (Fu, 2017; Walters et al., 2018). By +5 and +10 years, at least 50% and 80% of CWR species stored at the NLGRP will have germination protocols documented in GRIN-Global to support not only quality control, but also to increase the success rate for regenerating PGR that are difficult to grow (De Vitis et al., 2020; Pedrini and Dixon, 2020; White et al., 2018). To improve seed testing guidelines for CWR, NLGRP seed analysts will require additional on-the-job training (Component 1) and adjusted workflows to extend the seed testing period or change the test conditions (Baskin and Baskin, 1998). In partnership with information management personnel from GRIN-Global and other genebank units, data entry software must be adjusted to accommodate new methods of data collection and summary.

Viability testing of clonal propagules presents a significant bottleneck for both safety duplication (Component 4) and optimization of cryoexposure procedures (Pence et al., 2020; Panis and Nagel, 2020; Tanner et al., 2020; Volk et al., 2012; Reed, 2008). Applying in vitro techniques to acquire source material or to recover PGR from cryostorage constitutes part of the emerging field of cryobiotechnology (Pence et al., 2020). The challenges of implementing a strategy incorporating in vitro techniques include optimizing protocols for diverse taxa, where each type of clone might require specialized nutrient, hormone and lighting conditions for normal root and shoot development (Pence et al., 2020; Panis and Nagel, 2020; Reed, 2008). Faster assays that circumvent the in vitro step, such as measuring necrotic browning after a freezing challenge, can serve as early indicators of survival probability, but they do not predict the odds that healthy plantlets will be recovered. Consequently, the proof-of-concept that propagules retrieved from storage will grow into reproductive plants underpins PGR management and is an essential strategy for devising an effective preservation protocol (Pence et al., 2020; Panis and Nagel, 2020).

With the knowledge and capacities currently available at the NLGRP, testing and back-up for clonal PGR will concentrate strategically initially on crops with established protocols, e.g., *Malus* (apple), *Musa* (banana and plantain), *Solanum* (potato), *Citrus* and *Rubus* (raspberry), and proceed at rate of about 200 accessions tested annually to confirm that preservation has been successful. The required first step for backing-up other clonally propagated PGR begins with developing a reliable viability test, which is usually approached one genus at a time, making progress slow for collections with few accessions, e.g., *Carambola* (starfruit) and *Garcinia* (mangosteen), or PGR that are difficult to establish in vitro, e.g., *Persea* (avocado) and *Saccharum* (sugarcane). Successful back-up of NPGS's clonal PGR at the NLGRP will be accelerated by implementing a research program (see Applied Research below) with the strategy of specializing in developing biotechnologies for successful in vitro culture of diverse taxa, coordinated with research to expand knowledge of the fundamentals of cryoprotection and recovery metabolism. As mentioned earlier, significant additional resources (Component 1) are needed to conduct this research program

The viability of stored PGR must be tested periodically because samples can die in storage and the timing of death for any particular sample is unpredictable (Walters et al., 2004, 2005, 2010, 2018). Characteristic survival times are known for seeds of some crops stored under refrigerated conditions (41˚F, 5˚C; Walters et al., 2004, 2005; Nagel et al., 2009; Hay et al., 2015; Royal Botanic Gardens Kew, 2021). Accordingly, some genebank units (e.g., Aberdeen, Ames, Griffin, Sturgeon Bay) have implemented monitoring protocols in 5 to 10-year intervals (FAO, 2014; Hay and Sershen, 2020). In contrast, the survival period for seeds, pollen, and clonal propagules under freezer (-18˚C, 0˚F) and liquid nitrogen (-170˚C to -196˚C) temperatures have been estimated, often based on conflicting survival models (Walters et al., 2010; 2018; Royal Botanic Gardens Kew, 2021). This uncertainty arises because confirming data are sparse due to storage technologies that were implemented relatively recently (i.e., low temperature storage of PGR began only about 45 years ago). Considering this uncertainty, FAO's recommended strategy of a monitoring interval of 10 to 20 years is in line with conservative estimates of 50- to 100-year life expectancies for seeds stored in the freezer (Walters et al., 2004, 2005). Nonetheless, accumulating evidence of prolonged shelf life of seeds from some species (Walters et al., 2005; Nagel et al., 2009; Hay et al., 2015; Royal Botanic Gardens Kew, 2021) argues that the monitoring interval criterion can be extended strategically with the outcome of reducing unnecessary consumption of valuable seeds and accompanying high labor costs of testing.

Documentation of achieved longevity from ~45 years of maintenance data (20,000-30,000 viability observations per year) can verify and adjust many of the assumptions and models that currently drive PGR management recommendations. Therefore, it a high priority for the NPGS to assimilate the accumulating results from viability tests of seeds, stored for decades, during the next +5 years so that the known costs (e.g., highly skilled labor and consumed seeds) and benefits (e.g., mitigated risks of lost sample quality) can be reliably weighed (see Applied Research section below). Additional research capacity will enable more detailed exploration of longevity factors, such as weather during the growing season or harvest maturity, that contribute to within-species variation in survival under storage conditions (Hay et al., 2015; Fu, 2017). The NPGS will strive to develop the capacity to accurately assign "expiration dates" to individual samples in storage and thereby streamline monitoring efforts by focusing on the samples that are aging fastest.

A large backlog for accessions that have not been tested recently for viability has accumulated at the NLGRP and at genebank units that lack extensive seed testing programs (Fig. 5.2c). Unfortunately, the testing backlog at genebank units usually involves PGR which have not been duplicated at the NLGRP, meaning that they are more vulnerable to loss. Consequently, it is a priority to double the testing rates to 64,000+ accessions per year within +10 years (or ca. 6.2% of the total NPGS collection tested each year, Fig. 5.2a). Resources for expanded testing capacity at genebank units and the NLGRP (Component 1) will substantially reduce the time needed to decrease the backlogs from current average median of 15 and 237 years for genebanks units and the NLGRP, respectively, to 5 and 20 years at +10 years (Fig. 5.3b; Fig. S5.3).

The NLGRP's strategy to reduce backlogs in viability testing also involves low-cost changes in seed testing workflows. Streamlined retrieval of seeds for monitor-testing is expected to double the number of monitoring tests conducted from about 3,000 to 6,000 annually, totaling an extra 15,000 accessions tested during the next +5 years and reducing the backlog by about 7%. The

NLGRP is examining the feasibility of extending the standard monitoring interval from 15 to 20 years, a strategy which would reduce the required number of tests by 6,000 annually, effectively reducing the backlog by 13% in 5 years – although there would be an associated increased risk of undetected deterioration through time (see following paragraph). In addition, genebank units can transfer to the NLGRP samples of newly harvested seeds in sufficient numbers to replace older samples and reset the aging clock (Components 4 and 7). During the next +5 years, a priority of the NLGRP's applied research program, described below, will be to initiate technology transfer of new, more sensitive viability tests to other genebank units. Comparisons of traditional seed testing methods with new technologies applied to samples can lead to efficiencies that will increase the NLGRP's seed testing capacity by 5%. To enable viability testing when the numbers of seeds in samples are the limiting factor, the seedlings generated by the germination tests at the NLGRP could be returned to genebank units for planting. Collectively, these improved workflows can achieve the outcome of reducing the backlogs of germination tests conducted at the NLGRP by about 25% in +5 years. Ultimately, reducing the backlog will require a 3 to 4-fold increase in germination testing at the NLGRP through research to improve testing efficiency and additional trained staff, as detailed in Component 1, needed to implement the technological advances.

The threshold proportion of viable or germinating seeds, currently set at 85%, is based on the risks that too few seeds will be available for regeneration or that a sample might approach the onset of rapid mortality (FAO, 2014). Nonetheless, this standard could be too high for numerous seed samples, especially those from CWR, which might be impacted by pollination deficiencies during regeneration, leading to empty seeds or other quality factors that do not correlate with survival in storage (Mead and Gray, 1999; Walters et al., 2005). By +5 and +10 years, accumulated longevity data will enable comparisons of results from initial and viability monitoring tests of specific samples of accessions. Those data could also be applied to develop quality threshold standards tailored to specific crop types or species, or which are directly related to physiological changes during storage.

Applied Research for Testing PGR Germination, Viability, and Longevity

Successful conservation of the viability and vigor of PGR requires comprehensive knowledge of how to maintain and reproduce healthy plants. Increasingly, NPGS collections include plants, such as CWR, that are not domesticated. Cultivating those plants presents challenges to producing sufficient numbers of propagules for effective conservation, assessing their health, and identifying the factors that promote or limit normal development (White et al., 2018; Pedrini and Dixon, 2020; De Vitis et al., 2020). Applied research that leads to reliable markers of health can streamline testing or reduce the number of propagules consumed by testing (Fu, 2017). Such applied research is a priority for this Plan because it would also inform better agronomic or horticultural practices, especially for stimulating germination, flowering, fruit set and seed maturation for CWR (White et al., 2018).

Strengthening biotechnological approaches to promote healthy plant growth in vitro is an unaddressed need critical for generating source material for cryopreserving clonal propagules. Rather than addressing that need crop by crop, understanding basic biological characteristics common to large groups of different species might hasten progress overall, especially for highly vulnerable collections at tropical genebank units and the U.S. National Arboretum (Walters and

Pence, 2020; Pence et al., 2020). For example, elucidating the key metabolic pathways that cue basic developmental changes, such as organ development, seed maturation and germination, or cold acclimation, might furnish a priori knowledge applicable to plant species that have not been investigated previously (e.g., Phillips, 2004; Thomashow, 2010; Weitbrecht et al., 2011). Applied research will be conducted to combine the genomic information accumulated for diverse species (Component 10) with emerging knowledge of fundamental metabolic pathways in order to identify key limiting factors, across species, for healthy plant development. Knowledge of those factors can yield the outcome of more successful embryo or meristem rescue.

Uncertainty about the speed of aging necessitates the continual monitoring of PGR viability during storage. This problem is not unique to PGR: food, pharmaceutical and material industries invest heavily in research to determine the duration that a product performs (i.e., its expiration date; Walters et al., 2010). The difficulties with defining expiration dates for PGR viability in cold storage arise from the complex biochemical composition of plant cells, the extended time frames (i.e., decades) for measurement, and the subtle and unknown chemical and physical changes that culminate in sudden losses of viability and vigor. Consequently, it is a priority to understand numerous interacting effects related to genetic factors, growth and harvest of propagules, pretreatments, and storage conditions to explain the variation for survival in storage within species and among propagule types (Nagel et al., 2009; Hay et al., 2015). Identifying the biochemical and cellular byproducts of deterioration under storage is essential to understand the physiological and molecular thresholds that trigger loss of viability or vigor (Walters et al., 2010; Mira et al., 2016; Fleming et al., 2017, 2018, 2019) and to retrieve accessions from storage before this happens. The NLGRP's expanded leading-edge research capacities for aging and mortality of PGR will identify new biochemical markers that detect the earliest stages of PGR aging that can enable genebanks to develop better PGR management practices. Additionally, identifying genetic or epigenetic effects of aging will lead to more effective PGR regeneration schedules that avoid shifting an accession's genetic profile.

Eventual mortality of PGR maintained in storage is unavoidable, and often is preceded by morbidity, wherein living propagules fail to grow and develop normally. Biotechnological advances from NLGRP research will focus on the priority of enabling propagules with diminished or lost biological functions to be revived following aging during storage or retrieved following damage during cryoexposure. Developing methods to stimulate propagule metabolism; repair damaged cellular machinery; and block "self-destruct" pathways (i.e., programmed cell death) are NPGS priorities for increasing survival of valuable PGR that would otherwise be lost (Chen et al., 2013; Walters et al., 2013).

Data generated from the genotypic characterization program outlined in Component 10 will be critical to linking rapid, nucleotide sequence-based assays with slower, more difficult-to-measure phenotypic evaluations of propagule health, stress tolerance, and longevity during storage. Research at the NLGRP and other genebank units will reveal how variation in gene function and metabolic pathways interrelates to storage response of propagules and will enable applications of automated sampling and analyses with sequence-based tools (Weitbrecht et al., 2011). Such automation could reduce both the human labor and the consumption of PGR required for testing. It will also facilitate diagnosing the causes of failed preservation treatments, which could then refine the currently applied, broad and binary diagnostic categories that term PGR as "alive versus dead" or "normal versus abnormal."

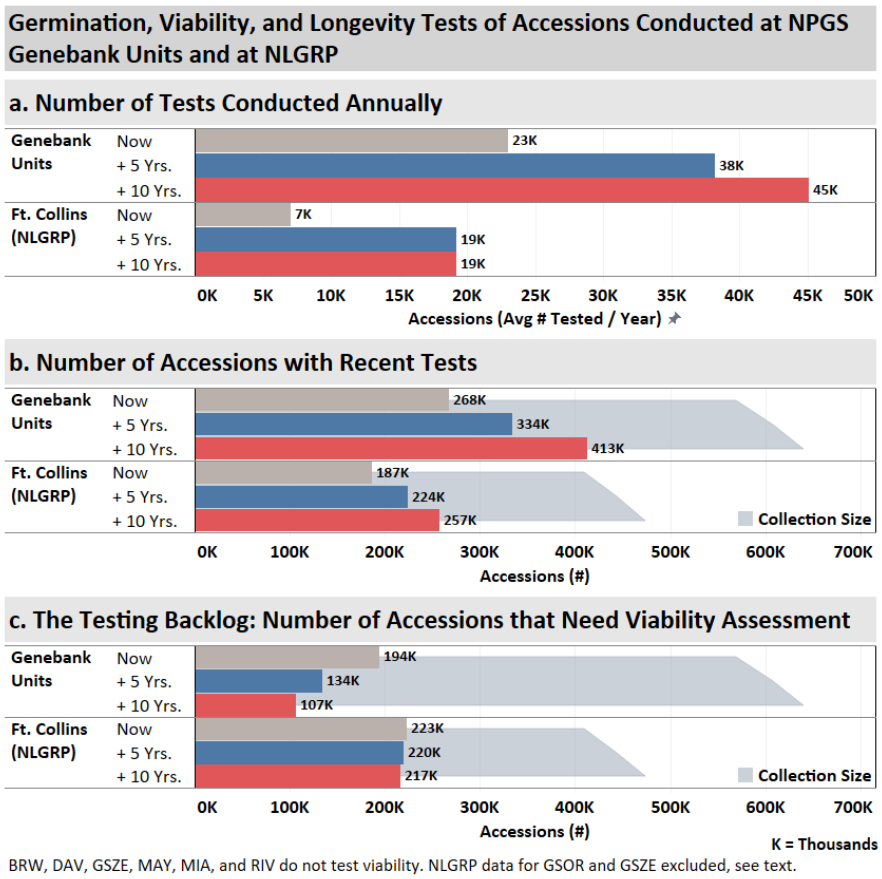


Fig. 5.1: Germination, Viability, and Longevity Tests of Accessions Conducted at NPGS Genebank Units and at NLGRP. Figure 5.1a describes number of tests conducted per year, Figure 5.1b the number of accessions with recent tests, and Figure 5.1c the size of the backlog (i.e., number of accessions that require viability assessment).

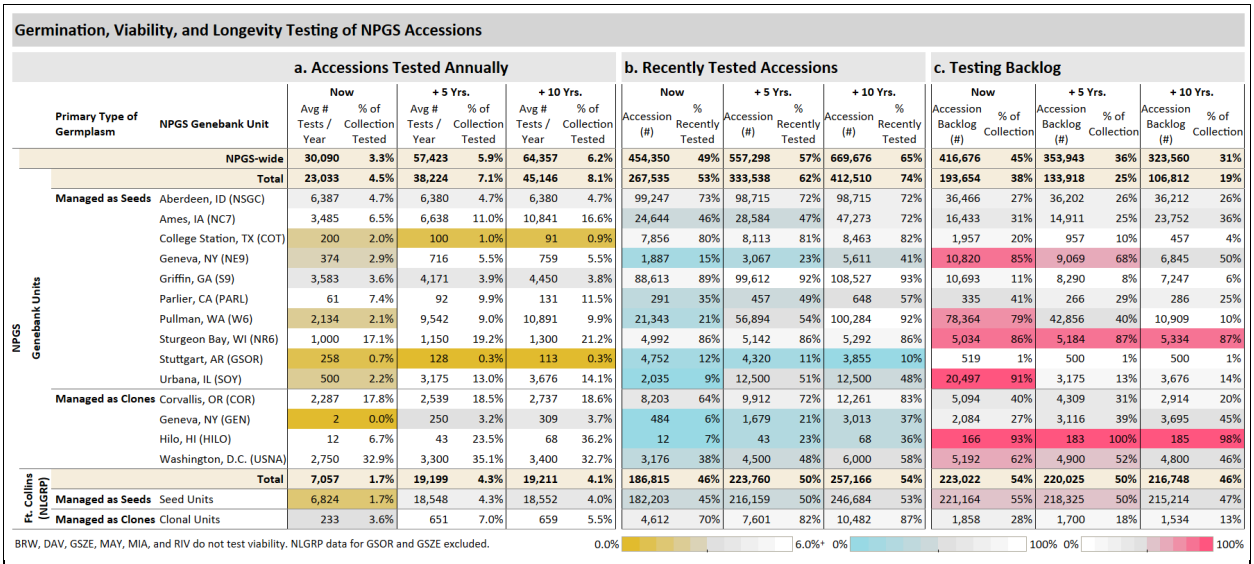
Fig. 5.1a depicts the current average annual numbers of NPGS accessions tested by the dark gray bars and goals for numbers of tests +5 and +10 years by blue and rust red bars, respectively. The figure presents separate summaries of PGR testing conducted by NPGS genebank units and by the NLGRP. Tests are the sum of initial germination (or viability, see text) tests, scheduled monitoring tests of seeds (genebank units and NLGRP), and tests for normal growth following cryoexposure of clonal propagules (NLGRP only).

Fig. 5.1b depicts by the dark gray bar the number of accessions that were tested in 2019 (when data were assembled) and a defined number of years before that date (i.e., "recent"). The numbers of years that defined "recent" were determined by genebank unit PGR managers, based on the factors associated with specific PGR. At the NLGRP, recent tests were defined as the 15-year interval between 2005 and 2019, inclusive, according to FAO standards (FAO, 2014). Projected future progress with testing assumes increased resources to expand testing capacities. The blue bars depict goals for increasing the number of accessions with recent tests for +5 years and the rust bars for +10 years. The figure presents separate summaries of recent PGR testing conducted by NPGS genebank units and by the NLGRP.

To facilitate a visual assessment of the proportion of NPGS accessions recently tested, 52% and 46% at the genebank units and the NLGRP, respectively, the light gray bars in Fig. 5.1b and Fig. 5.1c depict the current total number of accessions in the NPGS collection and the total numbers estimated for +5 and +10 years.

Fig. 5.1c depicts by the dark gray bars the numbers of accessions that required viability assessment in 2019 (i.e., the backlog). The numbers of accessions that constitute a backlog were determined by genebank unit PGR managers, based on the factors associated with specific PGR. The blue and rust red bars depict the goals for reducing the backlogs in +5 and +10 years, respectively. The figure presents separate summaries of recent PGR testing conducted by NPGS genebank units and by the NLGRP. Future progress projected to reduce the testing backlogs assumes increased resources to expand testing capacities.

BRW, DAV, GSZE, MAY, MIA and RIV currently do not conduct these types of tests. NLGRP data for GSOR AND GSZE are excluded; see text for explanation.



Germination, Viability, and Longevity Testing of NPGS Accessions

			a. Accessions Tested Annually						b. Recently Tested Accessions						c. Testing Backlog					
			Now		+ 5 Yrs.		+ 10 Yrs.		Now		+ 5 Yrs.		+ 10 Yrs.		Now		+ 5 Yrs.		+ 10 Yrs.	
	Primary Type of Germplasm	NPGS Genebank Unit	Avg # Tests / Year	% of Collection Tested	Avg # Tests / Year	% of Collection Tested	Avg # Tests / Year	% of Collection Tested	Accession (#)	% Recently Tested	Accession (#)	% Recently Tested	Accession (#)	% Recently Tested	Accession Backlog (#)	% of Collection	Accession Backlog (#)	% of Collection	Accession Backlog (#)	% of Collection
		NPGS-wide	**30,090**	**3.3%**	**57,423**	**5.9%**	**64,357**	**6.2%**	**454,350**	**49%**	**557,298**	**57%**	**669,676**	**65%**	**416,676**	**45%**	**353,943**	**36%**	**323,560**	**31%**
NPGS Genebank Units		**Total**	**23,033**	**4.5%**	**38,224**	**7.1%**	**45,146**	**8.1%**	**267,535**	**53%**	**333,538**	**62%**	**412,510**	**74%**	**193,654**	**38%**	**133,918**	**25%**	**106,812**	**19%**
	Managed as Seeds	Aberdeen, ID (NSGC)	6,387	4.7%	6,380	4.7%	6,380	4.7%	99,247	73%	98,715	72%	98,715	72%	36,466	27%	36,202	26%	36,212	26%
		Ames, IA (NC7)	3,485	6.5%	6,638	11.0%	10,841	16.6%	24,644	46%	28,584	47%	47,273	72%	16,433	31%	14,911	25%	23,752	36%
		College Station, TX (COT)	200	2.0%	100	1.0%	91	0.9%	7,856	80%	8,113	81%	8,463	82%	1,957	20%	957	10%	457	4%
		Geneva, NY (NE9)	374	2.9%	716	5.5%	759	5.5%	1,887	15%	3,067	23%	5,611	41%	10,820	85%	9,069	68%	6,845	50%
		Griffin, GA (S9)	3,583	3.6%	4,171	3.9%	4,450	3.8%	88,613	89%	99,612	92%	108,527	93%	10,693	11%	8,290	8%	7,247	6%
		Parlier, CA (PARL)	61	7.4%	92	9.9%	131	11.5%	291	35%	457	49%	648	57%	335	41%	266	29%	286	25%
		Pullman, WA (W6)	2,134	2.1%	9,542	9.0%	10,891	9.9%	21,343	21%	56,894	54%	100,284	92%	78,364	79%	42,856	40%	10,909	10%
		Sturgeon Bay, WI (NR6)	1,000	17.1%	1,150	19.2%	1,300	21.2%	4,992	86%	5,142	86%	5,292	86%	5,034	86%	5,184	87%	5,334	87%
		Stuttgart, AR (GSOR)	258	0.7%	128	0.3%	113	0.3%	4,752	12%	4,320	11%	3,855	10%	519	1%	500	1%	500	1%
		Urbana, IL (SOY)	500	2.2%	3,175	13.0%	3,676	14.1%	2,035	9%	12,500	51%	12,500	48%	20,497	91%	3,175	13%	3,676	14%
	Managed as Clones	Corvallis, OR (COR)	2,287	17.8%	2,539	18.5%	2,737	18.6%	8,203	64%	9,912	72%	12,261	83%	5,094	40%	4,309	31%	2,914	20%
		Geneva, NY (GEN)	2	0.0%	250	3.2%	309	3.7%	484	6%	1,679	21%	3,013	37%	2,084	27%	3,116	39%	3,695	45%
		Hilo, HI (HILO)	12	6.7%	43	23.5%	68	36.2%	12	7%	43	23%	68	36%	166	93%	183	100%	185	98%
		Washington, D.C. (USNA)	2,750	32.9%	3,300	35.1%	3,400	32.7%	3,176	38%	4,500	48%	6,000	58%	5,192	62%	4,900	52%	4,800	46%
		Total	**7,057**	**1.7%**	**19,199**	**4.3%**	**19,211**	**4.1%**	**186,815**	**46%**	**223,760**	**50%**	**257,166**	**54%**	**223,022**	**54%**	**220,025**	**50%**	**216,748**	**46%**
Ft. Collins (NLGRP)	**Managed as Seeds**	Seed Units	6,824	1.7%	18,548	4.3%	18,552	4.0%	182,203	45%	216,159	50%	246,684	53%	221,164	55%	218,325	50%	215,214	47%
	Managed as Clones	Clonal Units	233	3.6%	651	7.0%	659	5.5%	4,612	70%	7,601	82%	10,482	87%	1,858	28%	1,700	18%	1,534	13%

BRW, DAV, GSZE, MAY, MIA, and RIV do not test viability. NLGRP data for GSOR and GSZE excluded.

0.0% 6.0%+ 0% 100% 0% 100%

Fig. 5.2: Germination, Viability, and Longevity Testing of NPGS Accessions. The top row of Fig. 5.2a, shaded light beige, reports for the total NPGS collection the current average annual number of germination, viability, and/or longevity tests, and goals for increasing testing at +5 years and +10 years. The current average annual rate (percentage) of testing for the total collection, and goals for +5 years and for +10 years also are approximated. The same information then is provided for individual genebank units, listed by their geographical locations. Data for the NPGS genebank units that primarily manage PGR propagated as seeds are listed above data for genebank units that primarily manage PGR propagated as clones. The data for testing at the NLGRP are listed at the bottom of the figure. The lower the rate of testing for the individual NPGS collections, the darker the mustard hue, with 0% testing rate the darkest.

The top row of Fig. 5.2b, shaded light beige, reports for the total NPGS collection the current average number of germination, viability, and/or longevity tests conducted recently, and goals for +5 years and +10 years. The current average rate (percentage) of recent tests for the total collection, and goals for +5 years and for +10 years also are approximated. “Recently” is defined in the legend of Fig 5.1 and in the text. The same information then is provided for individual genebank units, listed by their geographical locations. Data for the NPGS genebank units that primarily manage PGR propagated as seeds are listed above data for genebank units that primarily manage PGR propagated as clones. The data for testing at the NLGRP are listed at the bottom of the figure. The lower the rate of recent tests for the individual NPGS collections, the darker the aqua hue, with 0% testing rate the darkest.

The top row of Fig. 5.2c, shaded light beige, reports for the total NPGS collection the current backlogs of numbers of NPGS accessions that require germination, viability, and/or longevity, and the goals for reducing the backlogs at +5 years and +10 years. The current rate (percentage) of NPGS accessions that require testing also is listed, as are goals for reducing the backlogs for +5 years and for +10 years. The same information then is provided for individual genebank units, listed by their geographical locations. Data for the NPGS genebank units that primarily manage PGR propagated as seeds are listed above data for genebank units that primarily manage PGR propagated as clones. The data for testing at the NLGRP are listed at the bottom of the figure. The higher the percentages of accessions at the individual NPGS genebank units that require testing, the darker the pink hue, with 100% that require testing at genebank units the darkest.

BRW, DAV, GSZE, MAY, MIA, and RIV do not test for viability. NLGRP data for GSOR and GSZE are excluded because they are genetic stocks; see text.

a. Time Needed to Reduce the Backlogs of Germination, Viability, and Longevity Testing of NPGS PGR

NPGS	Primary Type of Germplasm	NPGS Genebank Unit	Now MIN (# Years)	Now Avg. of Medians	Now MAX (# Years)	+5 Yrs. MIN (# Years)	+5 Yrs. Avg. of Medians	+5 Yrs. MAX (# Years)	+10 Yrs. MIN (# Years)	+10 Yrs. Avg. of Medians	+10 Yrs. MAX (# Years)	# of Crops & CWR
		NPGS-wide	**0**	**112**	**3,268**	**0**	**13**	**1,792**	**0**	**13**	**2,017**	**222**
Genebank Units		**Total**	**0**	**15**	**1,567**	**0**	**6**	**1,792**	**0**	**5**	**2,017**	**125**
	Managed as Seeds	Aberdeen, ID (NSGC)	1	5	10	1	4	10	0	3	10	10
		Ames, IA (NC7)	1	11	1,567	1	11	1,792	1	15	2,017	24
		College Station, TX (COT)	10	10	10	10	10	10	5	5	5	1
		Geneva, NY (NE9)	4	29	80	1	9	38	0	6	33	10
		Griffin, GA (S9)	1	3	17	0	2	5	0	1	5	25
		Parlier, CA (PARL)	1	6	20	1	4	10	1	2	5	5
		Pullman, WA (W6)	1	38	168	2	6	14	1	1	6	23
		Sturgeon Bay, WI (NR6)	5	5	5	5	5	5	5	5	5	1
		Stuttgart, AR (GSOR)	0	2	5	1	3	5	1	3	5	3
		Urbana, IL (SOY)	3	4	5	1	1	1	1	1	1	2
	Managed as Clones	Corvallis, OR (COR)	1	12	55	0	6	27	1	3	10	14
		Geneva, NY (GEN)	5	8	10	2	4	5	2	4	5	5
		Hilo, HI (HILO)	15	15	15	4	4	4	3	3	3	1
		Washington, D.C. (USNA)	0	1	3	0	1	3	0	1	3	1
Ft. Collins (NLGRP)		**Total**	**0**	**237**	**3,268**	**0**	**19**	**91**	**0**	**20**	**102**	**97**
	Managed as Seeds	Seed Units	1	236	3,268	0	24	91	0	26	102	92
	Managed as Clones	Clonal Units	0	240	654	0	8	75	0	7	77	5

b. Median Years Needed to Reduce the Backlogs

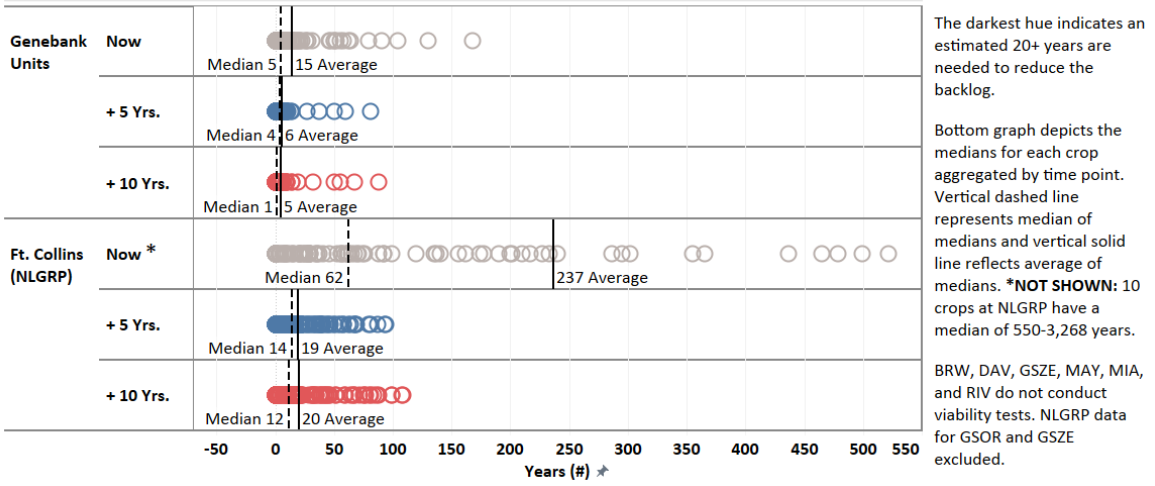


Fig. 5.3: Time Needed to Reduce the Backlogs of Germination, Viability, and Longevity Testing of NPGS PGR. The top row of Fig. 5.3a, shaded light beige, reports for the total NPGS collection the current extreme minima, extreme maxima, and the average median number of years needed to reduce the backlogs, as much as is feasible, in testing germination, viability, and longevity of NPGS PGR, and goals for reducing the backlogs for +5 years and +10 years. The range and median number of years needed to reduce the testing backlogs at individual NPGS genebank units, according to the best estimates of the PGR managers, then are listed below by the genebank units' geographical locations. The NPGS genebank units that primarily manage seed-propagated PGR are in the top portion of the figure, and those that primarily managed clonally-propagated PGR are below them. Data for the NLGRP are presented at the bottom of the figure. The more time needed to reduce the backlogs for the individual genebank unit collections, the darker the aqua hue. The darkest hue indicates an estimated 20+ years are needed to reduce the backlog. The numbers of crops and CWR managed by the NPGS overall, by the individual genebank units that manage PGR propagated by seeds and as clones, are listed in the column at the far right. Many of the longest backlogs result from a current lack of effective means for testing the PGR, which will be the focus of applied research in this Plan.

Figure 5.3b depicts the current medians, for all the NPGS PGR, for the numbers of years needed to reduce the backlogs for testing NPGS accessions, and the goals for reducing the backlogs at +5 years and +10 years. The current median numbers of years needed to reduce the backlogs in testing individual crops and CWR are depicted by light gray circles, the goals for reducing the backlogs at +5 years by blue circles, and the goals for +10 years by rust red circles. The medians of medians for the numbers of years, across all PGR, needed to reduce backlogs are depicted by dashed vertical lines, and averages of medians for the number of years, across all PGR, needed to reduce backlogs are depicted as solid vertical lines. *Ten crops safeguarded at the NLGRP that have median backlogs of 550-3,268 years are not shown here because of the scale format.

BRW, DAV, GSZE, MAY, MIA, and RIV are excluded because those genebank locations do not conduct viability tests. NLGRP data for GSOR and GSZE are excluded because they are genetic stocks; see text.

Component 6: Pathogen Testing and Clean-Up (Figs. 6.1-6.4)

Current Status

Accessions of certain PGR must be tested for the presence of known pathogens for optimal conservation, and to prevent the spread of plant diseases. Testing for pathogens is required to maintain PGR health; identify unknown microbes and suspected pathogens; and ensure compliance with phytosanitary regulations associated with international (and sometimes domestic) PGR exchange (Kumar et al., 2021). Such testing therefore plays an important role in the security of U.S. and global agricultural production. Pathogen tests can be particularly complicated to apply to PGR because of the wide genetic diversity not only among different taxa, but often within taxa and crops. Furthermore, for little-studied plant species, knowledge can be scant or completely lacking for relevant pathogens, harmless microbial symbionts, and physiological reactions to abiotic stresses that can mimic disease symptoms.

Backlogs have developed in the NPGS for pathogen testing the PGR that require it (Fig. 6.1; Fig. S6.1). Approximately 92,000+ accessions (ca. 28% of the total number of NPGS accessions, Fig. 6.2) currently require pathogen testing, but the average volumes and percentages (ca. 10,500+ accessions, 1.8% of the NPGS total, Fig. 6.2) tested annually are inadequate to meet current NPGS needs. The volume and percentages of accessions that have been tested; require testing; or are tested annually vary greatly across taxa and genebank units. For example, some cereal PGR require testing for few pathogens or no testing at all, whereas some clonally propagated PGR require extensive testing. Across the NPGS, accomplishing the needed testing and accompanying diagnostic analyses would currently require a range of 0-700+ years and an average median of 15 years (Fig. 6.1, Fig. S6.1).

As mentioned above, numerous clonally propagated crops at genebank units such as Corvallis, Riverside, Miami, Hilo, and Mayagüez require testing for pathogens. Citrus PGR at Riverside requires monthly testing for the presence of the huanglongbing (HLB) pathogen and other diseases (Fig. 6.2, Appendix B). When PGR of crops such as rice, sugarcane, and some tree fruits are imported into the United States, they undergo pathogen testing by APHIS during quarantine periods. Seedborne or suspected seedborne diseases, such as several bacterial and viral diseases of tomato (*Solanum*, at Geneva), pepper (*Capsicum*, at Griffin), and Stewart's wilt of maize (*Zea*, at Ames) are priorities for pathogen testing of seed-propagated crops, due to phytosanitary regulations and potentially deleterious effects on the plants. Accessions of potato (*Solanum*) and potato CWR are tested according to a regular schedule at Sturgeon Bay. Numerous accessions (34,000+) of the seed-propagated crops managed at Pullman require pathogen testing, but that genebank unit currently lacks testing capacity (Appendix B). For convenience's sake, soybean (*Glycine*, at Urbana) accessions subject to testing for adventitious presence of transgenes were included in this overall testing category, because the logistics of those tests resemble those for pathogens. At the current overall rates of testing, crop-specific median periods ranging from 1 to almost 400 years would be required to test accessions that currently require assays for pathogens (Fig. 6.1; Fig. S6.1). The causes for substantial backlogs of testing PGR for pathogens include insufficient operational capacities and lack of affordable, effective, and reliable pathogen testing procedures, which is particularly important for newly-identified pathogens occurring within the United States or within NPGS collections. The

preceding factors are especially relevant to reducing or eliminating the "backlog of…maintenance of existing accessions" of particular interest to the Congress.

With sufficient operational capacities, genebank units can address the priorities of eliminating (cleaning-up) pathogens particularly from clonally propagated PGR. Pathogen-tested and "cleaned-up" accessions then can be distributed to a greater range of users and jurisdictions than those that have not been tested, undergone therapy (often a heat treatment), or repropagated from buds to eliminate pathogens. Approximately 50,000+ accessions (8%+ of the total number; Fig. 6.3) require pathogen "clean-up", but the annual average volumes and percentages (650+ accessions, ca. 1% of those requiring "clean-up"; Fig. 6.3) that undergo therapy or are repropagated to remove pathogens are inadequate to meet NPGS needs. Therefore, a backlog has developed for pathogen "clean-up" of accessions (Fig. 6.4, Fig. S6.4). At the current overall rates, crop-specific median periods ranging from 1 to almost 400 years (for *Phaseolus* at the Pullman genebank unit) would be required to clean-up accessions from pathogens (Fig. 6.4, Fig. S6.4), with clonally-propagated crops particularly in need of attention. The causes for the substantial backlogs of cleaning-up pathogens from NPGS PGR include many of the same impediments to pathogen testing procedures noted earlier.

Strategies and Implementation

Over the entire NPGS collection, ca.110,000+ accessions (Fig. 6.2b) should be tested for pathogens during the next ten years to reduce the current backlog in testing (Fig. 6.2b). The strategy for accomplishing that goal is to increase the overall rate of testing to an average of ca. 12,800+ accessions annually +5 years from now (Fig. 6.2b). Priorities for expanded testing capacity include the seed-propagated crops managed at the Pullman genebank unit, and clonally propagated horticultural crops such as pecan at College Station; *Citrus* at Riverside; and subtropical and tropical crops at Hilo, Mayagüez, and Miami (Fig. 6.2b). In addition to expanding strategically the NPGS operational capacities for pathogen testing, research capacities to develop more efficient and effective pathogen-testing procedures will be expanded, especially to address the priorities of emerging and re-emerging pathogens that currently lack testing protocols (see Applied Research section below). Based on the significant increases in global trade and international travel during recent decades, and new quarantine and virus indexing regulations from APHIS, the number of pathogens for which PGR will require testing will likely increase in the future (Kumar et al., 2021). Similarly, as new genetically-engineered traits, particularly from genome editing (Li et al., 2020), are deployed, detection procedures for those traits will be needed.

Across the entire NPGS collection, 32,000+ accessions should be cleaned-up from pathogens (or from adventitious presence of transgenes in soybeans) via therapy or repropagation during the next +10 years to reduce the current backlogs by 60+% (Fig. 6.3). The strategy for doing so involves increasing the overall rate of clean-up to an average of 3,800+ accessions processed annually (Fig. 6.3) at +5 years.

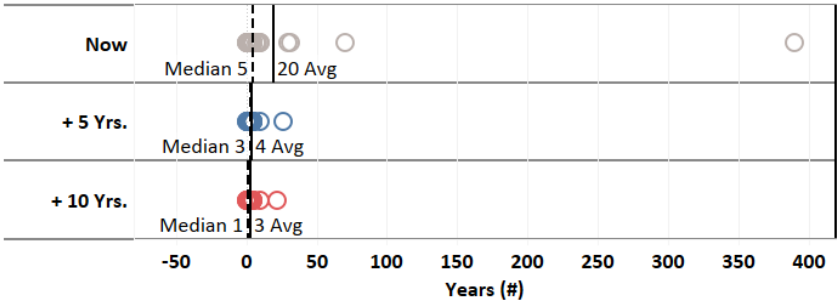
Applied Research for Pathogen Testing and Clean-Up

In addition to expanding strategically the NPGS operational capacities for pathogen testing and clean-up, additional research will focus on the goal of developing more efficient and effective testing, diagnostic, and clean-up procedures, focusing on priority pathogens of quarantine importance, and those that occur in, and/or damage, seeds or the propagules of clonally-propagated crops. Developing more efficient and effective methods are priorities for detecting, reducing infection or infestation, and cleaning-up PGR from seedborne pathogens, e.g., tomato brown rugose fruit virus from tomato (*Solanum*, Geneva), and seedborne pathogens of melons and cucumbers (*Cucumis*) at Ames. Similarly, better methods must be devised for *Citrus* disease indexing at Riverside, for detecting pathogens in sugarcane (*Saccharum*) at Miami, and for viruses and viroids in peppers (*Capsicum*) at Griffin. As an initial step, the size and scope for pathogen detection and clean-up capacities needed for grape (*Vitis*) and tart cherry (*Prunus*) at Geneva must be ascertained. For tropical crops, methods are required for detecting and cleaning-up viruses from coffee (*Coffea*) via tissue culture at Hilo, and from cacao (*Theobroma*) for quarantine release at Mayagüez and Miami. Finally, NPGS research priorities also include formulating strategies for managing key diseases that affect PGR maintained clonally in orchards, or that infect seed-propagated PGR through regeneration (Component 7).

a. Time Needed to Reduce the Backlogs of Testing NPGS Accessions for Pathogens

	NPGS Genebank Unit	Now MIN (# Years)	Now Avg. of Medians	Now MAX (# Years)	+ 5 Yrs. MIN (# Years)	+ 5 Yrs. Avg. of Medians	+ 5 Yrs. MAX (# Years)	+ 10 Yrs. MIN (# Years)	+ 10 Yrs. Avg. of Medians	+ 10 Yrs. MAX (# Years)	# of Crops & CWR
	NPGS-wide	**0**	**20**	**735**	**0**	**4**	**26**	**0**	**3**	**22**	**35**
Primary Type of Germplasm Managed as Seeds	Ames, IA (NC7)	1	1	1	1	1	1	1	1	1	2
	Griffin, GA (S9)	0	3	5	0	1	1	0	1	1	3
	Parlier, CA (PARL)	5	8	10	1	1	1	1	1	1	1
	Pullman, WA (W6)	1	104	735	1	8	26	1	6	22	5
	Sturgeon Bay, WI (NR6)	10	10	10	10	10	10	10	10	10	1
	Urbana, IL (SOY)	5	5	5	1	2	2	1	2	2	1
Primary Type of Germplasm Managed as Clones	College Station, TX (BRW)	10	10	10	5	5	5	0	0	0	1
	Corvallis, OR (COR)	0	4	7	1	3	5	1	3	5	8
	Geneva, NY (GEN)	5	5	5	3	3	3	2	2	2	5
	Hilo, HI (HILO)	0	1	1	0	0	1	0	0	1	4
	Mayaguez, PR (MAY)	1	4	5	3	3	5	4	3	5	2
	Riverside, CA (RIV)	0		1	1		5	1		5	2

b. Median Years Needed to Reduce Backlogs



Years 0 20+

The darkest hue indicates an estimated 20+ years are needed to reduce the backlog. Blank fields indicate that data could not be estimated.

COT, DAV, GSOR, GSZE, MIA, NE9, NSGC, and USNA do not conduct pathology testing or cannot estimate the time needed to reduce the backlog.

Fig. 6.1: Time Needed to Reduce the Backlogs of Testing of NPGS Accessions for Pathogens. Figure 6.1a depicts the current extreme (absolute minimum and maximum) range of years and the averages of the medians of years needed to reduce the backlogs in pathogen testing for all the PGR managed by specific NPGS genebank units, and the goals for reducing the backlogs for +5 and +10 years. The top row, shaded in light beige, shows the current overall extreme (absolute minimum and maximum) range of years and the averages of the medians of years needed to reduce the backlogs in pathogen testing for all the PGR in the NPGS that require testing. The data for the individual genebank units are listed below by their geographical locations. The genebank units that primarily manage seed-propagated PGR are grouped above those genebank units that primarily manage clonally-propagated PGR. The darker the aqua hue, the more years are needed to reduce the backlogs, with the darkest hue indicating 20+ years. The numbers of crops and CWR in each genebank unit that require pathogen testing are recorded in the far-right column and summed across all genebank units for an NPGS-wide total in the top beige-shaded row.

Figure 6.1b depicts the current medians, for all the NPGS PGR, for the numbers of years needed to reduce the backlogs in pathogen testing for NPGS accessions, and the goals for reducing the backlogs at +5 years and +10 years. The current median numbers of years needed to reduce the backlogs in pathogen testing for each of the crops or CWR are depicted by light gray circles, the goals for +5 years by blue circles, and the goals for +10 years by rust red circles. The medians of medians for the numbers of years, across all PGR, needed to reduce backlogs are depicted by dashed vertical lines, and averages of medians for the number of years, across all PGR, needed to reduce backlogs are depicted as solid vertical lines.

COT, DAV, GSOR, GSZE, MIA, NE9, NSGC, and USNA do not conduct pathology testing or cannot estimate the time needed to reduce the backlog.

Testing NPGS PGR for Pathogens

a. Progress with Pathogen Testing by NPGS Genebank Units

Primary Type of Germplasm	NPGS Genebank Unit	Now Accessions (#)	Now % of Collection	+ 5 Yrs. Accessions (#)	+ 5 Yrs. % of Collection	+ 10 Yrs. Accessions (#)	+ 10 Yrs. % of Collection
	NPGS-wide	**92,971**	**72%**	**57,957**	**84%**	**49,460**	**87%**
Managed as Seeds	Ames, IA (NC7)	4,196	92%	2,862	95%	2,517	96%
Managed as Seeds	Geneva, NY (NE9)	6,604	48%	6,654	50%	6,704	52%
Managed as Seeds	Griffin, GA (S9)	6,855	93%	1,705	98%	430	100%
Managed as Seeds	Parlier, CA (PARL)	281	76%	20	98%	10	99%
Managed as Seeds	Pullman, WA (W6)	34,042	66%	25,919	76%	22,219	80%
Managed as Seeds	Sturgeon Bay, WI (NR6)	5,834	0%	5,984	0%	6,134	0%
Managed as Seeds	Urbana, IL (SOY)	21,284	5%	2,500	90%	1,600	94%
Managed as Clones	College Station, TX (BRW)	4,108	0%	3,000	30%	500	89%
Managed as Clones	Corvallis, OR (COR)	5,028	61%	4,652	66%	4,765	68%
Managed as Clones	Geneva, NY (GEN)	3,124	59%	2,327	71%	1,583	81%
Managed as Clones	Hilo, HI (HILO)	363	70%	796	65%	1,172	65%
Managed as Clones	Mayaguez, PR (MAY)	437	64%	229	84%	238	84%
Managed as Clones	Miami, FL (MIA)	145	91%	370	80%	494	76%
Managed as Clones	Riverside, CA (RIV)	670	60%	939	46%	1,094	39%

b. Annual Pathogen Testing by NPGS Genebank Units

Primary Type of Germplasm	NPGS Genebank Unit	Now Accessions Tested (Avg #/ Yr)	Now % Tested that Need Testing	+ 5 Yrs. Accessions Tested (Avg #/ Yr)	+ 5 Yrs. % Tested that Need Testing	+ 10 Yrs. Accessions Tested (Avg #/ Yr)	+ 10 Yrs. % Tested that Need Testing
	NPGS-wide	**10,591**	**12%**	**12,883**	**25%**	**9,478**	**22%**
Managed as Seeds	Ames, IA (NC7)	2,654	63%	2,156	75%	2,061	82%
Managed as Seeds	Griffin, GA (S9)	4,402	64%	305	18%	180	42%
Managed as Seeds	Parlier, CA (PARL)	0	0%	50	100%	20	100%
Managed as Seeds	Pullman, WA (W6)	93	0%	2,226	9%	1,650	7%
Managed as Seeds	Sturgeon Bay, WI (NR6)	938	16%	963	16%	988	16%
Managed as Seeds	Urbana, IL (SOY)	0	0%	4,000	100%	1,600	100%
Managed as Clones	College Station, TX (BRW)	222	5%	500	17%	100	20%
Managed as Clones	Corvallis, OR (COR)	1,356	27%	1,114	24%	1,356	28%
Managed as Clones	Geneva, NY (GEN)	0	0%	466	20%	316	20%
Managed as Clones	Hilo, HI (HILO)	43	12%	132	17%	158	13%
Managed as Clones	Mayaguez, PR (MAY)	140	32%	71	31%	62	26%
Managed as Clones	Miami, FL (MIA)	73	50%	110	30%	112	23%
Managed as Clones	Riverside, CA (RIV)	670	100%	790	84%	875	80%

c. Progress with Pathogen Testing by Crop & CWR

Crop & CWR	NPGS Genebank Unit	Crop PGR	Now	+ 5 Yrs.	+ 10 Yrs.
Allium Garlic	Pullman, WA (W6)	Clonal	35%	80%	80%
Apple	Geneva, NY (GEN)	Clonal	20%	40%	50%
Apple CWR	Geneva, NY (GEN)	Clonal	75%	80%	90%
Avocado	Miami, FL (MIA)	Clonal	11%	8%	27%
Brassica	Ames, IA (NC7)	Seed	88%	74%	88%
Cacao	Mayaguez, PR (MAY)	Clonal	0%	87%	86%
Chickpea	Pullman, WA (W6)	Seed	0%	51%	97%
Citrus	Riverside, CA (RIV)	Clonal	57%	52%	45%
Coffee	Hilo, HI (HILO)	Clonal	100%	80%	75%
Cucurbita	Griffin, GA (S9)	Seed	24%	59%	93%
Date Palm	Riverside, CA (RIV)	Clonal	88%	0%	0%
Flax	Ames, IA (NC7)	Seed	99%	92%	92%
Grape	Geneva, NY (GEN)	Clonal	45%	70%	80%
Grape CWR	Geneva, NY (GEN)	Clonal	45%	70%	80%
Hops CWR	Corvallis, OR (COR)	Clonal	0%	7%	5%
Lentil	Pullman, WA (W6)	Seed	0%	52%	62%
Macadamia	Hilo, HI (HILO)	Clonal	93%	0%	0%
Musa	Mayaguez, PR (MAY)	Clonal	18%	12%	21%
Opuntia	Parlier, CA (PARL)	Clonal	0%	93%	96%
Pea	Pullman, WA (W6)	Seed	3%	52%	57%
Pecan	College Station, TX (BRW)	Clonal	0%	30%	89%
Pepper	Griffin, GA (S9)	Seed	0%	84%	94%
Ribes	Corvallis, OR (COR)	Clonal	0%	65%	94%
Saccharum	Miami, FL (MIA)	Clonal	100%	37%	0%
Soybean	Urbana, IL (SOY)	Seed	0%	89%	93%
Sunflower	Ames, IA (NC7)	Seed	34%	82%	83%
Tart Cherry	Geneva, NY (GEN)	Clonal	55%	65%	80%
Watermelon	Griffin, GA (S9)	Seed	58%	84%	99%

Crops and CWR with few and/or infrequent pathogen testing are not displayed (<5%). No pathogen testing conducted by COT, DAV, GSOR, GSZE, NR6, NSGC, SOY, and USNA

0% 100% 0% 50%+

Fig. 6.2: Testing NPGS PGR for Pathogens.

Fig. 6.2a shows in the first, light beige-shaded row the current number and percentage of NPGS accessions that require testing for which pathogen testing has been completed, and goals for increasing testing for +5 years and for +10 years. The preceding information is then presented for NPGS genebank units managing PGR requiring pathogen testing. Those genebank units that primarily manage accessions propagated by seeds are grouped above those that primarily manage accessions propagated clonally. The darker the blue hue, the greater the proportion of accessions at the specific genebank units that require pathogen testing.

Fig. 6.2b shows in the first, light beige-shaded row the current number and percentage of NPGS accessions that are tested annually for pathogens, and goals for increasing annual testing for +5 years and for +10 years. The preceding information is then presented for NPGS genebank units managing PGR conducting annual pathogen testing. Those genebank units that primarily manage accessions propagated by seeds are grouped above those that primarily manage accessions propagated clonally. The darker the lavender hue, the greater the proportion of accessions at the specific genebank units that conduct annual pathogen testing.

Fig. 6.2c lists specific crops and CWR with accessions that require pathogen testing. The NPGS genebank units that manage those accessions, categorized as clonally or seed-propagated, are listed. The percentages of accessions that currently require pathogen testing and have been tested are provided, as are goals for increasing testing for +5 years and +10 years. The darker the blue hue, the greater the percentages of accessions that require pathogen testing.

COT, DAV, GSOR, GSZE, NR6, NSGC, and USNA do not conduct pathogen testing. Crops and CWR that require few (<5%) and/or infrequent pathogen testing are not covered here.

Progress and Backlogs For Cleaning Up NPGS Accessions From Pathogens

a. Progress with Pathogen Clean-Up by NPGS Genebank Units

Primary Type of Germplasm Managed	NPGS Genebank Unit	Now Accessions (#)	Now % of Collection	+ 5 Yrs. Accessions (#)	+ 5 Yrs. % of Collection	+ 10 Yrs. Accessions (#)	+ 10 Yrs. % of Collection
	NPGS-wide	**50,551**	**83%**	**31,514**	**88%**	**18,749**	**93%**
as Seeds	Ames, IA (NC7)	3,224	94%				
as Seeds	Griffin, GA (S9)	3,005	96%	1,005	99%	205	100%
as Seeds	Parlier, CA (PARL)	40	97%	100	92%	5	100%
as Seeds	Pullman, WA (W6)	18,584	81%	15,157	85%	12,050	89%
as Seeds	Sturgeon Bay, WI (NR6)	46	99%	30	99%	15	100%
as Seeds	Urbana, IL (SOY)	14,900	30%	6,150	73%	550	98%
as Clones	College Station, TX (BRW)	4,500	0%	3,000	30%	500	89%
as Clones	Corvallis, OR (COR)	1,794	85%	1,564	88%	794	94%
as Clones	Davis, CA (DAV)	3,384	49%	3,424	56%	3,464	62%
as Clones	Geneva, NY (GEN)	155	98%	116	99%	80	99%
as Clones	Hilo, HI (HILO)	4	100%	0	100%	0	100%
as Clones	Miami, FL (MIA)	0	100%	150	92%	264	87%
as Clones	Riverside, CA (RIV)	915	46%	818	53%	822	55%

b. Annual Pathogen Clean-Up by NPGS Genebank Units

Primary Type of Germplasm Managed	NPGS Genebank Unit	Now Accessions Cleaned Up Annually (Avg #)	Now % Cleaned Up That Require Clean-Up	+ 5 Yrs. Accessions Cleaned Up Annually (Avg #)	+ 5 Yrs. % Cleaned Up That Require Clean-Up	+ 10 Yrs. Accessions Cleaned Up Annually (Avg #)	+ 10 Yrs. % Cleaned Up That Require Clean-Up
	NPGS-wide	**655**	**1.4%**	**3,846**	**13.7%**	**2,482**	**16.2%**
as Seeds	Ames, IA (NC7)	160	5.0%	160	0.1%	105	0.1%
as Seeds	Griffin, GA (S9)	10	0.3%	405	40.3%	25	12.2%
as Seeds	Parlier, CA (PARL)	0	0.0%	20	20.0%	2	40.0%
as Seeds	Pullman, WA (W6)	23	0.1%	647	4.3%	640	5.3%
as Seeds	Sturgeon Bay, WI (NR6)	2	4.3%	5	16.7%	5	33.3%
as Seeds	Urbana, IL (SOY)	0	0.0%	1,750	28.5%	1,120	100.0%
as Clones	College Station, TX (BRW)	300	6.7%	500	16.7%	100	20.0%
as Clones	Corvallis, OR (COR)	142	7.9%	243	15.5%	336	42.3%
as Clones	Geneva, NY (GEN)	0	0.0%	41	35.3%	54	67.5%
as Clones	Hilo, HI (HILO)	1	25.0%	0	0.0%	0	0.0%
as Clones	Miami, FL (MIA)	0	0.0%	30	20.0%	30	11.4%
as Clones	Riverside, CA (RIV)	17	1.9%	45	5.5%	65	7.9%

c. Progress with Pathogen Clean-Up by Crop

Crop & CWR	NPGS Genebank Unit	Crop PGR	Now	+ 5 Yrs.	+ 10 Yrs.
Allium Garlic	Pullman, WA (W6)	Clonal	10%	72%	94%
Apple	Geneva, NY (GEN)	Clonal	96%	97%	97%
Apple CWR	Geneva, NY (GEN)	Clonal	99%	99%	99%
Chickpea	Pullman, WA (W6)	Seed	90%	95%	100%
Citrus	Riverside, CA (RIV)	Clonal	40%	54%	62%
Cucumis melo	Ames, IA (NC7)	Seed	0%		
Date Palm	Riverside, CA (RIV)	Clonal	100%	50%	0%
Grape	Davis, CA (DAV)	Clonal	7%	26%	39%
	Geneva, NY (GEN)	Clonal	97%	99%	99%
Grape CWR	Geneva, NY (GEN)	Clonal	97%	98%	99%
Hazelnut	Corvallis, OR (COR)	Clonal	100%	99%	99%
Hops	Corvallis, OR (COR)	Clonal	0%	15%	42%
Hops CWR	Corvallis, OR (COR)	Clonal	9%	25%	81%
Lentil	Pullman, WA (W6)	Seed	90%	95%	96%
Lettuce	Pullman, WA (W6)	Seed	0%	25%	50%
Longan	Hilo, HI (HILO)	Clonal	96%		
Macadamia	Hilo, HI (HILO)	Clonal	93%	100%	100%
Opuntia	Parlier, CA (PARL)	Clonal	86%	64%	98%
Pea	Pullman, WA (W6)	Seed	90%	99%	99%
Pecan	College Station, TX (BRW)	Clonal	0%	30%	89%
Pepper	Griffin, GA (S9)	Seed	39%	80%	96%
Phaseolus	Pullman, WA (W6)	Seed	21%	30%	42%
Potato	Sturgeon Bay, WI (NR6)	Seed	99%	99%	100%
Ribes	Corvallis, OR (COR)	Clonal	42%	53%	94%
Rubus	Corvallis, OR (COR)	Clonal	71%	73%	74%
Saccharum	Miami, FL (MIA)	Clonal	100%	37%	0%
Soybean	Urbana, IL (SOY)	Seed	30%	73%	98%
Strawberry	Corvallis, OR (COR)	Clonal	96%	94%	91%
Sweet Potato	Griffin, GA (S9)	Seed	99%	99%	99%
Tart Cherry	Geneva, NY (GEN)	Clonal	98%	98%	99%
Vaccinium	Corvallis, OR (COR)	Clonal	73%	85%	95%

Blank fields indicate that data could not be estimated. COT, GSOR, GSZE, MAY, NE9, NSGC, and USNA do not conduct pathogen clean-up. DAV cannot estimate annual pathogen clean-up.

0.0% 25.0%+ 0% 100%

Fig. 6.3: Progress and Backlogs for Cleaning Up NPGS Accessions from Pathogens.

Fig. 6.3a shows in the first, light beige-shaded row the current number and percentage of NPGS accessions requiring pathogen clean-up that have been completed, and goals for increasing clean-up for +5 years and for +10 years. The preceding information is then presented for NPGS genebank units managing PGR requiring pathogen clean-up. Those genebank units that primarily manage accessions propagated by seeds are grouped above those that primarily manage accessions propagated clonally. The darker the lavender hue, the greater the proportion of accessions at the specific genebank units that require pathogen clean-up.

Fig. 6.3b shows in the first, light beige-shaded row the current number and percentage of NPGS accessions requiring pathogen clean-up that are cleaned-up annually, and goals for increasing annual pathogen clean-up for +5 years and for +10 years. The preceding information is then presented for NPGS genebank units managing PGR conducting annual pathogen clean-up. The genebank units that primarily manage accessions propagated by seeds are grouped above those units that primarily manage accessions propagated clonally. The darker the khaki hue, the greater the proportion of accessions at the specific genebank units that are cleaned-up annually.

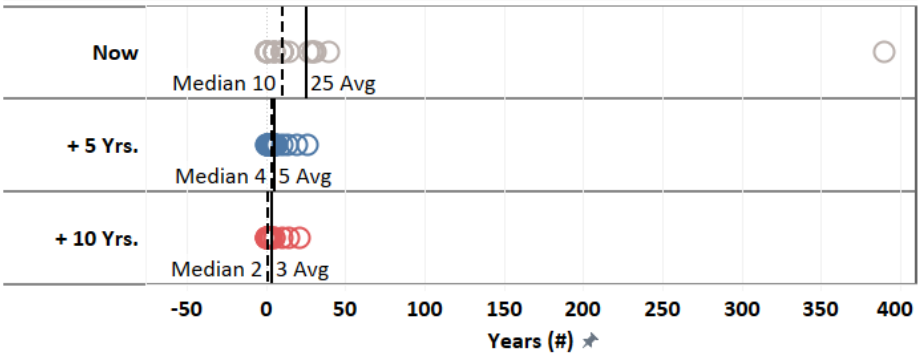
Fig. 6.3c lists specific crops and CWR with accessions that require pathogen clean-up. The NPGS genebank units that manage those accessions, categorized as clonally or seed-propagated, are listed. The percentages of accessions that currently require pathogen clean-up and have been cleaned-up are provided, as are goals for increasing clean-up for +5 years and +10 years. The darker the lavender hue, the greater the percentages of accessions that require pathogen clean-up.

COT, GSOR, GSZE, MAY, NE9, NSGC, and USNA do not clean-up PGR from pathogens. DAV cannot estimate annual pathogen clean-up. Blank fields indicated that data cannot be estimated.

a. Time Needed to Reduce the Backlogs of Cleaning Up NPGS Accessions from Pathogens

	NPGS Genebank Unit	Now MIN (# Years)	Now Avg. of Medians	Now MAX (# Years)	+ 5 Yrs. MIN (# Years)	+ 5 Yrs. Avg. of Medians	+ 5 Yrs. MAX (# Years)	+ 10 Yrs. MIN (# Years)	+ 10 Yrs. Avg. of Medians	+ 10 Yrs. MAX (# Years)	# of Crops & CWR
	NPGS-wide	**0**	**25**	**735**	**0**	**5**	**29**	**0**	**3**	**22**	**31**
Primary Type of Germplasm Managed as Seeds	Griffin, GA (S9)	1	16	30	1	3	5	1	1	1	3
	Parlier, CA (PARL)	10	15	20	5	5	5	2	2	2	1
	Pullman, WA (W6)	0	96	735	1	9	26	0	7	22	5
	Sturgeon Bay, WI (NR6)	10	10	10	10	10	10	10	10	10	1
	Urbana, IL (SOY)	10	10	10	2	3	3	2	3	3	1
Primary Type of Germplasm Managed as Clones	College Station, TX (BRW)	10	10	10	5	5	5	0	0	0	1
	Corvallis, OR (COR)	0	13	40	1	6	14	1	3	5	8
	Geneva, NY (GEN)	5	9	10	3	4	4	3	3	3	5
	Hilo, HI (HILO)	0	2	5	0	0	1	0	0	1	4
	Riverside, CA (RIV)	0		54	5		29	5		15	2

b. Median Years Needed to Reduce the Backlogs



Years 0 20+

The darkest hue indicates an estimated 20+ years are needed to reduce the backlog. Blank fields indicate that data could not be estimated.

COT, DAV, GSOR, GSZE, MAY, MIA, NC7, NE9, NSGC, and USNA do not conduct pathology clean up or cannot estimate the time needed to reduce the backlogs.

Fig. 6.4: Time Needed to Reduce the Backlogs of Cleaning Up NPGS Accessions from Pathogens. The top row of Figure 6.4a, shaded light beige, depicts the current extreme (absolute minimum and maximum) range of years and the averages of the medians of years needed to reduce the backlogs in pathogen clean-up for all the PGR managed by specific NPGS genebank units, and the goals for reducing those backlogs for +5 and +10 years. The data for the individual genebank units are listed below by their geographical locations. The genebank units that primarily manage seed-propagated PGR are grouped above those genebank units that primarily manage clonally-propagated PGR. The darker the teal hue, the more years are needed to reduce the backlogs. The numbers of crops and CWR in each genebank unit that require pathogen clean-up are recorded in the far-right column and summed across all genebank units for an NPGS-wide total in the top beige-shaded row.

Figure 6.4b depicts the current medians for the numbers of years needed to reduce the backlogs in pathogen clean-up for NPGS PGR, and the goals for reducing those backlogs for +5 years and +10 years. The current median numbers of years needed to reduce the backlogs in pathogen clean-up for each of the individual PGR are denoted by light gray circles, the goals for reducing the backlogs +5 years by blue circles, and the goals for +10 years by rust red circles. The medians of medians for the numbers of years, across all PGR, needed to reduce backlogs are depicted by dashed vertical lines, and averages of medians for the number of years, across all PGR, needed to reduce backlogs are depicted as solid vertical lines.

COT, DAV, GSOR, GSZE, MAY, MIA, NC7, NE9, NSGC, and USNA do not conduct PGR clean-up from pathogens or cannot estimate the time needed to reduce the backlogs. Blank fields indicated that data cannot be estimated.

Component 7: PGR Regeneration/Repropagation (Figs. 7.1-7.5)

Current Status

As the viability, quality, and quantity of seeds or vegetative propagules decrease in storage (Component 5) or under cultivation, and inventories are depleted through distribution (Component 8), accessions must be regenerated. The goals for regeneration or repropagation are to increase the quality and quantity of PGR to specific thresholds established to reduce the loss of genetic diversity (Components 4, 5; Clark et al., 1997; Sackville, Hamilton, and Chorlton, 1997; FAO, 2014). Furthermore, highly heritable morphological, agronomic, and horticultural traits are often assayed when NPGS accessions are regenerated (Components 10 and 11). As explained earlier, (see Fig. E) the volume and percentage of NPGS accessions that require regeneration or repropagation, and that are regenerated or repropagated each year, are critical determinants for effective and efficient PGR management and planning for the future (Pardey et al., 2001; Lusty et al., 2021).

The volumes and percentages of accessions that require regeneration or repropagation; which are regenerated or repropagated annually; and the years needed to reduce or eliminate backlogs for regeneration or repropagation; differ greatly across PGR and genebank units (Figs. 7.1-7.5; Figs. S7.1-S7.3). Many factors contribute to these differences. Some tree or vine PGR, such as stone fruits and almonds (*Prunus*) and grapes (*Vitis*) at the Davis genebank unit, require periodic repropagation because of disease infestation, the expanding size of individual trees, and other factors. Nonetheless, no land is currently available for repropagating these PGR in new fields free of diseases, establishing them in orchards with adequate tree spacing, and managing them according to recommended horticultural practices. Consequently, a repropagation backlog has ensued for these PGR.

Dissimilarities in the sizes of regeneration or repropagation backlogs (Figs. 7.1-7.5, Figs. S7.1-S7.3) are also associated particularly with different reproductive modes. As discussed above, clonally propagated PGR often require substantial land areas devoted solely to their maintenance and repropagation. Self-pollinated, seed-propagated PGR generally require less land and labor than do primarily cross-pollinated, seed-propagated PGR (Pardey et al., 2001), consequently regeneration backlogs can often be larger for the latter PGR. Furthermore, proportionately fewer accessions have been regenerated or repropagated from some NPGS collections, such as the Seeds of Success accessions at the Pullman genebank unit, which include relatively high percentages of CWR and other wild taxa. Effective PGR regeneration and repropagation procedures can be completely lacking for those taxa, or particularly problematic to implement.

Across the NPGS, 98,000+ accessions (or ca. 17% of the total number of NPGS accessions) currently require regeneration or repropagation (Fig. 7.1; Fig. S7.1). In an average year, 20,000+ accessions (or ca. 3.6% of the total number of NPGS accessions) are regenerated or repropagated (Fig. 7.2; Fig. S7.2), an amount inadequate to meet current needs, leading to substantial backlogs. Across the NPGS, an average median period of about 10 years and a range of 0 to 300+ years (for maize CWR at Ames) would be required to regenerate or repropagate the accessions that currently require regeneration or repropagation (Fig. 7.3, Fig. S7.3).

For seed-propagated crops, the cost and complexity of regeneration can contribute substantially to PGR maintenance backlogs. The 298,000+ accessions (ca. 52%+ of the total number of 523,000+ NPGS seed-propagated accessions) that are self-pollinated (Fig. 7.4)—comprising most of the accessions of small grains, soybeans (*Glycine)*, and pulses—can be regenerated through a process that is relatively efficient in terms of cost and resources. For instance, the approximate cost of regenerating an accession of primarily self-pollinated homozygous, homogeneous soybean PGR in the field at Urbana is approximately $55 per regeneration. In contrast, ca. 81,000+ NPGS seed-propagated accessions require regeneration through controlled insect or hand pollinations (Fig. 7.4)—a labor, resource, and cost-intensive process (Fu, 2017). The approximate cost of regenerating a heterozygous, heterogeneous accession via controlled pollination at Ames is ca. $600. Therefore, data for NPGS seed-propagated accessions requiring insect-pollination, hand-pollination, and other specialized and expensive regeneration or repropagation procedures were recorded separately to enable a closer examination of the current NPGS status, and to plan strategically for meeting future needs (Figs. 7.2, 7.4, 7.5; Fig. S7.2).

Currently, 43,000+ accessions (or ca. 8% of the total number of NPGS accessions) require regeneration by insect-pollination (Fig. 7.4). Those accessions are often of outcrossing crops (e.g., alfalfa (*Medicago*), brassicas, cucurbits, sunflowers (*Helianthus*), and ornamentals) that are pollinated by bees and/or flies. Currently, in an average year, 800+ accessions, 1.9% of the total number of accessions requiring insect pollination, are regenerated across the NPGS (Figs. 7.4, 7.5). This amount is inadequate to meet current needs and has led to substantial backlogs of accessions requiring regeneration by insect pollination. Another cause for the backlog is lack of knowledge of the insect pollinators for PGR such as CWR and other wild species that has impeded development of effective methods of controlled insect pollination (Richards, 2001).

In an average year, 37,000+ NPGS accessions (or ca. 6.5% of the total number of NPGS accessions) currently require regeneration by hand pollination (Fig. 7.4). Those accessions are often from outcrossing cereal PGR such as maize (*Zea*) and *Sorghum*, but some accessions pollinated "in nature" by insects, e.g., potatoes (*Solanum*), tomatoes (*Solanum*), and sunflower cultivars (*Helianthus*), must also be hand-pollinated. In an average year, 3,100+ accessions, 8% of the total number of accessions that require hand pollination, are regenerated (Figs. 7.4, 7.5). That amount is also inadequate to meet current needs and contributes to the substantial backlog of accessions requiring regeneration by hand-pollination.

At present, 112,000+ accessions (or ca. 20% of the total number of NPGS accessions; Fig. 7.4) are regenerated or repropagated by other specialized procedures, such as i) re-planting, grafting, and micropropagation for clonally-propagated accessions; and ii) pollinator exclusion, isolation, or cultivation in protected environments for some seed-propagated accessions (Fig. 7.4). In an average year, 5,500+ accessions of the total number of accessions requiring specialized procedures (including clonal propagation) are regenerated or repropagated (Fig. 7.5). As with the other regeneration and repropagation methods, this amount is inadequate to meet current needs, and has led to substantial backlogs.

Strategies and Implementation

To strategically reduce the backlogs in PGR regeneration, approximately 229,000+ accessions (or roughly 38% of the current total number in the NPGS) should be regenerated or repropagated at +10 years (Fig. 7.5; Fig. S7.2). To attain that outcome, the overall annual rate of regeneration and repropagation will be increased to ca. 23,000+ to reduce the current backlogs to a range of 0-60 years across the NPGS (Fig. 7.5; Fig. S7.3). The size of this increase was determined by a conservative approach that recognizes the logistical complexity of regeneration and repropagation operations that require not only additional personnel and budgetary resources for expansion, but also more field, greenhouse, and screenhouse space (Component 1). This is particularly a priority for the Davis genebank unit mentioned above, and the Parlier genebank unit that provides other genebank units with crucial PGR seed regeneration capacities in an arid, long-season environment (Appendix B). Conducting regeneration and repropagation according to the statistical designs discussed in greater detail in Component 11 will also necessitate more land.

The following strategy will be adopted to reduce the current NPGS backlogs (Fig. 7.5), during the next +10 years: i) a total of ca. 114,000+ self-pollinated accessions will be regenerated, at a rate of ca. 11,000+ accessions annually; ii) 12,000+ insect-pollinated accessions will be regenerated at a rate increasing to ca. 1,500+ accessions annually; iii) ca. 41,000+ hand-pollinated accessions will be regenerated at a rate increasing to 4,900+ accessions annually (Fig. 7.5). A total of 78,000+ accessions that require specialized procedures (which includes 32,000+ clonally propagated) will be regenerated or repropagated during the next +10 years, at an increased annual rate of 9,200+ accessions (Fig. 7.5). This strategy would include the complete clonal repropagation of several field collections of perennial crops, such as apple (*Malus*, Geneva genebank unit); *Macadamia* (Hilo); avocado (*Persea*) and sugarcane (*Saccharum*, Miami); date palm (*Phoenix*, Riverside); pistachio (*Pistacia*), walnuts (*Juglans*), almonds, cherries, and plums (all *Prunus*) at Davis; and banana and plantain (*Musa*), cacao (*Theobroma*), and other tropical tree crops at Mayagüez. In addition to expanding the operational capacities for repropagation, reducing current backlogs requires more efficient and effective methods, especially for clonally propagated accessions, and for CWR or other wild taxa (Brown et al., 1997; see Applied Research below).

Applied Research for Developing Optimal Regeneration/Repropagation Methods

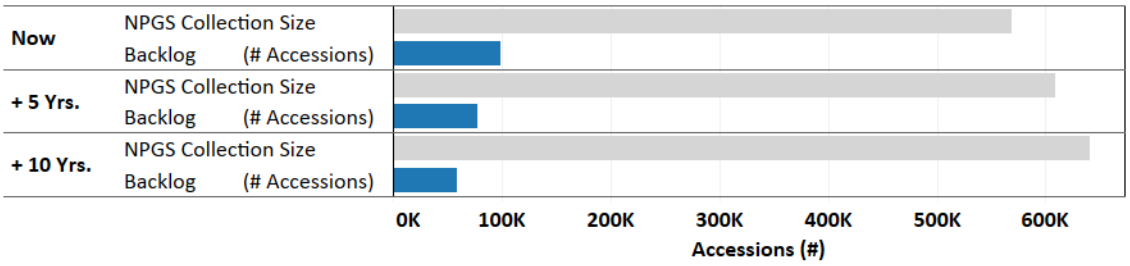
Research will be conducted to develop more efficient and effective approaches for effectively regenerating or repropagating:

- clonally-propagated taxa;
- self-pollinated genetic stocks, especially for barley and wheat, for which such procedures are often completely lacking;
- insect-pollinated PGR, especially of CWR or other wild taxa, such as those from the Seeds of Success program; and
- hand-pollinated PGR or devising alternative approaches for regenerating those PGR.

The reproductive modes (breeding systems, pollination mechanisms; Richards, 2001) of poorly known CWR and wild taxa (e.g., PGR from the Seeds of Success program at Pullman) and some PGR (e.g., papaya *Carica* at Hilo) must be ascertained to attain the goal of devising efficient and effective means for regenerating them. Tropical tree PGR require extensive research in this regard, including developing regimens to control and promote flowering, and methods for successfully grafting problematic PGR, e.g., mamey sapote (*Pouteria*) and *Manilkara* at Mayagüez, and pili nut (*Canarium*) at Hilo.

The efficacy of current regeneration and repropagation procedures for maintaining PGR "true-to-type" with minimal loss of genetic diversity (Clark et al., 1997) can be measured through genotypic characterizations (Component 10). Such genetic data are integral for discovering the genetic profiles of taxa and accessions, and the degree of outcrossing and self-pollination (Chebotar et al., 2003). Knowledge of those features is crucial for designing and operating efficient and effective PGR regeneration and repropagation programs (Sackville Hamilton and Chorlton, 1997), especially for poorly known CWR and other wild taxa. It is also needed for devising efficient and effective methods for regenerating genetic stocks, and maintaining them true-to-type, e.g., for small grains at the Aberdeen genebank unit.

a. NPGS PGR Regeneration/Repropagation Needs



b. NPGS PGR Regeneration/Repropagation Backlogs

	NPGS Genebank Unit	Now Backlog (# Accessions)	Now % of Collection	+ 5 Yrs. Backlog (# Accessions)	+ 5 Yrs. % of Collection	+ 10 Yrs. Backlog (# Accessions)	+ 10 Yrs. % of Collection
	NPGS-wide	**98,842**	**17%**	**78,124**	**13%**	**59,383**	**9%**
	PGR specialization	**88,346**	**17%**	**68,074**	**12%**	**49,906**	**9%**
Managed as Seeds	Aberdeen, ID (NSGC)	7,301	5%	6,100	4%	5,600	4%
Managed as Seeds	Ames, IA (NC7)	18,032	34%	15,272	25%	9,733	15%
Managed as Seeds	College Station, TX (COT)	3,500	36%	2,100	21%	600	6%
Managed as Seeds	Geneva, NY (NE9)	2,934	23%	2,777	21%	1,794	13%
Managed as Seeds	Griffin, GA (S9)	17,514	17%	13,604	12%	11,817	10%
Managed as Seeds	Parlier, CA (PARL)	368	31%	129	10%	94	6%
Managed as Seeds	Pullman, WA (W6)	24,622	25%	12,797	12%	4,883	4%
Managed as Seeds	Sturgeon Bay, WI (NR6)	1,345	23%	1,345	22%	1,345	22%
Managed as Seeds	Stuttgart, AR (GSOR)	80	0%	200	1%	190	0%
Managed as Seeds	Urbana, IL (GSZE)	10,000	24%	11,000	22%	12,000	22%
Managed as Seeds	Urbana, IL (SOY)	2,650	12%	2,750	11%	1,850	7%
	PGR specialization	**10,496**	**23%**	**10,050**	**20%**	**9,477**	**17%**
Managed as Clones	College Station, TX (BRW)	100	2%	50	1%	0	0%
Managed as Clones	Corvallis, OR (COR)	5,417	42%	4,991	36%	3,681	25%
Managed as Clones	Davis, CA (DAV)	1,233	17%	2,248	26%	2,538	26%
Managed as Clones	Geneva, NY (GEN)	925	12%	200	3%	200	2%
Managed as Clones	Hilo, HI (HILO)	543	45%	865	38%	1,446	43%
Managed as Clones	Mayaguez, PR (MAY)	259	21%	359	26%	494	33%
Managed as Clones	Miami, FL (MIA)	733	47%	775	43%	599	29%
Managed as Clones	Riverside, CA (RIV)	86	5%	287	16%	319	18%
Managed as Clones	Washington, D.C. (USNA)	1,200	14%	275	3%	200	2%

Primary Type of Germplasm

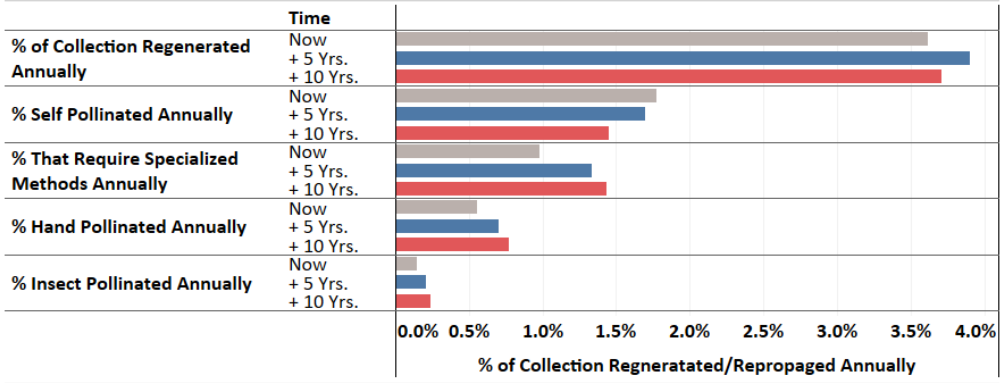
0% 50%+

Fig. 7.1: NPGS PGR Regeneration/Repropagation Needs and Backlogs. Figure 7.1a depicts by the light gray bars the total numbers of accessions currently in the NPGS PGR collection and collection size projected for +5 and +10 years. The blue bars depict the total numbers of accessions in the NPGS PGR collection currently requiring regeneration or repropagation and the goals for regenerating those accessions for +5 and +10 years.

The top light beige-shaded row of Fig. 7.1 b shows the numbers and percentages of all NPGS accessions that currently require regeneration/repropagation, and the goals for reducing those backlogs for +5 years and for +10 years. The same information is then presented for individual NPGS genebank units, listed below by their geographical locations. The genebank units that primarily manage seed-propagated accessions are grouped above those that primarily manage clonally-propagated accessions. The light beige-shaded rows above each group of genebank units presents the overall numbers and percentages of accessions for the group that currently require regeneration/repropagation, and the goals for reducing backlogs in regeneration/repropagation for +5 years and +10 years for each group of genebank units. The PGR specialization sub-headings in beige highlight the differences in regeneration rates between seed-propagated and clonally-propagated accessions. For individual genebank units, the numbers and percentages of accessions that currently require regeneration/repropagation, and the goals for reducing regeneration/repropagation backlogs for +5 years and for +10 years, are color-coded. The higher the percentages of accessions at the individual NPGS genebank units that require regeneration/repropagation, the darker the green hue, with 50% that require regeneration/repropagation at genebank units the darkest.

Annual Regeneration/Repropagation of NPGS PGR

a. Percentages of NPGS PGR Regenerated/Repropagated Annually



b. Numbers and Percentages of NPGS PGR Regenerated/Repropagated Annually

Primary Type of Germplasm	NPGS Genebank Unit	Now: Annually Regenerated (Avg # Accessions)	Now: % of Collection Regenerated Annually	+ 5 Yrs.: Annually Regenerated (Avg # Accessions)	+ 5 Yrs.: % of Collection Regenerated Annually	+ 10 Yrs.: Annually Regenerated (Avg # Accessions)	+ 10 Yrs.: % of Collection Regenerated Annually
	NPGS-wide	**20,588**	**4%**	**23,728**	**4%**	**23,753**	**4%**
	PGR specialization	**17,447**	**3%**	**20,427**	**4%**	**20,413**	**3%**
Managed as Seeds	Aberdeen, ID (NSGC)	6,660	5%	6,625	5%	6,625	5%
Managed as Seeds	Ames, IA (NC7)	1,047	2%	2,095	3%	2,978	5%
Managed as Seeds	College Station, TX (COT)	350	4%	300	3%	250	2%
Managed as Seeds	Geneva, NY (NE9)	170	1%	342	3%	385	3%
Managed as Seeds	Griffin, GA (S9)	2,765	3%	3,192	3%	3,174	3%
Managed as Seeds	Parlier, CA (PARL)	66	6%	97	8%	55	4%
Managed as Seeds	Pullman, WA (W6)	1,909	2%	2,936	3%	3,008	3%
Managed as Seeds	Sturgeon Bay, WI (NR6)	1,000	17%	1,000	17%	1,000	16%
Managed as Seeds	Stuttgart, AR (GSOR)	40	0%	40	0%	38	0%
Managed as Seeds	Urbana, IL (GSZE)	1,000	2%	1,100	2%	1,200	2%
Managed as Seeds	Urbana, IL (SOY)	2,440	11%	2,700	11%	1,700	7%
	PGR specialization	**3,141**	**7%**	**3,301**	**6%**	**3,340**	**6%**
Managed as Clones	College Station, TX (BRW)	100	2%	50	1%	0	0%
Managed as Clones	Corvallis, OR (COR)	1,237	10%	1,374	10%	1,502	10%
Managed as Clones	Davis, CA (DAV)	761	11%	727	9%	582	6%
Managed as Clones	Geneva, NY (GEN)	185	2%	183	2%	220	3%
Managed as Clones	Hilo, HI (HILO)	197	16%	173	8%	296	9%
Managed as Clones	Mayaguez, PR (MAY)	234	19%	255	18%	283	19%
Managed as Clones	Miami, FL (MIA)	116	8%	181	10%	157	8%
Managed as Clones	Riverside, CA (RIV)	86	5%	108	6%	100	6%
Managed as Clones	Washington, D.C. (USNA)	225	3%	250	3%	200	2%

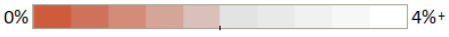


Fig. 7.2: Annual Regeneration/Repropagation of NPGS PGR. The gray bars in Fig 7.2a depict the current average percentages of the total number of NPGS accessions regenerated/repropagated annually. The goals for increasing the average percentages of accessions regenerated/repropagated at +5 years are depicted by the blue bars, and for +10 years by the rust red bars. The same information is provided separately for accessions regenerated/repropagated by self-pollination, specialized methods (as explained in the text), hand pollination, and insect pollination.

The top row of Fig. 7.2b shaded light beige depicts the average number and percentage of the total numbers of NPGS accessions that are currently regenerated/repropagated annually and goals for increasing the numbers and percentages for +5 and +10 years. The numbers and percentages for repropagations/regenerations are depicted in the other two rows shaded light beige for the group of genebank units that primarily manage seed-propagated accessions and those that primarily manage clonally-propagated accessions. For individual genebank units, the average total number and percentages of accessions at the genebank units that currently are regenerated/repropagated annually, and the goals for increasing those numbers and percentages for +5 and +10 years, are provided. The darker the brown hue, the lower the average percentage of accessions that are regenerated/repropagated annually at the genebank units, with the darkest hue 0% regenerated/repropagated annually.

a. Time Needed to Reduce Backlogs for Regenerating/Repropagating NPGS Accessions

	NPGS Genebank Unit	Now MIN (# Years)	Now Avg. of Medians (# Years)	Now MAX (# Years)	+ 5 Yrs. MIN (# Years)	+ 5 Yrs. Avg. of Medians (# Years)	+ 5 Yrs. MAX (# Years)	+ 10 Yrs. MIN (# Years)	+ 10 Yrs. Avg. of Medians (# Years)	+ 10 Yrs. MAX (# Years)	# of Crops & CWR
	NPGS-wide	**0**	**10**	**371**	**0**	**5**	**60**	**0**	**4**	**60**	**185**
Managed as Seeds	Aberdeen, ID (NSGC)	1	2	5	1	2	3	1	2	3	10
	Ames, IA (NC7)	1	20	371	1	12	60	1	12	60	21
	College Station, TX (COT)	10	10	10	5	5	5	3	3	3	1
	Geneva, NY (NE9)	1	11	32	1	7	18	0	4	12	12
	Griffin, GA (S9)	1	12	230	0	4	25	0	2	20	26
	Parlier, CA (PARL)	0	5	20	0	4	12	0	3	8	7
	Pullman, WA (W6)	0	22	95	1	5	12	1	2	7	23
	Sturgeon Bay, WI (NR6)	0	0	0	0	0	0	0	0	0	1
	Stuttgart, AR (GSOR)	1	1	2	1	2	2	1	2	2	3
	Urbana, IL (GSZE)	10	10	10	10	10	10	10	10	10	1
	Urbana, IL (SOY)	1	1	2	1	1	2	1	1	2	2
Managed as Clones	College Station, TX (BRW)	10	10	10	5	5	5	0	0	0	1
	Corvallis, OR (COR)	1	10	55	1	6	27	1	4	10	17
	Davis, CA (DAV)	1	2	3	1	2	3	1	2	3	10
	Geneva, NY (GEN)		3			3			3		5
	Hilo, HI (HILO)	0	11	50	1	7	20	1	6	20	18
	Mayaguez, PR (MAY)	0	2	7	0	2	7	0	2	7	12
	Miami, FL (MIA)	1	3	5	1	3	5	1	3	5	12
	Riverside, CA (RIV)	1	1	1	1	1	1	1	1	1	2
	Washington, D.C. (USNA)	1	10	30	1	10	30	1	10	30	1

Primary Type of Germplasm

b. Median Years Needed to Reduce the Backlogs

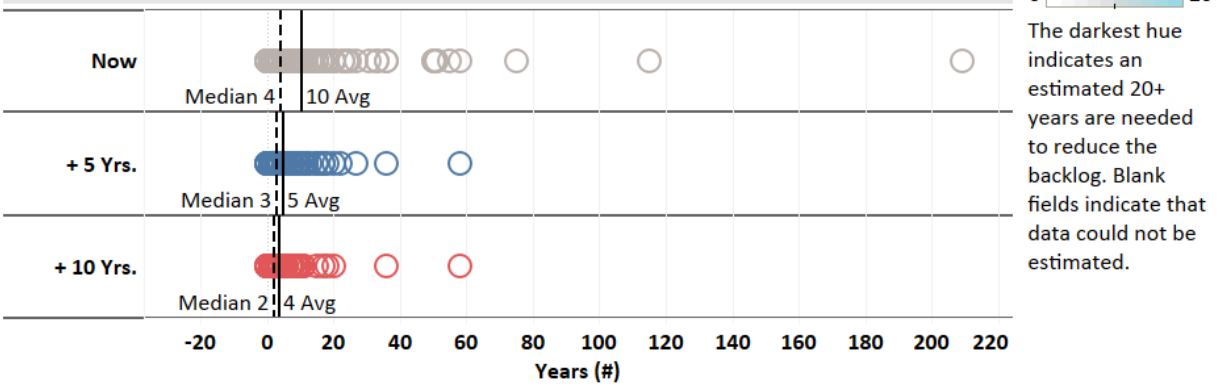


Fig. 7.3: Time Needed to Reduce Backlogs for Regeneration/Repropagation of NPGS Accessions. The top row of Fig. 7.3a, shaded light beige, shows the current overall extreme (absolute minimum and maximum) range of years and the averages of the medians of years needed to reduce the backlogs in regeneration/repropagation for all the PGR in the NPGS. The data for the individual genebank units are listed below by their geographical locations. The genebank units that primarily manage seed-propagated PGR are grouped above those that primarily manage clonally-propagated PGR. The darker the aqua hue, the more years are needed to reduce the backlogs, with the darkest hue 20+ years. The numbers of PGR in each genebank unit that require regeneration/repropagation are recorded in the far-right column and summed across all genebank units for an NPGS-wide total in the top beige-shaded row. Many of the longest backlogs result from a current lack of effective means for regenerating/repropagating PGR, which will be the focus of applied research in this Plan. Blank fields indicate that data could not be estimated.

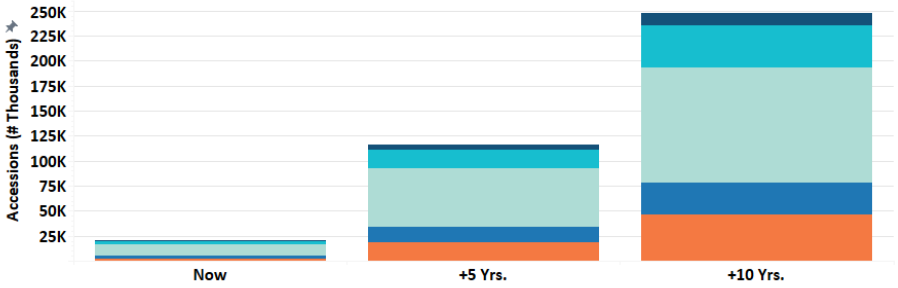
Figure 7.3b depicts the current medians for the numbers of years needed to reduce the backlogs in regeneration/repropagation for NPGS accessions overall, and the goals for reducing the backlogs for +5 years and +10 years. The current median numbers of years needed to reduce the backlogs in regeneration/repropagation for individual PGR are denoted by gray circles, the goals for reducing backlogs at +5 years by blue circles, and the goals for +10 years by rust red circles. The medians of medians for the numbers of years, across all PGR, needed to reduce backlogs are depicted by dashed vertical lines, and averages of medians for the number of years, across all PGR, needed to reduce backlogs are depicted as solid vertical lines.

Types of Regeneration/Propagation Methods for NPGS Accessions

		Percent of Collection			Number of Accessions		
		Now	+ 5 Yrs.	+ 10 Yrs.	Now	+ 5 Yrs.	+ 10 Yrs.
NPGS-wide	Insect Pollinated	8%	8%	8%	43,923	46,403	49,190
	Hand Pollinated	7%	6%	5%	37,548	36,966	34,174
	Self Pollinated	52%	50%	48%	298,307	304,044	309,113
	Clonally Propagated	14%	17%	20%	76,877	101,944	128,785
	Specialized Techniques	20%	20%	19%	112,542	119,027	119,152

Fig. 7.4: Types of Regeneration/Repropagation Methods for NPGS Accessions. The percentages of NPGS accessions currently regenerated/repropagated are depicted at the left, and estimates for +5 and +10 years, through insect-pollination, hand-pollination, self-pollination, clonal propagation, and that require specialized regeneration/repropagation methods. The data at the right provide the total numbers of NPGS accessions currently regenerated/repropagated by the preceding methods and estimates for regeneration/repropagation for +5 years and +10 years.

a. Regeneration/Repropagation of NPGS Accessions



b. Cumulative Totals for NPGS Accession Regenerations/Repropagations

	Now	+5 Yrs.	+10 Yrs.
NPGS-wide Regenerations	20,588	110,790	229,505
Insect Pollinated	813	5,213	12,386
Hand Pollinated	3,139	18,530	41,869
Self Pollinated	11,184	57,774	114,817
Clonally Propagated	3,131	15,990	32,124
Specialized Regeneration*	2,443	18,290	46,065

c. Average Number of NPGS Accessions Regenerated Annually

	Now	+5 Yrs.	+10 Yrs.
NPGS-wide Regenerations	20,588	23,728	23,753
Insect Pollinated	813	1,272	1,543
Hand Pollinated	3,139	4,273	4,931
Self Pollinated	11,184	11,997	11,017
Clonally Propagated	3,131	3,264	3,202
Specialized Regneration*	2,443	4,874	6,009

Regeneration Method
- Insect Pollinated
- Hand Pollinated
- Self Pollinated
- Clonally Propagated
- Specialized Regeneration*

Specialized* includes accessions which require specialized regeneration procedures and are maintained at NPGS genebank units which manage primarily seed-propagated PGR

Fig. 7.5: Regeneration/Repropagation of NPGS Accessions. The stacked bar charts in Figure 7.5a depict the number of NPGS accessions currently regenerated/repropagated annually, and the goals for cumulative numbers of NPGS accessions regenerated/repropagated between the present time and +5 years (labelled +5 Yrs.) and between the present time and +10 years (labelled +10 Yrs.). The numbers of insect pollinated accessions are depicted by navy blue, hand pollinated by aqua, self-pollinated by light aqua, clonally-propagated by blue, and specialized regeneration procedures by orange.

Figure 7.5b lists the cumulative numbers of NPGS accession regenerations/repropagations and goals for increasing the numbers of regeneration/repropagations for +5 years and +10 years; these data are depicted above in Fig. 7.5a. The top row lists cumulative numbers of NPGS accessions regenerated/repropagated overall; the numbers of NPGS accessions regenerated/repropagated by insect, hand, and self-pollination, or by clonal propagation or specialized methods are listed below.

Figure 7.5c lists the average numbers of NPGS accessions currently regenerated/repropagated annually and goals for increasing the annual numbers at +5 and +10 years. The top row lists total number of NPGS accessions regenerated/repropagated on average annually. The average numbers of NPGS accessions regenerated/repropagated annually by insect, hand, and self-pollination, or by clonal propagation or specialized methods are listed below.

Component 8: PGR Availability and Distribution (Fig. 8)

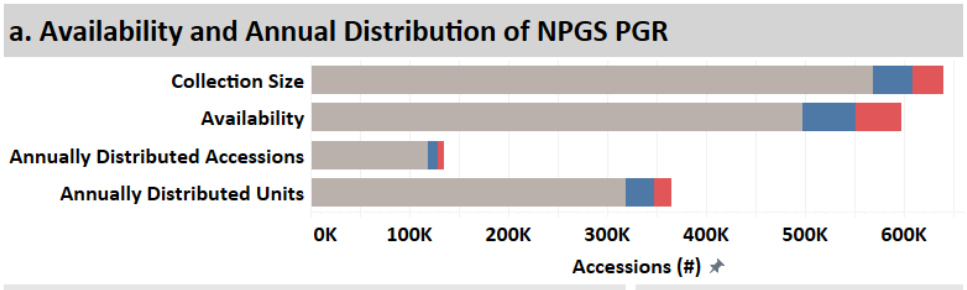
Current Status

The volume and percentage of accessions available for distribution constitute invaluable metrics for assessing the overall status and functioning of a PGR management system, its constituent genebank units, and their PGR collections. Essentially all the other aspects of PGR management discussed in this Plan must be synchronized and function effectively for conserving PGR successfully and distributing them to users. At present, 497,000+ NPGS accessions are available for distribution to users, comprising the great majority of (87+%) of the overall current NPGS collections covered by this Plan (Fig. 8; Fig. S8b). Nevertheless, proportionately fewer accessions are available from some PGR collections, such as apple (*Malus*) and grape (*Vitis*) CWR, and Seed of Success accessions at Pullman, which contain relatively large quantities of CWR and other wild taxa. As described in other Components, effective PGR maintenance, testing, and regeneration procedures can be completely lacking for those taxa, or are particularly complicated and expensive to implement, leading to reduced availability to users. Pecan (*Carya*) accessions at College Station (BRW) are currently unavailable for distribution because of quarantine restrictions (Fig. 8, Fig. S8b).

The average volumes and percentages of accessions and seed packets or propagation units distributed to users, and the average volume of PGR orders filled annually, also constitute valuable indicators for the demand for those accessions and to the value that the user community places on the NPGS. At present, the average annual volumes of seed packets or propagation units distributed (ca. 250,000+-300,000+), and the numbers and percentages of accessions distributed (118,000+, 21%+ of the total number of NPGS accessions, Fig. 8; Fig.S8c) by the NPGS are among the highest of any national or international genebank system (Fu, 2017). Those volumes and percentages vary substantially across PGR collections and genebank units, with PGR of soybean (*Glycine*, Urbana), potato (*Solanum*, Sturgeon Bay), maize (*Zea*, Ames), vegetables (Geneva) and temperate fruits (Corvallis) in particularly high demand (Fig. 8; Fig. S8c). The overall high demand for and volume of PGR distributed are primary causes for the relatively frequent regenerations/repropagations of some accessions, and the associated extensive quality control (germination and viability testing, pathogen testing, and clean-up) efforts throughout the NPGS (Components 5,6,7).

Strategies and Implementation

By +10 years, 93+% of the total number of NPGS accessions should be available for distribution (Fig. 8; Fig. S8b). To attain that outcome, many of the PGR management backlogs described earlier in this Plan must be substantially reduced, and a larger future NPGS collection must be effectively managed, with the PGR maintenance operations (Components 4-7) well-synchronized and functioning efficiently. Furthermore, the demand for NPGS PGR is forecast to continue to increase in the coming +10 years (especially for vegetable crops), with a forecast ca. 15,000+ more accessions distributed annually to researchers, breeders, and producers (Fig. 8; Fig. S8c). Fulfilling these expanded demands will require expanding strategically the NPGS's infrastructure and PGR management capacities, as documented in Components 1 and 2.



b. Availability of NPGS Accessions | **c. Annual Distribution of NPGS Accessions**

Primary Type of Germplasm	NPGS Genebank Unit	Now	+ 5 Yrs.	+ 10 Yrs.	Now	+ 5 Yrs.	+ 10 Yrs.
	NPGS-wide	**87%**	**90%**	**93%**	**21%**	**21%**	**21%**
	PGR Specialization	**88%**	**92%**	**95%**	**20%**	**21%**	**20%**
Managed as Seeds	Aberdeen, ID (NSGC)	98%	98%	98%	13%	13%	13%
Managed as Seeds	Ames, IA (NC7)	78%	77%	86%	40%	38%	37%
Managed as Seeds	College Station, TX (COT)	69%	78%	78%	22%	16%	12%
Managed as Seeds	Geneva, NY (NE9)	77%	79%	85%	43%	41%	40%
Managed as Seeds	Griffin, GA (S9)	86%	91%	93%	26%	25%	24%
Managed as Seeds	Parlier, CA (PARL)	73%	89%	93%	20%	20%	18%
Managed as Seeds	Pullman, WA (W6)	77%	88%	96%	11%	12%	11%
Managed as Seeds	Sturgeon Bay, WI (NR6)	97%	97%	97%	43%	42%	41%
Managed as Seeds	Stuttgart, AR (GSOR)	94%	96%	96%	9%	10%	10%
Managed as Seeds	Urbana, IL (GSZE)	100%	100%	100%	13%	11%	10%
Managed as Seeds	Urbana, IL (SOY)	98%	98%	98%	50%	60%	65%
	PGR Specialization	**77%**	**78%**	**78%**	**26%**	**26%**	**26%**
Managed as Clones	College Station, TX (BRW)	0%	2%	4%	0%	1%	2%
Managed as Clones	Corvallis, OR (COR)	97%	97%	96%	48%	49%	49%
Managed as Clones	Davis, CA (DAV)	87%	91%	96%	14%	12%	11%
Managed as Clones	Geneva, NY (GEN)	44%	46%	49%	29%	33%	35%
Managed as Clones	Hilo, HI (HILO)	61%	42%	33%	30%	19%	29%
Managed as Clones	Mayaguez, PR (MAY)	65%	77%	80%	45%	44%	44%
Managed as Clones	Miami, FL (MIA)	98%	99%	100%	38%	38%	38%
Managed as Clones	Riverside, CA (RIV)	100%	100%	89%	31%	32%	33%
Managed as Clones	Washington, D.C. (USNA)	100%	100%	100%	8%	5%	5%

Fig. 8: Availability and Annual Distribution of NPGS PGR. The gray bars in Fig. 8a depict the number of accessions currently managed by the NPGS, the number of those accessions available for distribution, the average number of accessions distributed annually, and the average number of samples or units of accessions distributed annually. The projected values for +5 years are depicted by the blue bars, and for +10 years by the rust red bars.

The top row of Fig. 8b, shaded light beige, depicts the percentage of NPGS accessions currently available for distribution and goals for increasing availability for +5 and +10 years. The percentages of accessions available are depicted in the other two rows, shaded light beige, for the group of genebank units that primarily manage seed-propagated accessions and for those that primarily manage clonally-propagated accessions. For individual genebank units, the average percentages of accessions that currently are available, and the goals for increasing those percentages for +5 and +10 years, are provided. The darker the green hue, the lower the percentage of accessions that are available at the genebank units, with the darkest hue 0% available.

The top row of Fig. 8c, shaded light beige, depicts the average percentage of NPGS accessions currently distributed annually and projected distributions for +5 and +10 years. The average percentages of accessions distributed are depicted in the other two rows, shaded light beige, for the group of genebank units that primarily manage seed-propagated accessions and for those that primarily manage clonally-propagated accessions. For individual genebank units, the average percentages that currently are distributed, and projected increases for those percentages for +5 and +10 years, are provided. The darker the blue hue, the lower the percentage of accessions that are distributed annually from the genebank units, with the darkest hue 0% distributed.

Plan Components 9-11: PGR Characterization and Evaluation

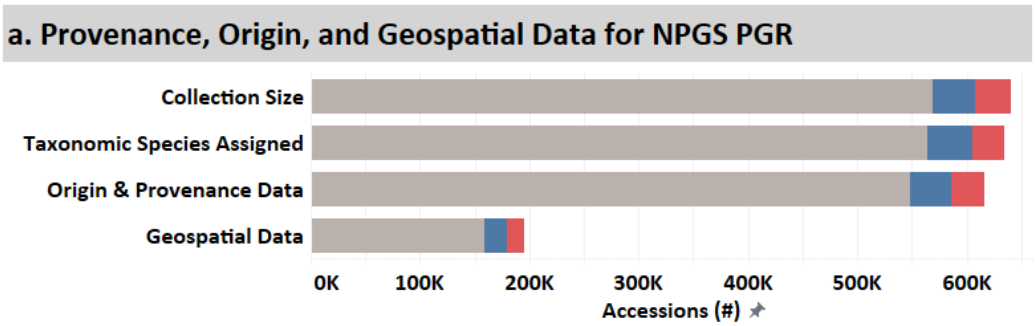
Component 9: PGR Documentation (Fig. 9)

Current Status

The information management system GRIN-Global serves as a primary source of "passport data", the basic descriptive information about NPGS PGR that is critical for effective PGR management, and as a reference for potential requestors. The provenance or origin has been documented for nearly all (548,000+ accessions; 96 % of the total number) of the current NPGS accessions (Fig. 9). More precise geospatial (longitude, latitude, elevation) data are currently available for fewer (158,000+ accessions; ca. 28 % of total) NPGS accessions (Fig. 9). Notably, such geospatial information is relevant primarily for accessions of wild taxa, CWR, and traditional cultivars, but not for the many NPGS accessions of "scientifically-bred" cultivars, so those lower percentages are to be expected. Generally speaking, the more precise their taxonomic identification, the more valuable are PGR for research and breeding (Lusty et al., 2021). Essentially all (563,000+ accessions, Fig. 9) of the NPGS accessions have been identified at least to the taxonomic level of species, according to the current understandings of systematic relationships.

Strategies and Implementation

The preceding data demonstrate that NPGS PGR are well-characterized with respect to their origins and taxonomic identification. It is projected that, at +10 years, the provenance or origin for a greater number (613,000+) of NPGS accessions will have been documented (Fig. 9), an outcome achieved primarily because newly acquired accessions should be accompanied by those data. Notably, the total number and percentage of accessions with that information will have upper bounds because, except for unusual circumstances, it will be infeasible to uncover more details for provenance and origin for accessions acquired long ago. Similar upper bounds are applicable for ascertaining more precise geospatial locality coordinates for such accessions (Fig. 9). With expanded knowledge of PGR systematic relationships generated from genotypic characterizations (Component 10), more of the NPGS accessions (630,000+ accessions, 96% of total, Fig. 9) could be identified at +10 years at least to the taxonomic level of species. Furthermore, the preceding data will have the impact of providing more accurate taxonomic classifications for many crop taxa, especially those with complicated phylogenies, with accompanying changes in assignments to species.



b. NPGS Accessions with Provenace & Origin Data

c. NPGS Accessions with Geospatial Data

Primary Type of Germplasm Managed	NPGS Genebank Unit	Now	+ 5 Yrs.	+ 10 Yrs.	Now	+ 5 Yrs.	+ 10 Yrs.
	NPGS-wide	**96%**	**96%**	**96%**	**28%**	**33%**	**34%**
as Seeds	Aberdeen, ID (NSGC)	100%	100%	100%	46%	46%	46%
as Seeds	Ames, IA (NC7)	95%	96%	95%	26%	35%	38%
as Seeds	College Station, TX (COT)	84%	84%	85%	1%	2%	2%
as Seeds	Geneva, NY (NE9)	100%	100%	100%	9%	8%	8%
as Seeds	Griffin, GA (S9)	97%	97%	97%	11%	12%	13%
as Seeds	Parlier, CA (PARL)	99%	99%	99%	23%	29%	25%
as Seeds	Pullman, WA (W6)	99%	99%	99%	41%	44%	47%
as Seeds	Sturgeon Bay, WI (NR6)	82%	83%	83%	69%	69%	70%
as Seeds	Stuttgart, AR (GSOR)	95%	94%	94%	3%	3%	3%
as Seeds	Urbana, IL (GSZE)	100%	100%	100%			
as Seeds	Urbana, IL (SOY)	100%	100%	100%	38%	46%	52%
as Clones	College Station, TX (BRW)	95%	95%	95%	50%	50%	50%
as Clones	Corvallis, OR (COR)	99%	98%	97%	37%	37%	37%
as Clones	Davis, CA (DAV)	40%	37%	35%	6%	7%	8%
as Clones	Geneva, NY (GEN)	94%	94%	95%	40%	42%	44%
as Clones	Hilo, HI (HILO)	99%	100%	100%	21%	98%	99%
as Clones	Mayaguez, PR (MAY)	75%	76%	77%	9%	18%	24%
as Clones	Miami, FL (MIA)	88%	89%	91%	0%	0%	0%
as Clones	Riverside, CA (RIV)	86%	89%	91%	1%	6%	10%
as Clones	Washington, D.C. (USNA)	46%	54%	61%	46%	54%	61%

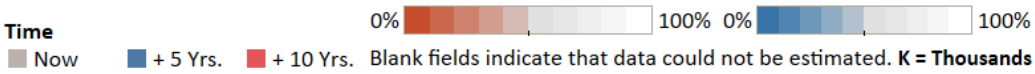


Fig. 9: Provenance, Origin, and Geospatial Data for NPGS PGR. In Fig. 9a, the number of accessions currently managed by the NPGS, the number of those accessions with taxonomic species assigned, documented origin and provenance, and geospatial (latitude, longitude, and/or elevation) information, are depicted by the gray bars. The number of accessions with this information is estimated for +5 years by the blue bars, and for +10 years by the rust red bars.

Figure 9b depicts the percentage of NPGS accessions with provenance and origin information and projected percentages of accessions with that information at +5 and +10 years. The top row, shaded in light beige, shows the overall percentage across the entire NPGS. Percentages for individual genebank units are listed below by their geographical locations. The data for genebank units that primarily manage seed-propagated PGR are grouped above those for genebank units that primarily manage clonally-propagated PGR. The darker the brown hue, the lower the percentage of accessions at individual NPGS genebank units with provenance and origin information.

Figure 9c depicts the percentage of NPGS accessions currently with geospatial data for their origin/provenance and projected percentages for +5 years and +10 years. The top row, shaded in light beige, shows the overall percentage across the entire NPGS. Percentages for individual genebank units are listed below by their geographical locations. The data for genebank units that primarily manage seed-propagated PGR are grouped above data for those genebank units that primarily manage clonally-propagated PGR. The darker the blue hue, the lower the percentage of accessions at individual NPGS genebank units with geospatial data for their origin/provenance and the lower the estimated percentages for +5 and +10 years. Data could not be estimated for blank fields.

Component 10: PGR Genotypic Characterization (Figs. 10.1-10.2)

Current Status

Genotypic characterizations with DNA markers such as simple-sequence repeats (SSRs) or single nucleotide polymorphisms (SNPs) generate information that is invaluable for efficient and effective PGR management, and for enabling requestors to select the best NPGS PGR for their research or breeding projects. Statistical analyses of the genetic data generated from those characterizations can yield "genetic profiles" for accessions that describe their overall genetic variability content, the structure of that variability within the accessions, and the systematic/phylogenetic relationships among accessions. Such profiles can contribute strongly to PGR management efficiency by ascertaining evolutionary or breeding histories; guiding genetic gap analyses for PGR acquisition strategies (Component 3); detecting shifts in accessions' genetic contents due to inadvertent gene flow, admixture, and genetic drift (Components 5,7); estimating optimal sample sizes and pollination methods for efficient regeneration and repropagation (Component 7); detecting misidentified and mislabeled accessions; setting priorities for accession regeneration and evaluation (Component 11); assisting in delimiting core subsets and trait evaluation arrays (Component 11); and guiding the design of initial pre-breeding or breeding programs (Component 12) focused on broadening the base of genepools or selectively incorporating high-value traits (Bretting and Widrlechner, 1995; Corek et al., 2019; Hinze et al., 2017; Otyama et al., 2020; Romay et al., 2013).

At present, most (ca. 390,000+ or 70%) of the NPGS accessions have been assessed with highly heritable morphological traits, some of which, such as fruit size, shape, and color, are valuable both for PGR management and for research and breeding (Fig. 11). Until recently, genotypic characterization with DNA genetic markers has been relatively expensive and technically complicated. Thus, as of this writing, relatively few (ca. 80,000 accessions, or ca. 14% of total) of the NPGS accessions have been characterized systematically and thoroughly by a uniform set of genetic markers, with such data subsequently accessible either directly from GRIN-Global, or through links with allied databases (Fig. S10.1). During the last decade, the costs for SNP genotypic characterizations and data analyses have dropped, enabling genotypic characterization of, for example, essentially all 21,000+ accessions of the NPGS soybean (*Glycine*) collection by a uniform set of 50,000 SNPs (Song et al. 2015), and most of the 2,500 NPGS maize (*Zea)* inbred line accessions by a uniform set of 500,000 SNPs (Romay et al. 2013). The data from the preceding characterizations reside in the SoyBase (https://www.soybase.org/) and Maize GDB (https://www.maizegdb.org/) genome databases, respectively. Soybean and maize are diploid (only two sets of chromosomes); crops with multiple sets of chromosomes (polyploid) are more expensive and complicated to characterize genotypically. These types of genotypic characterization and data analysis have mainly been conducted as part of research projects supported by external grant funds, rather than by NPGS programmatic resources. Because of the nature of support for those projects, genotypic characterizations of NPGS PGR have proceeded episodically and somewhat unpredictably, rather than strategically, resulting in substantial variability across different collections for the number of accessions that have been genotypically characterized and for the number of characterization datapoints (Fig. S10.1). Up to this point, most of these genotypic characterizations have not been coordinated with phenotypic evaluations either.

Strategies and Implementation

As directed by Congress, this Plan must "address the significant backlog of characterization and maintenance of existing accessions…" (2018 Farm Bill). It has been challenging to formulate a detailed strategy for addressing the backlog of "characterization" for NPGS PGR. First, apparently no standards (such as FAO, 2014 for PGR maintenance) exist for genotypic characterization of PGR. Consequently, determining whether extant characterizations are adequate or whether a backlog exists for NPGS PGR characterization would necessitate applying somewhat idiosyncratic sets of metrics to genetically quite different forms of PGR (e.g., CWR vs. elite cultivars). Second, significant technical breakthroughs in nucleotide sequencing methods, bioinformatics, and statistical analytical approaches are occurring so frequently and rapidly that the approaches preferred at this writing might be superseded by novel, superior methods by the time the Plan is implemented. Third, analytical strategies for genetically heterogeneous, heterozygous accessions (populations) are not yet well developed, as compared to homogeneous, homozygous PGR. Consequently, the proposed plan for genotypic characterizations of NPGS accessions comprises the broad outlines for an approach. Major strategic elements are identified below, but specific, crop-by-crop operational details necessarily will remain fluid, and will be adjusted as experience accumulates during the initial years of the Plan.

During the next ten years, ca. 450,000 accessions–which constitute ca. 75% of the total projected number of ca. 600,000+ NPGS accessions–should be genotypically characterized (Fig. 10.1). Depending on their sizes and complexities, the resulting datasets will be incorporated into or directly interlinked with GRIN-Global, increasing the average number of genotypic characterization records per NPGS accession to a projected ca. 200+ (KASP markers, see below and Fig. 10.2). As explained above, rapidly evolving genotypic characterization and analytic technologies enable only general forecasts of future conditions. Consequently, the average volume of such data generated annually in the future cannot be ascertained precisely at present, especially considering that high through-put phenotypic evaluations will be conducted concurrently (Component 11).

Nonetheless, it can be projected that, to avoid backlogs in data and information availability, data and information management capacities (personnel and equipment) must be expanded at individual genebank units and for GRIN-Global operations (Components 1, 2). Additional resources will be required not only for internal NPGS operations, but also to fund partnerships with university and private-sector genotyping laboratories that will likely generate much of the new genotypic characterization data. University collaborators, private-sector partners, and ARS researchers can exploit the broad spectrum of genetic diversity readily accessible from NPGS collections as ideal "testing grounds" for identifying and developing sets of genetic markers applicable to the full range of variation within and among large collections of PGR.

The following comprehensive implementation plan for genotypic characterization of NPGS accessions differs from the planned expansions in recurrent NPGS operations and budgetary support to address PGR maintenance backlogs described in Components 4-7. The plan for genotypic characterization is organized according to discrete sequential Phases (Fig. 10.2). Each

Phase considers costs and technologies, including the genotyping platforms available; marker types and numbers needed; and throughput for analyzing accessions. It is estimated that Phase 1 will require a budget of $2 million+; Phase 2 $2.25 million+; Phase 3 $7.2 million+; Phase 4 $5.22 million initially, plus a $237,800-$290,000 annual recurrent cost for quality control genotyping of NPGS accessions (with an additional $40.5 million required for an optional whole genome sequencing [WGS] of a genetically representative 150,000 accession subset over 10 years); and Phase 5 $1.5 million+. The overall budget for the five phases would be roughly $18 million in "one-time costs," an annual recurrent cost of perhaps $300,000 for quality assurance genotyping, plus the optional WGS analysis ($40.5 million+). Appendix C "Technical Details and Cost Calculations for Genotypic Characterization of NPGS Plant Genetic Resources" contains additional technical details and cost calculations. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*

The schedules and priorities for genotypic characterization of accessions will depend strongly on the genomic research tools (reference genome sequences, genetic maps, and genetic marker sets) currently available, or their forecasted availability, for particular PGR. The needs of NPGS genebank unit personnel and crop user communities contributed to formulating the schedules and priorities of each Phase, as did the experience and knowledge gained from developing and implementing the ongoing USDA/ARS-Cornell University Breeding Insight Project (see https://www.breedinginsight.org/). Technologies for genotypic characterization and their costs are evolving so rapidly that the plan will require periodic revision, as explained in the Implementation Roadmap section.

Numerous accessions for a few NPGS collections of major crops (e.g., maize, soybean) have been well characterized by SNP markers; some accessions of other collections have been genotyped for few SNP or SSR markers, but the accessions of most NPGS collections have not been genotyped. Additionally, although for many crops at least one high quality, high depth of coverage, publicly accessible reference genome sequence exists, that is not the case for all crops nor most CWR and wild species. Some of the prior genotypic characterizations have generated data sets that might be incomplete, poorly annotated, or not combinable with other data sets. Accordingly, with relatively few exceptions such as those mentioned above, this plan is designed to be applicable to essentially all the accessions in NPGS collections and will generate compatible data sets that can be analyzed jointly. Factors determining the numbers of plants and accessions for adequate genotypic characterization of NPGS PGR include the accessions' overall genetic diversity (especially heterozygosity or heterogeneity), reproductive systems, (e.g., selfing vs. outcrossing, clonal vs. seed-propagated), and user needs. Factors determining optimal depth of coverage (i.e., the number of SNPs to be assayed) include the prior factors, plus the accessions' ploidy level. Those factors will be taken into account when formulating strategies tailored to each of the ca. 200 crops and CWR—a total of ca. 13,000 species.

The ultimate goal of this genotypic characterization plan is to generate data that will inform PGR management decisions. To generate data for this purpose efficiently, accessions would generally be genotyped strategically with fewer markers per plant, but more plants would be assayed per accession. However, because many of the research tools and genotypic data generated will also have far-reaching benefits to other researchers working on these PGR, some accessions will be genotyped with more markers per plant, but fewer plants assayed per accession. For the purposes

of this plan for genotypic characterization, the needs of PGR managers will be prioritized. The tools and data created will contribute to and dovetail with phenotypic evaluations (Component 11) and ongoing activities of breeders and geneticists that are outside the scope of this plan, such as the Breeding Insight project.

For some species, a SNP chip assay is already available with enough SNP markers (i.e., 50,000) to enable many types of analyses, including gene identification studies such as Genome-Wide Association Studies (GWAS), but most species lack this genomic tool. The costs of developing or conducting SNP chip assays have not decreased; however, the cost of nucleotide sequencing has. Nucleotide sequence reading and alignment and SNP genotyping procedures can generate hundreds of thousands to millions of SNP markers per species. Several other user-friendly methods can generate ~ 200 SNP markers in a cost-efficient manner, such as the Kompetitive Allele Specific PCR (KASP) system (Livak et al, 1995; Robinson and Ganske, 2012). Accessions of polyploid or highly heterozygous, outcrossing species might not be amenable to genotyping via 200 KASP SNP markers and therefore might require additional SNP markers or a different genotyping platform for unambiguous genotyping. Service providers can extract DNA, perform assays, and rapidly deliver data and bioinformatic tools or services to visualize the data. Each genebank unit will confer with other units, NPGS leadership, authorities in genotypic characterization, and service providers, to determine strategically if they will genotype accessions in-house or through a service provider.

Genotypic Characterization of NPGS Accessions:

Drawing on the preceding factors, during the next 5-10 years, the planned genotypic characterization effort will focus as a priority on ca. 450,000 of the total ca. 600,000+ NPGS accessions that are cultivars, landraces, or wild relatives of the ~200 crops (comprising ca. 1,000-3000 different species) of significant economic importance to the United States and internationally (Fig. 10.1). Genotypic characterizations for those 450,000 accessions encompass the following five Phases (Fig. 10.2):

1. Construction of new reference genome sequences: A reference genome must be sequenced sufficiently, thoroughly, and accurately for the purposes of SNP marker discovery. If such a reference genome sequence exists for a crop or CWR, then genotypic characterization of accessions from those taxa will proceed to Phase 2 below. If it does not already exist, a high quality, annotated reference genome for each crop will be generated at the beginning of this characterization plan's implementation. The high-quality sequence from a genetically representative individual plant will also enable many more types of genomic research, making the end products applicable to scientific endeavors far beyond this plan (Jackson, 2016). The cost of creating a high-quality reference genome sequence is currently approximately $8,000 - $9,000 per individual using PacBio or Illumina technology. Naturally, larger genomes will cost more to sequence, and smaller ones less, so this is an estimated average cost across all crops and CWR. This includes the cost of DNA extraction from plant cells. For adequate funding to enable bioinformatic analysis and ensure public data availability, an additional $1,000 per sample is needed. Approximate cost of Phase 1 = $2 million, which is $10,000/crop species X the approximately 200 crops in the NPGS.

2. Creation of new Practical Haplotype Graphs (PHG): The reference genome sequences can serve as the bases for breeding and genetic research, especially when they enable construction of a Practical Haplotype Graph (PHG; Rizzi et al, 2002; Xie and Wang, 2007). A PHG is created by high-throughput, lower density sequencing (termed "skim" sequencing) or whole genome sequencing (WGS) of accessions that are genetically representative of most of the overall diversity within the crop species or CWR, or accessions that might be "founders" of important crop genepools and frequently incorporated into breeding programs. A PHG enables SNP marker discovery and correcting for missing or erroneous data (a process termed "imputation") and can also contribute to identifying variants key for crop improvement (Della Coletta et al., 2021). Creation of PHGs through WGS of 95 accessions per NPGS crop, for a genome of average size (1 Gb (gigabase) or smaller), would cost $12,750 per crop. Approximate cost of Phase 2 = $2.55 million, which is $12,750 X the ca. 200 NPGS crops.

3. Identification of SNP marker sets and analytical protocols: The preceding reference genome sequences and PHGs can yield a subset of high-quality SNP markers that can be assayed by numerous methods, including KASP assays or SNP genotyping with WGS. A set of low-density markers (up to 200 KASP SNP markers) will be sufficient for many PGR management needs, i.e., initial genotypic characterization to provide "baseline genetic profiles" for current and newly acquired accessions; to ensure accessions' identity and purity; to identify off-types in an accession or in a collection; and to define subsets of accessions in the collection, which facilitate management and use. Assaying the same marker set repeatedly will generate a consistent survey of the same loci in all accessions and generations, creating a genetic fingerprint and facilitating direct comparisons of different data sets for accessions within a crop (see Phase 4, below).

   Creation and validation of 200 KASP SNP markers per crop will enable characterization of NPGS accessions of not only crops, but also CWR and wild taxa. It can guide the prioritization of NPGS accessions for phenotypic evaluations (Component 11). The SNP marker datasets can also furnish significant research tools for plant geneticists and breeders working to tap the valuable genetic variation within NPGS collections through the genetic enhancement programs outlined in Component 12. Approximate one-time cost of Phase 3, including creation of a low-density, high-quality KASP SNP marker set for all 200 NPGS crops = $7.2 million.

4. Genotypic characterizations: The genotypic characterizations completed during this Phase will create key research data for those PGR for which SNP markers are not currently available. The initial genotyping of the ca. 450,000 accessions (individual plant or bulks of up to 12 plants, depending on the accession) from the ~200 NPGS crops with the preceding 200 KASP SNP assays would cost $5,220,000 (=450,000 accessions X $11.60 per accession). Preparing the resulting genotypic data for delivery to users would involve an estimated one-time cost of $500,000. Approximately 10 years would be required to complete the initial genotypic characterization of those ca. 450,000 accessions, depending on how rapidly technological approaches evolve, and the knowledge gained from the initial Phases.

An estimated maximum of ca. 5% (or ca. 20,000) of the total of ca. 400,000 NPGS accessions of seed propagated crops considered herein are regenerated each year, a complicated procedure that requires quality assurance to maintain the accessions' genetic integrity (Component 7). Accordingly, a comprehensive program of quality assurance genotyping for the regenerated accessions would cost ca. $232,000 per year: $11.60 for each of the ca. 20,000+ seed propagated accessions regenerated annually. For accessions of clonally propagated crops maintained as plants in orchards or greenhouses, quality assurance genotyping would be conducted as needed, e.g., when orchard plantings are re-propagated, mislabeling is suspected, etc. Some years, very few clonally propagated accessions would need genotyping. Consequently, the annual costs for quality assurance genotyping of the ca. 40,000 accessions of clonally propagated crops would be highly variable and likely range between $4,640 - $46,400: $11.60 for each of the estimated 1% (400) to 10% (4,000) of the ca. 40,000 clonally propagated accessions that might require quality assurance genotyping in a given year.

For NPGS accessions of particular interest to researchers, breeders, or PGR managers, further genotyping via WGS or a high-density SNP chip could be accomplished in 10 years. Characterization via WGS is particularly applicable for determining species boundaries, total genetic diversity of a PGR collection, genetic gap analyses, creating and utilizing core subsets of collections, and for understanding how the genetic profiles of different accessions have inadvertently changed during PGR management. Whole genome sequencing currently costs ~$300 per accession, including bioinformatic analyses. A priority subset of perhaps ~1/3 of the total 450,000 NPGS accessions considered herein might include much of the total genetic variation encompassed by the entire collection. This is not because the accessions in the collection are extensively duplicated, but rather because the same DNA sequence variation at any given place on a chromosome could be shared by many individuals, and broad combinations of these sequence variants might be represented by fewer than the total number of accessions. Based on the results of the initial 200 KASP SNP assays, a subset of 150,000 of the total 450,000 NPGS accessions considered here could be identified and WGS conducted during a 10-year period, ideally in collaboration with cooperative ARS-university-private-sector research projects that could share costs. Without such cost-sharing, WGS of the preceding subset of 1/3 of the total 450,000 accessions considered herein would cost ca. $40.5 million in total (=subset of 150,000 NPGS accessions X $300 per accession).

To sum, the cost of Phase 4 is estimated as $5.22 million initially, plus a $237,800-$290,000 annual recurrent cost for quality control genotyping of NPGS accessions. In addition, as much as $40.5 million would be required for WGS of the genetically representative 150,000 accession subset of the entire NPGS collection, a project that is of lower priority and could be conducted over 10 years.

5. Maintaining and delivering information: Reference genome sequences generated by Phase 1 would best be stored in crop-specific genome databases such as Gramene,

SoyBase, etc., or in the NIH National Center for Biological Information website, which is a globally accepted hub for maintaining and delivering reference genome sequences and would be the most convenient and central public repository for the reference genome sequence data. The best place to store genotypic characterization data for NPGS accessions is GRIN-Global (Component 2), with interconnections via the accessions' PI numbers to crop-focused genome databases such as Maize GDB, SoyBase, Gramene, etc., when they are available. GRIN-Global already stores genetic marker data for some NPGS accessions. GRIN-Global can accommodate the much greater volume of genotypic characterization data generated by the Plan and can perform basic "on the fly queries" of the data, including generating subsets or combinations of data sets, and filtering for data quality or type, in a user-friendly manner through the USDA/ARS BrAPI 2.0 interface. Genotypic characterization data would need to be extracted from existing data sets, transformed, and loaded into the GRIN-Global database. The genotypic characterization data will contribute to the efficient and effective management of NPGS PGR—enhancing essentially all the Components of the overall NPGS Plan. Some of the genotypic characterization data generated will also yield information about genetic variability associated with high-priority, high-value crop traits (e.g., yield, host-plant resistance, adaptation, and product quality; Component 11) in those NPGS accessions. Consequently, whenever possible NPGS accessions will be thoroughly characterized genotypically before phenotypic evaluations are conducted. This Phase 5 is a one-time, labor-intensive operation with an estimated cost of $1.5 million and requiring two to three years for completion.

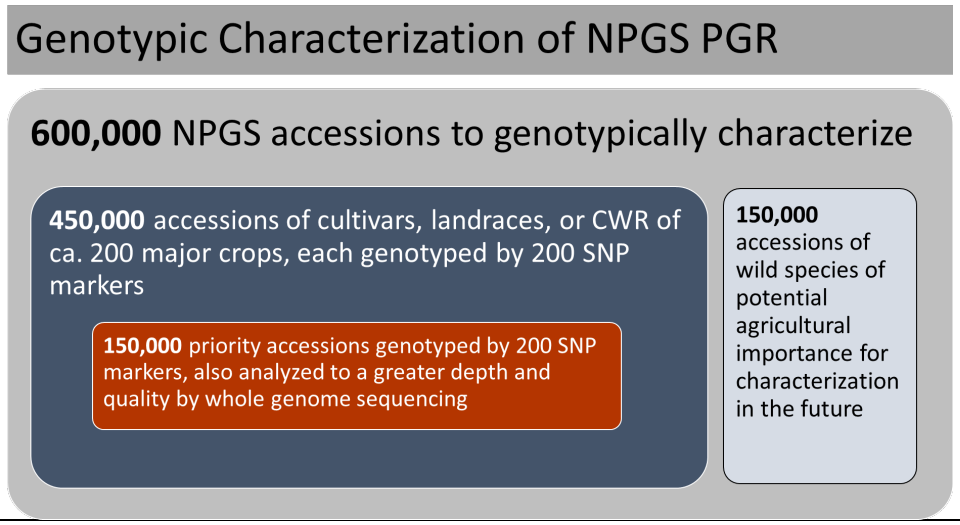


Fig. 10.1: Genotypic Characterization of NPGS PGR. Graphical depiction of the plan for genotypic characterization of the current total of ca. 600,000 NPGS accessions (gray bubble). Initially a subset of 450,000 accessions of cultivars, landraces, and CWR of 200 major crops will be genotyped by 200 SNP markers (navy blue bubble). A priority subset of 150,000 of the preceding 450,000 accessions also will be genotyped by whole genome sequencing (rust red bubble). Finally, 150,000 accessions of wild species (light blue bubble) of potential agricultural importance will be genotyped in the future after completion of the prior characterization phases (See Fig. 10.2).

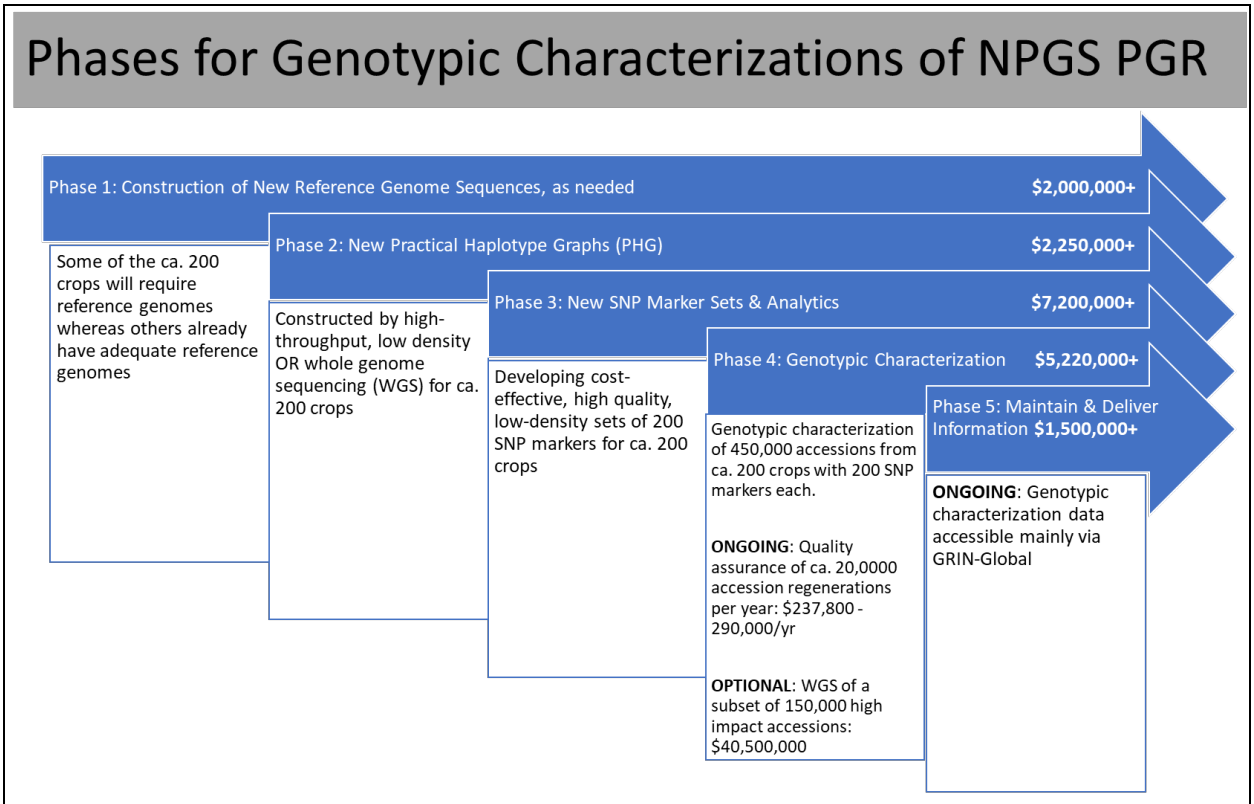


Fig. 10.2: Phases for Genotypic Characterizations of NPGS PGR. Figure 10.2 depicts the five phases for the planned genotypic characterizations of NPGS PGR. Individual phases and their estimated costs are provided in the blue shaded arrows. Additional information for the phases appears in the white boxes beneath the shaft of each individual, blue-shaded phase arrow. The chronological sequence for the phases runs from the earliest, Phase 1, at the left to the latest, Phase 5, at the right. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*

Component 11: PGR Phenotypic Evaluation, Digital Imaging (Figs. 11.1-11.3)

Current Status

To date, phenotypic evaluations of traits from NPGS PGR have generally been more extensive than genotypic characterizations and have focused on individual priority traits. The accessions are frequently evaluated at NPGS genebank units during regeneration by seeds or repropagation during maintenance of clonally-propagated PGR (Component 7). Because the primary goal is to increase the supplies of seeds or plants, phenotypic evaluations conducted during seed increases or clonal propagations usually focus on traits that can be measured without damaging the plant tissue and without replication across environments. These evaluated traits are usually well-established descriptors--highly heritable features that are readily measured during one field season and then recorded in GRIN-Global (Component 2).

Public or private-sector researchers also conduct phenotypic evaluations of NPGS accessions for specific traits, often across multiple seasons and multiple locations. Those evaluations are generally supported by grants, internal institutional resources, or private-sector funding. The resulting data are infrequently submitted to or incorporated into GRIN-Global. But other phenotypic evaluations of NPGS accessions conducted by public or private-sector researchers, usually with the guidance of CGCs, are supported by NPGS funding. As a requirement for receiving NPGS funding, data from those phenotypic evaluations, and associated metadata, must be submitted for entry into GRIN-Global.

As described earlier under Components 4-7, clonally propagated PGR, usually of horticultural crops, are generally maintained as field or greenhouse plantings, or in vitro tissue cultures. Because of the extended juvenility phases of some woody horticultural crops and their large mature size, they are evaluated phenotypically less frequently than other crop types. Clonally propagated PGR are more likely to be evaluated at genebank units during regular horticultural maintenance and monitoring. Data from such phenotypic evaluations of clonally propagated PGR can be more valuable when the plantings of accessions have been established according to a statistical experimental design. For example, the cacao (*Theobroma*) PGR collection at the Mayagüez genebank unit was planted in a replicated randomized complete block experimental design. Consequently, the data from phenotypic evaluations of cacao PGR are more amenable to statistical analyses than are those from other PGR plantings.

At present, the volume and proportion of the NPGS accessions with at least some trait phenotypic evaluation data (391,000+ accessions, ca. 69% of the total number of accessions; Fig. 11.1; Fig. S11.1) accessible via GRIN-Global are relatively high. On average, there are approximately 20 phenotypic datapoints per accession maintained by or directly interlinked with GRIN-Global. Many of these data describe variation in highly heritable morphological traits primarily useful for PGR management purposes, such as maintaining accessions true-to-type. Nonetheless, evaluations of PGR for other traits, such as tolerance to environmental extremes, host-plant resistance to pest and pathogens, and key product quality and production characteristics would enable requestors to choose more precisely the best accessions for specific research or breeding objectives. Moreover, higher quality metadata associated with phenotypic evaluations that are accessible via GRIN-Global could reduce superfluous requests for PGR.

Access to ample trait data of interest to breeders and geneticists is crucial for expanded but more efficiently targeted use of PGR for research, breeding, and the genetic enhancement program described in Component 12.

The rate and degree to which NPGS collections have been evaluated phenotypically vary greatly among different crops and genebank units, and are often associated with variation in funding available for this purpose (Fig. 11.2; Fig. S11.2). For example, maize (*Zea*) at Ames, pulses at Pullman, small fruits and pear (*Pyrus)* at Corvallis, small grains at Aberdeen, and soybean (*Glycine*) at Urbana have been more extensively evaluated than many other crops. Not surprisingly, some crops with active CGCs and greater financial resources available for this purpose (e.g., horticultural crops) have been more comprehensively evaluated phenotypically; in some cases, such as sugarbeet, accessions have evaluated phenotypically according to a long-term strategic plan. As with genotypic characterizations, other phenotypic evaluations have been supported by grant funding and, consequently, progress with phenotypic evaluations across NPGS PGR has often proceeded episodically and somewhat unpredictably.

Digital images of key phenotypic traits (e.g., plant architecture; fruit/seed size, shape, color) strongly assist requestors with choosing the optimal accessions for their specific research and breeding objectives. These images also enable PGR managers to detect off-types, sample admixtures, and misidentified accessions efficiently and effectively. Consequently, digital images can both substantially assist PGR maintenance and facilitate PGR use. The volume and proportion of NPGS accessions with digital images of phenotypes maintained in GRIN-Global have grown substantially in recent years (currently, 242,000+ accessions, ca. 46% of the total number of NPGS accessions; Fig. 11.3). Although some NPGS collections (e.g., cotton, *Gossypium* at College Station) are currently conducting systematic digital imaging efforts, relatively few accessions (12,000+, 2+% of the total number of NPGS accessions) are imaged annually on average (Fig. 11.3). The extent to which PGR have been documented via digital images has been limited by some of the same factors currently limiting other phenotypic evaluations of traits, such as the rate of accession regeneration (Component 7), and available budgetary support (Component 1). For example, the systematic digital imaging of NPGS cotton PGR has required external grant funding.

The available land, budgetary support, operational capacities, and technical limitations of current phenotypic evaluation protocols have contributed to a backlog of NPGS accessions that require evaluation. The preceding factors have also limited the volume of evaluation data for agronomically and horticulturally-important traits that breeders and researchers require for optimal PGR use. At present, the demand for phenotypic trait data for NPGS PGR substantially exceeds the resources available for comprehensive evaluations. For example, fewer than half of the proposals submitted to horticultural crop CGCs for small-scale (< $30,000) evaluation projects can be supported from the modest total funding (ca. $250,000 annually) available for this purpose.

Strategies and Implementation

Across most crops, the demand for additional phenotypic evaluations is projected to expand substantially in the future, especially as phenomic analytical pipelines are developed (see below).

Precise, accurate, and replicated phenotypic evaluation data are needed not only for PGR management, but also for genetic enhancement (Component 12), traditional pedigree selection breeding, and map-based marker-assisted breeding. High-quality trait phenotyping is a crucial prerequisite to map traits to genomic regions and identify the causal genes regulating phenotypes of interest.

Consequently, during the next +10 years, the number of NPGS accessions evaluated phenotypically should increase strategically. Initially, phenotypic evaluations will likely focus on individual traits or related groups of traits. Genebank units will require statistical and experimental design support to ensure that field plots are positioned to maximize the utility of the phenotypic evaluation data collected. For evaluation of annual, seed propagated accessions and non-replicated plantings of clonal accessions, following the strategy of planting the same crop-specific "check varieties" can enable statistically more robust cross-comparisons. Piepho and Williams (2016) demonstrated that planting a few replicated, randomly placed check varieties could enable more statistically robust phenotypic evaluation data to be generated from unreplicated plantings of accessions. Moreover, over time, inclusion of check varieties in phenotypic evaluations can enable stability analysis of accession performance across a range of optimal to suboptimal environmental conditions while providing insights into genotype-by-environment interactions for critical traits. Thus, implementing this practice can enhance the value and utility of phenotypic evaluations conducted during PGR regeneration or repropagation (Component 7) and immediately improve the quality of trait evaluation data, independent of the advanced phenomic evaluation methods described below.

Evaluation of roots has always been problematic and expensive, and very few data are available for root phenotypes of NPGS PGR. Root phenotypes have traditionally been measured by destructive field-based methods requiring intense physical labor to excavate and rinse soil from plant root systems (appropriately termed "shovelomics"; Trachsel et al., 2011). New lab-based methods improve measurement resolution and decrease physical labor, but these methods and equipment are expensive and not high-throughput. Field sensors and simulation models could be combined with some lab-based phenotyping systems to enable root traits to be more quickly estimated from PGR accessions (Tracy et al., 2020).

During the next 10 years, at least 200,000 phenotypic evaluations of priority NPGS accessions should be conducted for priority traits determined by NPGS PGR managers and associated CGCs (Fig. 11.2). Once incorporated into or directly interlinked with GRIN-Global, the resulting datasets would increase the average number of phenotypic evaluations per accession substantially, especially if the phenomic approaches described herein can be adopted. Thus, the annual data collection goals (evaluation of 32,000+ accessions annually, constituting 4+% of the total number of NPGS accessions at +10 years; Fig. 11.2) constitute a general strategy based on current technologies. Future phenotypic evaluation priorities can shift according to unpredictable factors, including the emergence of virulent pathogens and pests, dynamic environmental factors, and unforeseen market forces. Furthermore, the research and technological advances described below could substantially expand the number of traits evaluated phenotypically, once the 40+ CGCs and NPGS PGR managers can effectively identify priority traits for evaluation. If the phenomic approaches described below can be implemented, the concept of a "trait" would be

redefined, making it infeasible to estimate the future volumes of phenotypic evaluation data by the current metric of "average number of phenotypic datapoints per accession."

The early developmental status for phenomic technologies and data analytical pipelines, and the biological differences among crops, do not permit the overall cost of an expanded NPGS trait evaluation program incorporating phenomic approaches to be estimated to the same degree of detail as for genotypic characterizations (Component 10). Nonetheless, in addition to the increased support for NPGS infrastructure and personnel described in Component 1, devoting at least $25 million annually to support collaborative NPGS-cooperator phenotypic and phenomic evaluations guided by the 40+ CGCs can serve as a preliminary budget estimate for strategically expanding phenotypic evaluations for 50-100 individual NPGS crop collections (*The costs to implement this Plan are estimated and do not constitute a USDA request for funding).* The process of assigning priorities for crops and traits to evaluate phenotypically will incorporate genotypic characterization data (Component 10), information about customers/stakeholder needs communicated through CGCs, and the available capacity for incorporating the data and traits into genepools through genetic enhancement (Component 12).

Initially, much of the preceding increased budget will be devoted to conducting the extensive research needed to perfect some of the current prototype phenomic technologies currently under development. Then the focus will shift to applying the technologies to phenomic evaluations of NPGS PGR. The costs to genebank units of upgrading equipment to capture phenomic evaluation data are thought to be relatively inexpensive (<$100,000 per genebank unit, every five years; S. Murray, pers. comm.). The major expense for expanded phenotypic evaluations and implementing phenomic approaches will be the personnel who collect, process, analyze, and deliver the data, and the initial development of the phenomic data capture, handling, and analytical pipelines.

The preceding budgetary estimates can be adjusted based on the results of the initial research and development phase, and as practical experience accrues with the new approaches and technologies for phenomic trait evaluation (see Implementation Roadmap). "Best practices" and standard operating procedures can then be formulated and shared with genebank sites and with researchers collecting phenomic evaluation data. Capturing and processing data through standard phenomic evaluation procedures should substantially enhance operational efficiencies and ultimately decrease the overall expense for phenotypic evaluations, as calculated per trait and per crop.

Phenomic evaluation strategies

In addition to expanding the NPGS capacity for phenotypic evaluation as described above, the methods for PGR phenotypic evaluation must be improved to reduce current backlogs. The phenomic approaches to evaluation described below could substantially increase the volume of such evaluation data and their availability. This strategy will serve both to increase the value of the PGR to plant breeding and research, and also aid PGR maintenance, e.g., managing disease-free orchards and nurseries via automated aerial disease detection (Wiesner-Hanks et al., 2019).

Phenotyping is the act of measuring or quantifying specific physical characteristics of the plant over its lifetime (Soulé, 1967; Schilling et al., 1999); phenomics refers to large-scale, high-dimensional phenotyping assisted by advanced data-collecting technologies and software. Phenomic approaches capture measurements, or predict expression, of many traits simultaneously. Considering the rapid development of phenomic technologies and the high value of trait evaluation data, this Plan will incorporate phenomic strategies increasingly into PGR evaluation programs in the future. Once a phenomics pipeline is established, overall costs per datapoint for PGR evaluations might be reduced considerably from current levels. Technological improvements in imaging and sensing (e.g., inexpensive, high resolution, visual, hyperspectral and thermal cameras; e.g., Hershberger et al. 2021), measurement platforms (robots, ground vehicles, and unoccupied aerial systems or UAS), computer hardware and software (faster processors, image stitching, and graphical processing units) and algorithms (temporal analysis, AI; Houle et al., 2010; Yang et al., 2020) are prerequisites for implementing those phenomic strategies efficiently.

As with the genotypic characterization plan described in Component 10, reducing the current backlog of phenotypic evaluation for NPGS PGR offers a uniquely valuable opportunity to apply the strategy of creating and deploying novel technological approaches tailored to the properties and characteristics of diverse PGR. The fields, orchards, and greenhouses where annual, perennial, and clonal accessions are grown can serve as living laboratories that in the future will enable systems studies through interrelating phenomic and genomic datasets, as well as datasets of associated environmental factors. The scheduling for phenotypic evaluations might no longer be determined primarily by regeneration or repropagation schedules. The availability of genotypic characterization data, sufficient supplies of seeds, and adequate land and personnel to conduct replicated field trials will become increasingly important determinants for scheduling phenotypic evaluations.

Highly reproducible phenomic strategies could substantially decrease the costs and increase the number of accessions evaluated by capturing and interpreting digital images routinely throughout PGR management operations. The images will enable specific trait phenotypes to be measured or estimated, even complicated traits such as grain yield (Lane et al., 2020). In some cases, these estimates have already proven to be more accurate and repeatable than are traditional manual measurements (e.g., plant height in maize; Pugh et al. 2018). As new phenomic measurement approaches are developed, they can be retroactively applied to historical imagery to estimate phenotypes from plants cultivated in the past in orchards or for seed increases.

The additional resources discussed earlier will be required not only for expanded phenotypic evaluations conducted at genebank units, but also for partnerships with university and private-sector collaborators as a strategy for fully exploiting the value of the NPGS investment in phenomic evaluations of priority traits. For example, interrelating long-term meteorological and phenological data could reveal how climate change affects plant reproduction and identify PGR with potentially greater resilience to rapid environmental changes. These data could also compensate for environmental influences that make comparing data across seasons or across locations challenging. The data from phenomic evaluations will enable requestors to select the

best accessions for accelerating the progress of research substantially; increasing genetic gain from breeding; and efficiently interrelating patterns of genotypic and phenotypic variation.

Training current NPGS staff and hiring newly trained staff (see Component 1) will be crucial for refining and implementing an overall phenomic evaluation strategy. In addition to the guidance for trait evaluation priorities received from CGCs, a technical steering group, equivalent to the group that assisted the development of GRIN-Global, should be formed to help develop phenomic strategies, approaches, and standard operating procedures. Contracting with software developers to provide analytical pipelines for the interpretation of digital images and definition of phenotypes might be necessary during early phases of implementing phenomic evaluations, as was the case with GRIN-Global development.

Phenomic evaluations for PGR of annual field crops involve different logistical and scheduling factors as compared to large tree crop PGR in orchards. Nonetheless, the core elements for the phenomic evaluation strategy and analytical pipeline will be similar for essentially all NPGS PGR, and will comprise the following three components:

Conventional ground-based field or indoor digital imagery – As more powerful and affordable image analysis software, drones, and other automated image-capturing technologies evolve and become readily available, digital images of NPGS PGR will become ever more instrumental for optimal PGR management and utilization. Most NPGS genebank units currently capture, via digital cameras and/or flatbed scanners operating under controlled lighting conditions, standardized digital images of PGR at selected key growth stages, such as fruits, inflorescences, and seeds at harvest. With current procedures, an estimated total of 360,000+ accessions, or ca. 56% of the total NPGS collection (Fig. 11.3) could be digitally imaged at +10 years, especially when systematic projects can be conducted, with a goal of 14,000+ accessions or 2% of total NPGS accessions imaged annually (Fig. 11.3). Future imaging efforts will be expanded strategically to encompass additional organs, growth stages and tissues, potentially including roots, and incorporate evaluations by both RGB and hyperspectral imagery through automated procedures. Hyperspectral imagery by laboratory instruments and processing by algorithms that can interpret and analyze intrinsic traits and qualities will generate phenotypic evaluation data that facilitate PGR use. Relatively inexpensive instruments, such as hand-held spectrophotometers, can evaluate phenotypic traits inexpensively, and add value to digital images (Hershberger et al., 2021).

The rate and extent of digital image documentation for NPGS PGR will be determined by many of the same limiting factors discussed above. The volume and proportion of accessions with digital images maintained in GRIN-Global (currently 242,000+ accessions, ca. 46% of the total, Fig. 11.3) should grow substantially in the future. Additionally, the evolution of powerful and affordable precision-agriculture imaging methods can transform PGR management approaches. Phenotypic annotation of existing and future images could serve as a resource for training machine learning models that could be applied widely to specific crops or to many different crops (M. Gore, pers. comm.). Image processing and analytical software, applied in conjunction with UAS and automatic robotic image-capturing technologies, would also generate the extensive digital datasets for NPGS PGR needed to support subsequent research and breeding applications.

Aerial field imagery – With field plantings of PGR for regeneration or repropagation, and replicated field trials specifically designed for phenomic evaluations, periodic UAS overflights (or possibly passes by terrestrial field vehicles) will be conducted by vehicles equipped with instrumentation that is the most cost-effective at the time. The timing of the flights or passes by terrestrial field vehicles would be determined strategically for each type of PGR and depend on the specific phenotypes deemed most useful, or the most difficult to obtain through traditional phenotypic evaluation methods. For example, newly acquired hemp PGR at the Geneva genebank unit will undergo phenomic evaluations via red, green, blue (RGB) and multispectral UAS imagery that assess three morphological and seven physiological indices to generate data to be incorporated into GRIN-Global. Standard image capture protocols with rigorous quality control will be followed in the field, including ground control points for identifying image location, orthomosaic stitching, and spectral correction (Shi et al., 2016).

Weather data – The sites of NPGS genebank units, and arguably major field and orchard sub-units, should host a standardized weather station, ideally connected to a mesonet network of environmental monitoring stations, to capture meteorological data that can be analyzed in conjunction with phenomic evaluation data. Accurate hyper-local weather data can contribute to an enhanced understanding of the effects of climate change on plant growth and development, such as growing-degree days until flowering.

Management of phenotypic evaluation data

As with genomic analyses, storing, cataloging, curating, and analyzing data have replaced data generation or capture as the bottlenecks for phenomic evaluations. Additional data management capacity is needed to process, manage, and deliver the large volumes of data generated by the phenomic strategies as well as to develop and deploy new phenomic evaluation technology. Which data are stored permanently in GRIN-Global, and in what format, must be determined by the community of potential users. Appropriate GRIN-Global database schema enhancements (Component 2) must be developed to handle metadata associated with phenomics pipelines. The expanded capacity will encompass additional data management hardware, software, communications bandwidth, data storage, plus personnel skilled in remote sensing, data architecture, data storage and retrieval, and applications to PGR management. Importantly, users will require ready access to both raw data and processed data because the former can be more useful than the latter as new algorithms for image processing and trait extraction are developed (S. Murray, pers.com.). Selected metadata included with the data should be designed and collected with maximum efficiency; for example, uploading weather data automatically to a mesonet (an integrated network of weather monitoring stations).

Images generate large digital files (ranging in size from 0.5 MB to 30+ MB per image). Consequently, to avoid backlogs in uploading to GRIN-Global and to make those images readily available to researchers and breeders, data and information management capacities must be expanded as described earlier. Fortunately, increases in computer storage capacity and communications bandwidth are keeping pace with the demands for managing phenomic evaluation data. As phenomic evaluation pipelines are developed and implemented, traits will no longer be viewed only as discrete elements, but rather collectively can serve as an overall

evaluation of the plant's agronomic or horticultural potential, just as a complete DNA sequence of a genome can serve as a catalogue of the plant's overall genetic potential (S. Murray, pers. comm.). Phenotypic evaluations via digital image phenotyping are typically highly labor and data intensive and will require expanded personnel and information management capacities at individual genebank units and for GRIN-Global operations at the NGRL (Components 1 and 2).

Future NPGS PGR genotypic characterizations (Component 10), phenotypic/phenomic evaluations, genetic enhancement programs (Component 12) and ARS crop breeding programs can become increasingly integrated, as with the digital ecosystems under development by groups such as the ARS/Cornell Breeding Insight Project (https://www.breedinginsight.org/). Specific, tablet-based data collection applications such as Field Book (CGIAR/Excellence in Breeding https://www.excellenceinbreeding.org) can also substantially enhance the efficiency of capturing and processing phenomic evaluation data. Networked data collection tools can enable standardization of trait measurement across a broad range of collaborators; streamline data integration pipelines; and provide real-time feedback throughout the duration of the phenomic evaluations. Through application programming interfaces (APIs) such as BrAPI (https://brapi.org/), trait evaluation datasets can be directly incorporated into future versions of GRIN-Global, which will soon feature a BrAPI 2.0 interface enabling ready interoperability with numerous advanced trait phenomic data capture and management programs. These might include the Texas A&M University approach of enabling UAS imagery to contribute data and insights to a broad spectrum of agricultural research, from plant breeding to weed science (Shi et al. 2018), and the development of BreedBase and ImageBreed by Cornell University (Morales et al., 2020; Hershberger et al., 2021). Implementing within genebank units these tools from Breeding Insight and other developers will enhance phenomic evaluation efficiencies and function as a developmental "test bed" encompassing a wide diversity of new crops and test cases. The experience and knowledge gained from implementing such phenomic data capture and analyses at genebank units can help effectively expand the applicability of new phenomic image storage, analysis, and retrieval tools to a wider scope of crops and traits.

Phenotypic Evaluation Data Currently Maintained Within GRIN-Global or Directly Linked to Corresponding Data in GRIN-Global

	NPGS Genebank Unit	a. Accessions with Phenotypic Evaluation Data: Accessions (#)	a. % of Collection	b. Average Number of Phenotypic Evaluation Datapoints per Accession for Crops Maintained by the NPGS: Avg # Datapoints per Accession	# of Crops & CWR
	NPGS-wide	**391,280**	**69%**	**20**	**183**
	PGR Specialization	**375,925**	**72%**	**13**	**115**
Primary Type of Germplasm Managed as Seeds	Aberdeen, ID (NSGC)	124,115	91%	10	10
	Ames, IA (NC7)	41,952	78%	17	25
	College Station, TX (COT)	7,856	80%	12	1
	Geneva, NY (NE9)	7,939	62%	5	13
	Griffin, GA (S9)	76,411	76%	12	28
	Parlier, CA (PARL)	437	37%	20	7
	Pullman, WA (W6)	79,192	79%	15	24
	Sturgeon Bay, WI (NR6)	5,656	97%	14	1
	Stuttgart, AR (GSOR)	5,345	14%	14	3
	Urbana, IL (GSZE)	5,442	13%	2	1
	Urbana, IL (SOY)	21,580	96%	23	2
	PGR Specialization	**15,355**	**34%**	**30**	**68**
Primary Type of Germplasm Managed as Clones	College Station, TX (BRW)	700	17%	18	1
	Corvallis, OR (COR)	5,402	42%	43	17
	Davis, CA (DAV)	3,474	49%	39	10
	Geneva, NY (GEN)	3,815	50%	17	5
	Hilo, HI (HILO)	445	47%	34	16
	Mayaguez, PR (MAY)	432	39%	17	9
	Miami, FL (MIA)	287	22%	15	7
	Riverside, CA (RIV)	800	47%	15	2
	Washington, D.C. (USNA)	0	0%	10	1

USNA does not maintain existing evaluation data within GRIN-Global

0% 100% 0 30+

Fig. 11.1: Phenotypic Evaluation Data Currently Maintained Within GRIN-Global or Directly Linked to Corresponding Data in GRIN-Global. The top row of Fig. 11.1a shaded light beige depicts the current number and percentage of NPGS accessions with phenotypic evaluation data maintained within GRIN-Global or directly linked to corresponding data in GRIN-Global. The numbers and percentages of accessions with phenotypic evaluation data are depicted in the other two rows shaded light beige for the group of genebank units that primarily manage seed-propagated accessions and for those that primarily manage clonally-propagated accessions. Information for individual genebank units are listed by geographical location. The darker the blue hue, the lower the percentage of accessions at the genebank units with phenotypic evaluation data, with the darkest hue 0% accessions with such data.

The top row of Fig. 11.1b shaded light beige depicts the current average number of phenotypic evaluation datapoints per crop or CWR accession maintained within GRIN-Global or directly linked to corresponding data in GRIN-Global, and the total number of crops or CWR with PGR managed by the NPGS. The same information is depicted in the other two rows shaded light beige for the group of genebank units that primarily manage seed-propagated accessions and for those that primarily manage clonally-propagated accessions. Information for individual genebank units are listed by geographical location. The darker the brown hue, the lower the average number of phenotypic evaluation datapoints per accession at the individual genebank units, with the darkest hue indicating zero datapoints per accession.

Average Number and Percentage of Accessions Annually Evaluated Phenotypically with Data Incorporated into GRIN-Global or Directly Linked to Corresponding Data in GRIN-Global

	NPGS Genebank Unit	Now: Accessions Annually Evaluated (Avg #)	Now: Accessions Annually Evaluated per Crop (Avg #)	Now: % of Collection Annually Evaluated	+5 Yrs.: Accessions Annually Evaluated (Avg #)	+5 Yrs.: Accessions Annually Evaluated per Crop (Avg #)	+5 Yrs.: % of Collection Annually Evaluated	+10 Yrs.: Accessions Annually Evaluated (Avg #)	+10 Yrs.: Accessions Annually Evaluated per Crop (Avg #)	+10 Yrs.: % of Collection Annually Evaluated	# of Crops & CWR
	NPGS-wide	**16,344**	**89**	**2.9%**	**26,809**	**146**	**4.4%**	**32,803**	**179**	**5.1%**	**183**
	Unit Specialization	**14,956**	**130**	**2.9%**	**20,021**	**174**	**3.6%**	**25,515**	**222**	**4.4%**	**115**
Managed as Seeds	Aberdeen, ID (NSGC)	6,585	659	4.8%	7,545	755	5.5%	11,645	1,165	8.5%	10
Managed as Seeds	Ames, IA (NC7)	1,330	53	2.5%	1,898	76	3.1%	2,641	106	4.0%	25
Managed as Seeds	College Station, TX (COT)	300	300	3.1%	250	250	2.5%	250	250	2.4%	1
Managed as Seeds	Geneva, NY (NE9)	159	12	1.2%	343	26	2.6%	386	30	2.7%	13
Managed as Seeds	Griffin, GA (S9)	2,132	76	2.1%	2,665	95	2.4%	2,721	97	2.3%	28
Managed as Seeds	Parlier, CA (PARL)	0	0	0.0%	10	1	0.8%	6	1	0.4%	7
Managed as Seeds	Pullman, WA (W6)	2,327	97	2.3%	5,016	209	4.7%	5,473	228	5.0%	24
Managed as Seeds	Sturgeon Bay, WI (NR6)	565	565	9.7%	565	565	9.4%	565	565	9.2%	1
Managed as Seeds	Stuttgart, AR (GSOR)	48	16	0.1%	29	10	0.1%	28	9	0.1%	3
Managed as Seeds	Urbana, IL (GSZE)	1,000	1,000	2.4%	1,100	1,100	2.2%	1,200	1,200	2.2%	1
Managed as Seeds	Urbana, IL (SOY)	510	255	2.3%	600	300	2.5%	600	300	2.3%	2
	Unit Specialization	**1,388**	**20**	**3.1%**	**6,788**	**100**	**13.5%**	**7,288**	**107**	**13.1%**	**68**
Managed as Clones	College Station, TX (BRW)	0	0	0.0%	4,300	4,300	100.0%	4,500	4,500	100.0%	1
Managed as Clones	Corvallis, OR (COR)	550	32	4.3%	550	32	4.0%	500	29	3.4%	17
Managed as Clones	Davis, CA (DAV)	190	19	2.7%	759	76	8.9%	939	94	9.5%	10
Managed as Clones	Geneva, NY (GEN)	45	9	0.6%	180	36	2.3%	210	42	2.5%	5
Managed as Clones	Hilo, HI (HILO)	168	11	17.7%	241	15	12.2%	280	18	9.3%	16
Managed as Clones	Mayaguez, PR (MAY)	163	18	14.6%	125	14	10.0%	107	12	7.8%	9
Managed as Clones	Miami, FL (MIA)	257	37	19.3%	513	73	32.9%	602	86	33.6%	7
Managed as Clones	Riverside, CA (RIV)	15	8	0.9%	60	30	3.4%	90	45	5.0%	2
Managed as Clones	Washington, D.C. (USNA)	0	0	0.0%	60	60	0.6%	60	60	0.6%	1

Primary Type of Germplasm

0.0% 4.0%+

Fig. 11.2: Average Number and Percentage of Accessions Annually Evaluated Phenotypically with Data Incorporated into GRIN-Global or Directly Linked to Corresponding Data in GRIN-Global. Figure 11.2 depicts the average numbers and percentages of NPGS accessions annually evaluated phenotypically and the data incorporated into GRIN-Global or directly linked to corresponding data in GRIN-Global. The top row, shaded in light beige, shows the overall average number of accessions across the NPGS genebank units that currently are annually phenotypically evaluated, the average number of accessions annually evaluated per NPGS crop or CWR, and the average percentage of the total number of NPGS accessions evaluated phenotypically. Goals for increasing the numbers and percentages of accessions evaluated at +5 and +10 years are provided. The data are summarized across the genebank units that primarily manage seed-propagated PGR and summarized across genebank units that primarily manage clonally-propagated PGR as depicted in the other two beige shaded rows. The same data are presented for individual genebank units listed by their geographical locations. The darker the lavender hue, the lower the percentage of accessions at individual NPGS genebank units that are annually evaluated, with 0% accessions annually evaluated the darkest. In the far-right column, the numbers of crops and CWR annually evaluated are presented. NPGS PGR managers provided goals for the numbers and percentages at +5 and +10 years, based on current approaches and capacities for phenotypic evaluations. Component 11 of this Plan describes alternative approaches that will be implemented to generate substantially more phenotypic evaluation data for all NPGS PGR.

Digital Images of NPGS Accessions Created and Maintained Within GRIN-Global or Directly Linked to Corresponding Data in GRIN-Global

a. Accessions with Digital Images

Primary Type of Germplasm Management	NPGS Genebank Unit	Now: Accessions with Images (#)	Now: % of Collection with Images	+5 Yrs.: Accessions with Images (#)	+5 Yrs.: % of Collection with Images	+10 Yrs.: Accessions with Images (#)	+10 Yrs.: % of Collection with Images
	NPGS-wide	**242,178**	**46%**	**309,237**	**55%**	**359,351**	**61%**
	PGR Specialization	**228,624**	**48%**	**285,450**	**56%**	**330,068**	**62%**
Managed as Seeds	Aberdeen, ID (NSGC)	134,694	99%	135,433	99%	135,913	99%
Managed as Seeds	Ames, IA (NC7)	16,477	31%	28,231	47%	41,640	64%
Managed as Seeds	College Station, TX (COT)	0	0%	7,856	78%	9,106	88%
Managed as Seeds	Geneva, NY (NE9)	3,381	27%	5,093	38%	6,790	48%
Managed as Seeds	Griffin, GA (S9)	26,563	27%	35,604	33%	43,611	37%
Managed as Seeds	Parlier, CA (PARL)	452	38%	784	61%	914	61%
Managed as Seeds	Pullman, WA (W6)	34,800	35%	51,331	48%	68,071	62%
Managed as Seeds	Sturgeon Bay, WI (NR6)	513	9%	1,028	17%	1,543	25%
Managed as Seeds	Stuttgart, AR (GSOR)	3,580	9%	3,740	9%	3,880	10%
Managed as Seeds	Urbana, IL (SOY)	8,164	36%	16,350	67%	18,600	72%
	PGR Specialization	**13,554**	**30%**	**23,787**	**47%**	**29,283**	**53%**
Managed as Clones	College Station, TX (BRW)	700	17%	4,300	100%	4,500	100%
Managed as Clones	Corvallis, OR (COR)	5,330	41%	8,165	59%	10,740	73%
Managed as Clones	Davis, CA (DAV)	1,192	17%	2,652	31%	3,020	31%
Managed as Clones	Geneva, NY (GEN)	4,044	53%	4,294	54%	4,895	59%
Managed as Clones	Hilo, HI (HILO)	369	39%	531	27%	636	21%
Managed as Clones	Mayaguez, PR (MAY)	787	71%	1,225	98%	1,366	100%
Managed as Clones	Miami, FL (MIA)	175	13%	263	17%	369	21%
Managed as Clones	Riverside, CA (RIV)	500	30%	650	37%	800	44%
Managed as Clones	Washington, D.C. (USNA)	457	5%	1,707	18%	2,957	28%

GSZE does not store images in GRIN-Global.

b. Average Number of Accessions Annually Imaged

Now: Accessions Imaged Annually (Avg #)	Now: % of Collection Imaged Annually	+5 Yrs.: Accessions Imaged Annually (Avg #)	+5 Yrs.: % of Collection Imaged Annually	+10 Yrs.: Accessions Imaged Annually (Avg #)	+10 Yrs.: % of Collection Imaged Annually	# of Crops & CWR
12,695	**2.4%**	**13,678**	**2.5%**	**14,126**	**2.4%**	**180**
11,509	**2.4%**	**11,186**	**2.2%**	**12,398**	**2.3%**	**113**
6,565	4.8%	605	0.4%	605	0.4%	10
805	1.5%	2,247	3.7%	2,608	4.0%	24
0	0.0%	250	2.5%	200	1.9%	1
158	1.2%	342	2.6%	385	2.7%	13
844	0.8%	1,870	1.7%	1,766	1.5%	28
0	0.0%	69	5.4%	29	1.9%	7
1,896	1.9%	2,968	2.8%	3,674	3.3%	24
103	1.8%	103	1.7%	103	1.7%	1
48	0.1%	32	0.1%	28	0.1%	3
1,090	4.8%	2,700	11.1%	3,000	11.5%	2
1,186	**2.6%**	**2,492**	**4.9%**	**1,728**	**3.1%**	**67**
0	0.0%	860	20.0%	0	0.0%	1
640	5.0%	635	4.6%	635	4.3%	17
116	1.6%	371	4.4%	480	4.9%	10
50	0.7%	100	1.3%	100	1.2%	5
57	6.0%	103	5.2%	127	4.2%	15
35	2.9%	77	5.8%	40	2.8%	9
28	2.1%	36	2.3%	36	2.0%	7
10	0.6%	60	3.4%	60	3.3%	2
250	3.0%	250	2.7%	250	2.4%	1

0% 100% 0.0% 2.4%+

Fig. 11.3: Digital Images of NPGS Accessions Created and Maintained Within GRIN-Global or Directly Linked to Corresponding Data in GRIN-Global. The top row of Figure 11.3a, shaded in light beige, depicts the number and percentage of NPGS accessions currently documented by digital images maintained within GRIN-Global or directly linked to corresponding data in GRIN-Global. Goals for +5 and +10 years for increasing the numbers and percentages of accessions documented by digital images are provided. The other rows shaded light beige show the numbers and percentages of NPGS accessions documented by digital images summarized across the genebank units that primarily manage seed-propagated accessions and those that primarily manage clonally-propagated accessions. The same information is presented for individual genebank units listed by their geographical locations. The darker the teal hue (0% the darkest), the lower the percentage of accessions at individual NPGS genebank units documented by digital images.

The top row of Figure 11.3b, shaded in light beige, depicts the average number and percentage of NPGS accessions that currently are annually imaged digitally. Goals for +5 and +10 years for increasing the average numbers and percentages of accessions that are annually imaged digitally are provided. The other rows shaded in light beige depict the same information for the genebank units that primarily manage seed-propagated accessions and for those that primarily manage clonally-propagated accessions. The same information for individual genebank units is listed by their geographical locations. The darker the peach hue (0% darkest), the lower the average percentage of accessions at individual genebank units that are annually imaged digitally. In the top row of the far-right column, the total number of NPGS crops and CWR annually imaged digitally are summarized. The numbers of NPGS crops and CWR are also summarized for the genebank units that primarily manage seed-propagated PGR, and for those that primarily manage clonally-propagated PGR. The same information is provided for the individual genebank units.

GSZE does not store images in GRIN-Global.

Component 12: PGR Genetic Enhancement/Pre-Breeding, and Breeding (Fig. 12)

Current Status

The ultimate goal of integrated PGR management, whether conducted by individual genebanks or a national system such as the NPGS, is to enable that PGR and associated information to benefit as many farmers, agricultural producers, and consumers as possible. "Genetic enhancement" or "pre-breeding" can be key to the research and development process that delivers such benefits. Genetic enhancement involves developing novel breeding genepools; incorporating desired traits from unadapted PGR into adapted breeding populations; and improving PGR for adaptation, as a prelude to varietal breeding (Falk, 2016). To date, the NPGS genebank units for the most part have not possessed the capacity to conduct and lead genetic enhancement programs. Consistent with their primary mission and the available resources, NPGS genebank units have focused on PGR management operations (Components 2-11) that provide PGR and information to public-sector and private-sector genetic enhancement and cultivar breeding programs and then have conserved PGR generated by the latter programs. Some NPGS PGR management programs have selected or sub-lined certain genotypes with particularly valuable traits (e.g., ornamental features, or pollen sterility important for hybrid breeding) from PGR accessions—but those efforts would not be categorized as comprehensive genetic enhancement or pre-breeding programs.

At present, NPGS genebank units provide crucial support for numerous crop genetic enhancement and breeding programs. Currently, ca. 115+ crop breeding or genetics programs conduct genetic enhancement projects in close, direct collaboration with a genebank unit (e.g., the Germplasm Enhancement of Maize (GEM) Project, Pollak and Salhuana 2001 with the Ames genebank unit; potato (*Solanum*) genetic enhancement, Jansky et al. 2012 with the Sturgeon Bay genebank unit). Approximately 120+ crop breeding programs that release cultivars for commercial use or for incorporation into pre-commercial or commercial breeding stocks currently collaborate closely with genebank units (Fig. 12; Fig. S12). The genebank units co-located at SAES/land-grant universities have been especially well-positioned to contribute to genetic enhancement and breeding programs. For example, genebank units at Corvallis, Davis, Pullman, and Stuttgart participate in or collaborate closely with genetic enhancement and breeding programs at nearby land-grant universities (Fig. 12). In turn, the host land-grant university faculty, in close collaboration with NPGS personnel, can educate students about PGR and their contributions to genetic enhancement and breeding.

Research projects funded by the NIFA Specialty Crop Research Initiative (SCRI) and Coordinated Agricultural Projects (CAP) have enlisted NPGS PGR managers as key partners, not only to provide PGR, but also to ensure that data or PGR generated by the projects are conserved for future research and breeding. A recent multi-disciplinary, multi-institutional SCRI project evaluated NPGS carrot (*Daucus*) and CWR PGR for pest resistance, as well as nutritional and market traits and incorporated those traits into adapted backgrounds. The products of that PGR evaluation and genetic enhancement project are conserved and distributed by the Ames genebank unit (Simon, 2016). Similarly, the CucCAP project conducted advanced genomic analyses of cucurbit crop and CWR accessions from the Ames genebank unit and other sources to develop genetically-enhanced populations resistant to economically important diseases that

impact squash and pumpkins (*Cucurbita*), and cucumber and melons (*Cucumis*; Grumet et al., 2015; Fig. S12).

Strategies and Implementation

At +10 years, an estimated ca. 140+ genetic enhancement programs, including extensions of the current long-term efforts mentioned above, will be conducted in close, direct collaboration with genebank units (Fig. 12; Fig. S12). Similarly, 140+ breeding programs that release cultivars for commercial use or incorporation into pre-commercial or commercial breeding programs are projected to cooperate closely with genebank units at +10 years (Fig. 12; Fig. S12). The specific goals and priorities for such genetic enhancement and breeding programs usually will be determined by crop or commodity-specific factors. Nevertheless, generally speaking, they include resistance to diseases and pests; tolerance to abiotic stresses; improved agronomic/horticultural production factors; and superior product quality and nutritional content. Furthermore, greater tolerance to environmental extremes, adaptation to climate change, and resistance to new pests and pathogens affecting new production regions are assuming ever greater importance (Kilian et al., 2020). For example, it was recognized recently that U.S. coffee production was threatened not only by virulent pathogens and insect pests, but also by inadequate access to coffee PGR with resistance to those threats. Consequently, the Congress provided critical support to develop a combined U.S. coffee PGR collection and genetic enhancement capacity crucial for the security of the domestic and international coffee crop.

The primary responsibilities of genebank units will continue to be delivering PGR accessions and associated genotypic and phenotypic information to genetic enhancement and breeding programs via the operations described in Components 2-11 of this Plan. Nonetheless, the Congress requested a "national strategic germplasm and cultivar collection assessment and utilization plan." Therefore, this Plan has considered approaches for supporting the capacities of NPGS genebank units to generate new breeding populations or cultivars critical for delivering the intrinsic value of NPGS PGR to U.S. farmers, producers, processors, and consumers. To meet rapidly evolving challenges to crop production, plant breeders and researchers frequently have voiced the need for more populations and lines, developed from PGR accessions, with new traits incorporated into genetic backgrounds that facilitate PGR utilization (e.g., Byrne et al., 2018; Dempewolf et al., 2017). Facilitating PGR usage is a primary goal for this NPGS Plan: consequently, with expanded resources, selected genebank units could extend their missions to support more extensively such programs that expand crop genepools, generate new cultivars, and make key traits more readily available for crop genetic improvement.

Plant breeders and researchers have stressed that availability of more, high quality genotypic and phenotypic data is crucial to progress with genetic enhancement and breeding (Dempewolf et al., 2017). Availability of numerous SNP genetic markers generated by expanded future NPGS-wide genotypic characterizations (Component 10) and many new PGR phenotypic evaluation data (Component 11) should strengthen future genetic enhancement and breeding efforts, especially for priority goals such as superior yield and adaptation to rapidly changing environmental and market conditions.

Specifically, several NPGS genebank units have already received the budgetary support needed to implement genetic enhancement programs for several crops. In addition to assembling and managing a new PGR collection for coffee, the genebank units at Hilo and Mayagüez will conduct coffee genetic enhancement and cultivar breeding programs focused on improving host-plant resistance to coffee leaf rust and nematodes--accompanied by high end-product quality. The genebank unit at Geneva has initiated a new PGR management program for hemp, and subsequently will implement a complementary genetic enhancement program for this new crop focused on priority industry needs, such as adaptation, yield, tolerance of environmental stresses, host-plant resistance to diseases and pests, and traits important for end-uses such as fiber length and quality and biochemical content. The soybean genetic enhancement project conducted for decades as part of the Urbana soybean genebank unit's overall PGR conservation and genetic improvement program (Nelson and Johnson, 2006; Hegstad et al., 2019) will expand to address additional priorities for this commodity. The genetic enhancement efforts will contribute to, rather than detract from, the core PGR management missions of these genebanks.

During the next +10 years, additional genetic enhancement and cultivar breeding programs located at, or associated with, NPGS genebank units and focused on horticultural or "specialty crops" will be conducted in coordination with the ongoing USDA/ARS-Cornell University Breeding Insight program (https://www.breedinginsight.org/) described under Component 11. As the Breeding Insight program and other such efforts expand and evolve, genebank units that have achieved or are achieving the +5 year and +10 year goals for PGR maintenance and characterization would then be assessed for their capacity to participate in or lead genetic enhancement programs to generate new genetically-structured populations, to incorporate high priority traits, and to conduct multi-locational and multi-seasonal performance trials. Specific crop genetic enhancement priorities would be determined in coordination with the results of genotypic characterizations (Component 10) and phenotypic evaluations (Component 11). If PGR are not adequately characterized and evaluated then their contributions to genetic enhancement can be limited by insufficient knowledge to identify priority traits for incorporation, or the need for expanding the over genetic variability in particular genepools.

Notably, new and precise genetic engineering methods collectively termed "gene editing" (e.g., Li et al. 2020) could also prove to be primary drivers of future demand for phenotypic evaluations, because the genetic variation in PGR could serve as "templates" for engineering valuable alleles identified in accessions into other genetic backgrounds without otherwise disrupting genomic content or organization, and without lengthy cycles of introgression through crossing and selection. Notably, although gene editing has become a universally applicable method for research, employing it for crop breeding should be guided by public acceptance of products developed by this approach.

Considering the highly diverse and sometimes unpredictable future priorities for developing new crop traits and cultivars, future PGR genetic enhancement and breeding programs involving the NPGS during the next +10 years should currently best be described in general terms. The magnitude of additional budgetary support and infrastructure needed for implementing and operating genetic enhancement and/or breeding programs varies widely according to the biological features of the crop (e.g., large, long-lived outcrossing tropical trees require more land and labor than do compact, annual inbreeding grasses), the specific goals of the programs,

existing complementary genotypic characterization, phenotypic evaluation, genetic enhancement projects, and opportunities for external partnerships and cost-sharing with public-sector and/or private-sector collaborators.

Nonetheless, based on the history of the 25+ year old USDA/ARS GEM Project, and recent experience with establishing the NPGS coffee and hemp PGR and genetic enhancement/breeding projects mentioned earlier, recurrent base funding increases in the range $500,000 to $1.5 million would be needed to implement and sustain each new genetic enhancement and/or breeding program for a specific crop or related group of crops. The NPGS currently manages PGR of ca. 200 crops, about half of which would likely need new or supplementary genetic enhancement and/or breeding programs to facilitate the effective future utilization of NPGS PGR. Therefore, a rough estimate for the collective recurrent costs for implementing such programs for 100 crops would range from $50 million to $150 million annually (*The costs to implement this Plan are estimated and do not constitute a USDA request for funding).*

. That cost is separate from and independent of the new budgetary support and infrastructure estimated in Component 1 for reducing backlogs in PGR maintenance (Components 2-8), as well as characterization and evaluation (Components 9-11). Consequently, the estimated budgetary needs for genetic enhancement of NPGS PGR has been considered separately from the expanded support needed for the core NPGS PGR management mission. As comprehensive genotypic characterization and phenotypic evaluation programs near completion for particular crops, NPGS personnel, land, equipment, and other infrastructure could be redirected to supporting genetic enhancement of those crops, with the outcomes of making available high-priority traits and genetically more diverse genepools.

Genetic Enhancement/Pre-Breeding and Breeding Programs Conducted at or in Close Collaboration with NPGS Genebank Units

NPGS Genebank Unit		Now	+ 5 Yrs.	+ 10 Yrs.
NPGS-wide	Genetic Enhancement/Pre-Breeding Program	**117**	**146**	**148**
	Breeding Program	**123**	**137**	**142**
Ames, IA (NC7)	Genetic Enhancement/Pre-Breeding Program	3	3	2
	Breeding Program	3	3	3
College Station, TX (BRW)	Genetic Enhancement/Pre-Breeding Program	1	1	1
	Breeding Program	1	1	1
College Station, TX (COT)	Genetic Enhancement/Pre-Breeding Program	2	2	2
	Breeding Program	3	3	3
Corvallis, OR (COR)	Genetic Enhancement/Pre-Breeding Program	74	74	74
	Breeding Program	85	85	85
Davis, CA (DAV)	Genetic Enhancement/Pre-Breeding Program	0	0	0
	Breeding Program	9	5	5
Geneva, NY (GEN)	Genetic Enhancement/Pre-Breeding Program	0	3	3
	Breeding Program	0	0	0
Geneva, NY (NE9)	Genetic Enhancement/Pre-Breeding Program	1	1	1
	Breeding Program	1	1	1
Griffin, GA (S9)	Genetic Enhancement/Pre-Breeding Program	3	10	13
	Breeding Program	1	8	11
Hilo, HI (HILO)	Genetic Enhancement/Pre-Breeding Program	1	5	5
	Breeding Program	1	4	6
Mayaguez, PR (MAY)	Genetic Enhancement/Pre-Breeding Program	2	3	3
	Breeding Program	1	1	1
Miami, FL (MIA)	Genetic Enhancement/Pre-Breeding Program	0	2	2
	Breeding Program	2	3	3
Parlier, CA (PARL)	Genetic Enhancement/Pre-Breeding Program	0	1	0
	Breeding Program	0	0	0
Pullman, WA (W6)	Genetic Enhancement/Pre-Breeding Program	13	22	22
	Breeding Program	8	14	14
Riverside, CA (RIV)	Genetic Enhancement/Pre-Breeding Program	0	1	1
	Breeding Program	2	3	3
Sturgeon Bay, WI (NR6)	Genetic Enhancement/Pre-Breeding Program	2	0	0
	Breeding Program	2	0	0
Stuttgart, AR (GSOR)	Genetic Enhancement/Pre-Breeding Program	11	12	13
	Breeding Program	1	1	1
Urbana, IL (SOY)	Genetic Enhancement/Pre-Breeding Program	2	2	2
	Breeding Program	1	1	1
Washington, D.C. (USNA)	Genetic Enhancement/Pre-Breeding Program	2	4	4
	Breeding Program	2	4	4

The darkest hue indicates 10 or more collaborative programs.
GSZE and NSGC do not conduct nor anticipate any collaborative genetic enhancement/pre-breeding or breeding programs

# of Collaborative Programs

Fig. 12: Genetic Enhancement/Pre-Breeding and Breeding Programs Conducted at or in Close Collaboration with NPGS Genebank Units. The top rectangle, shaded in light beige, shows in the top row the total numbers of genetic enhancement/pre-breeding programs and the row below it the total numbers of breeding programs currently conducted at or in close collaboration with NPGS genebank units, and estimates for +5 years and +10 years. The same information is provided for individual genebank units listed by their geographical locations. The darker the red hue, the more such programs are conducted at or in close collaboration with individual NPGS genebank units, with 10+ programs the darkest.

Based on current approaches and capacities, NPGS PGR managers provided estimates for the number of such programs that their genebank units could conduct or collaborate with at +5 and +10 years. Component 12 of this Plan describes an alternative approach that would implement genetic enhancement/pre-breeding programs for as many as 100 major crops, either conducted by or in close collaboration with individual NPGS genebank units.

GSZE and NSGC do not anticipate that any genetic enhancement/pre-breeding or breeding programs will be conducted at or in close collaboration with those genebank units.

Component 13: Cross-Cutting Strategies and Roadmap for Plan Implementation (Fig. 13.1 – 13.9)

Cross-Cutting Strategies

As this Plan shows, PGR management comprises a complicated series of operations requiring highly divergent skills, equipment, facilities, and approaches, such as propagating trees by grafting (Component 7); developing DNA genetic markers for PGR with polyploid genomes (Component 10); constructing digital "pipelines" for analyzing large volumes of genotypic characterization and phenomic evaluation data (Component 10 and 11); identifying and filling collection gaps (Component 3); diagnosing diseases, pests, and physiological disorders (Component 6); cryobiology (Components 4 and 5); and data science and information management (Component 2). Because of that diversity, the individual PGR management operations have been analyzed and discussed for this Plan in 12 separate Components.

Nonetheless, in practice these seemingly separate operations must be concurrently integrated and coordinated for successful implementation of this Plan, and to enable effective PGR management and utilization. Furthermore, as shown by the different operations and needs of the individual genebank units (Appendix B; Fig. B.1), coordinated approaches for addressing PGR management backlogs and other challenges must be tailored to the specific conditions at individual genebank units and their constituent PGR collections. Despite that diversity, several cross-cutting strategies and priorities for addressing the current backlogs in PGR management operations at all NPGS genebank units have emerged and are described in the first half of this section. These NPGS-wide strategies will be applied whenever possible throughout the implementation of the Plan and will be highlighted in the overall roadmap and schedule for implementing this Plan that are presented in the second half of this section and also in the companion "Synopsis" document.

Costs of managing PGR accessions: Information about the current budgetary support and estimated future needs for supporting overall NPGS operations was presented in Component 1. To effectively implement this Plan, the costs of managing different types of NPGS accessions require analyses. Estimates for the annual per accession costs for individual core PGR management operations such as back-up/duplication, viability testing, pathogen testing and clean-up, and regeneration or repropagation (Components 4-7) are confounded because those different operations are often performed by the same personnel and involve the same facilities and other genebank unit resources. Consequently, overall annual PGR management costs per accession were estimated herein via a heuristic approach. The annual recurrent base funding per genebank unit divided by the number of accessions managed by that genebank unit has served as a proxy for comparing the relative annual cost per accession for core PGR management operations. To date, the funding levels for individual NPGS genebank units sometimes have been fully or partially determined by factors unrelated to the number of PGR accessions managed (e.g., historical events, crop/commodity-specific priorities, etc.). Nonetheless, this heuristic approach has yielded cross-PGR comparisons instructive for this Plan.

Because of the comprehensive operational differences between PGR managed as clones and those managed in the form of seeds, the management costs for those two types of PGR were

examined separately. As shown by Fig. 13.1, the average annual per accession funding at genebank units devoted primarily to clonally-maintained crops can be several times greater than for genebank units devoted primarily to maintaining accessions as seeds, with the highest per accession average annual funding at the Hilo, Mayagüez, Miami, and Riverside genebank units that are dedicated primarily to managing genetically-diverse tropical and sub-tropical tree crops. Consistent with the analyses of Pardey et al. (2001), for PGR maintained as seeds, genetically-diverse accessions requiring more costly controlled pollination during regeneration (e.g., some crops at Ames, Pullman, and Griffin genebank units) and, on average, require more resources than self-pollinated, relatively genetically homogeneous small grains and rice accessions managed at the Aberdeen and Stuttgart genebank units. These differences are reflected by the budgetary needs projected for +5 and +10 years for individual genebank units (Appendix B), and by the strategies discussed below and throughout this Plan for addressing operational backlogs and enhancing the efficiencies of PGR management.

PGR accessions maintained as clones: The biological features (e.g., genetic structure and content; plant physiological functions) that determine optimal PGR management operations are often poorly understood for crops maintained and propagated as clones, relative to those maintained in the form of seeds. At present, accessions of many such crops can be safeguarded only via duplicate plantings rather than by storage at the NLGRP. Considering the many threats to field plantings and the comparatively high costs of clonal PGR maintenance, research to devise and implement effective procedures for long-term preservation of vegetative propagules at the NLGRP is a high strategic priority (Component 4). Genotypic characterizations (Component 10) to ascertain the identity of accessions in orchard or greenhouse plantings, or as plants or tissue in vitro, are crucial for maintaining genetic integrity and for avoiding the expense of maintaining redundant or misidentified individuals or accessions (e.g., Irish et al., 2010). Furthermore, genotypic characterizations can reveal the extent to which NPGS collections of clonal PGR contain the genetic diversity needed for research and breeding, and identify accessions that should be priorities for phenotypic evaluations (Component 11) and genetic enhancement (Component 12). That knowledge can also sharpen the focus of PGR acquisitions (Component 3) to fill key gaps in genetic coverage in a targeted and economical manner.

PGR accessions maintained as seeds: Successful, cost-effective regeneration (Component 7) is crucial for enabling progress in nearly all other management operations for PGR maintained as seeds. Without a sufficient supply of numerous, healthy seeds, PGR management operations are impeded or precluded. As a result, the technical and logistical barriers to regenerating genetic stocks, unadapted crop varieties, weedy species, and CWR have contributed to numerous operational backlogs. It is therefore an NPGS strategic priority to discover the reproductive modes (breeding systems, pollination vectors) of those PGR and apply that knowledge to devise and implement more effective regeneration/multiplication methods (Component 7) that make the best use of the available genebank capacities.

Regeneration costs comprise the primary expenses for managing accessions maintained as seeds, not only for NPGS genebank units but also for other genebank systems (Pardey et al., 2001; Lusty et al., 2021). Reducing the need for accession regenerations can reduce backlogs not only for that PGR maintenance operation, but also for duplication/back-up (Component 4), viability/germination testing (Component 5), and pathogen testing and clean-up (Component 6).

The longer seeds can be stored without deteriorating, the better—both to control PGR management costs, and to reduce the risk of losing genetic diversity that can occur during regeneration. It is an NPGS strategic priority to conduct research to devise and implement effective methods for longer-term storage of seeds, especially those that currently cannot be preserved under standard reduced-temperature regimens (Component 4), and to develop sufficient long-term storage capacity (usually 0˚F, -18 ˚C) for this PGR at the NLGRP and other genebank units. Research to develop new seed treatments that improve germination of historical/legacy seeds could rescue invaluable genes and traits that might be otherwise lost. Additionally, priority research is needed to formulate new germination/viability tests to predict impending deterioration of seed vigor and viability before such reductions occur and without destroying numerous seeds in the process (Component 5). Furthermore, the genotypic characterization tools developed through Component 10 can be applied following harvest of regenerated seeds to ensure that they are true-to-type and contain no undesired outcrosses or seed admixtures.

Information and data management: As this Plan is implemented, publicly accessible information associated with PGR will increase both in volume (Component 2) and in the value it can contribute to research, breeding, and PGR management. Genotypic data (Component 10) and information from the novel phenomic strategies for trait phenotypic analyses (Component 11) can enable requestors to choose more precisely the PGR that meet their specific needs. Reducing the backlogs in delivering data and information associated with NPGS PGR can increase the overall cost-effectiveness of crop agricultural research, development, and production enterprises. New digital "pipelines" to generate and distribute genotypic and phenomic data through seamless integration of the data generation, storage, analysis, interpretation, and visualization steps will be created and implemented by data scientists and NPGS personnel collaborating across genebank units, because many protocols will be applicable to numerous types of PGR. New ways to depict the complicated data generated through those new pipelines, e.g., efficient quantitative descriptions of the variability in heterogeneous/heterozygous accessions and populations, will be key for facilitating PGR maintenance and utilization. As the NPGS PGR become more thoroughly described and the accompanying data and information are more readily accessible, artificial intelligence (AI) applications could be developed and applied strategically to autonomously answer queries from PGR requestors/users and serve as decision-making tools for PGR management (Bretting, 2018). Consequently, advanced information management and analytical tools could contribute to the outcome of tangibly increasing operational effectiveness for NPGS genebank units.

Genotypic characterization, phenotypic evaluation, and genetic enhancement

As outlined in Components 10-12, additional budgetary resources (Fig. 1.7) beyond those included in Components 1 and 2 are needed for applied research to develop leading edge genotypic characterization, phenotypic evaluation, and genetic enhancement strategies. Some of those characterization and evaluation operations might be more efficiently conducted by centralized service laboratories, operated by the USDA/ARS or the private-sector, which are accessible to all NPGS genebank units and other USDA/ARS research projects. Newly generated genotypic characterization data will refine priorities for PGR management, for example, via definition of core subsets and evaluation arrays, as well as provide researchers with valuable

information about associations of those data with phenotypic traits. Consulting collection records, descriptive information, and genotypic characterization data, PGR managers could identify potentially redundant accessions to archive, and accessions with lower PGR management priorities. The genetic data, trait information, and superior, genetically-enhanced PGR are strategically crucial for implementing this Plan and for the outcome of delivering PGR and associated information that enable researchers, breeders, and PGR managers to attain their research and PGR management goals.

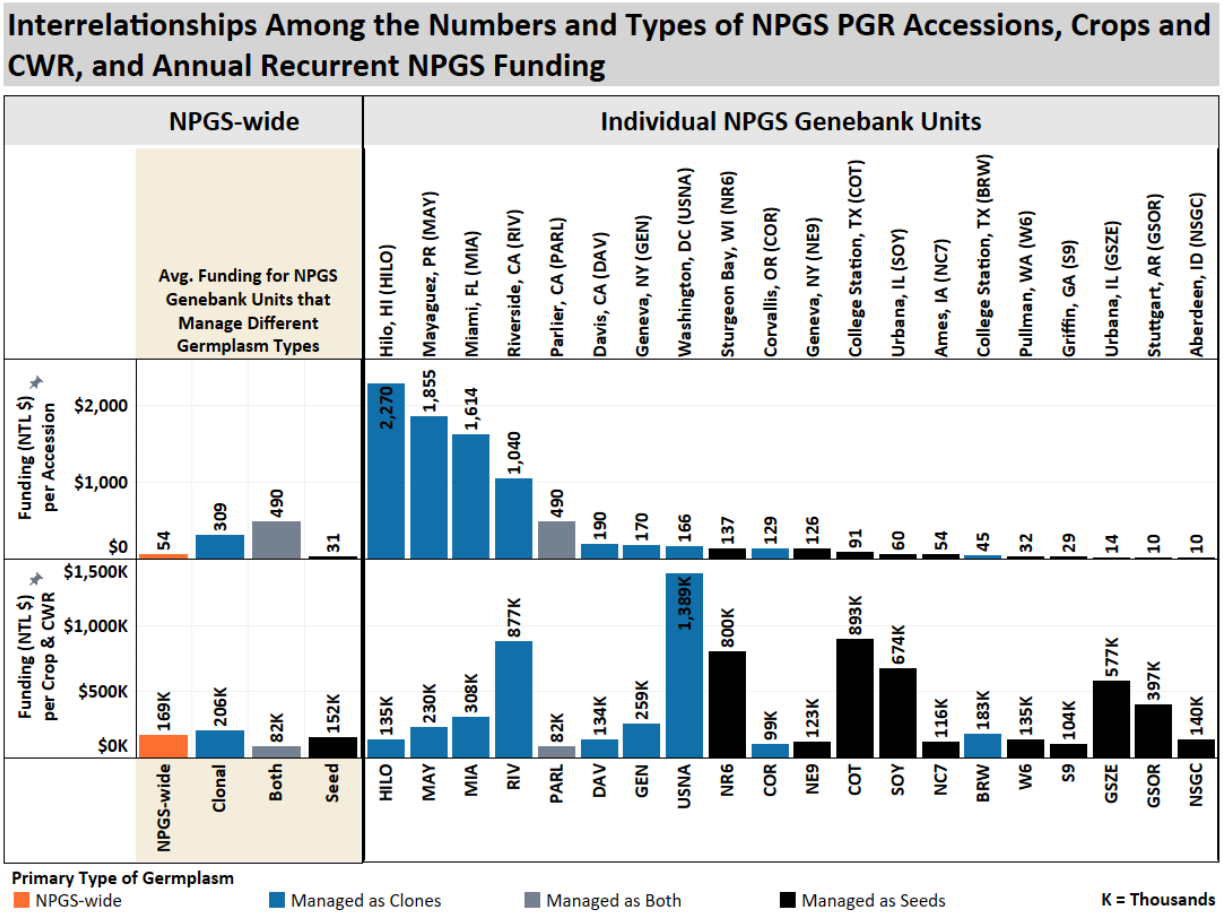


Fig. 13.1: Interrelationships Among the Numbers and Types of NPGS PGR Accessions, Crops and CWR, and Annual Recurrent NPGS Funding. In the top row of data, the orange bar at the far left depicts the ratio of the current average annual recurrent funding for the overall operations of the 22 NPGS genebank units divided by the current total number of accessions in the NPGS. The other three bars also listed under the "NPGS-wide" header summarize the same ratios for overall operations in NPGS genebank units that primarily manage i) clonally-propagated PGR (blue bar), ii) an equivalent number of clonally-propagated and seed-propagated PGR (gray bar—just Parlier), and iii) seed-propagated PGR (black bar). The colored bars in the top row at the right depict the same information for individual genebank units.

The colored bars in the bottom row of data depict the ratios of the current average annual recurrent funding for overall operations in NPGS genebank units to the current numbers of crops and CWR (as defined by PGR managers) at those genebank units. The colored bars at the bottom row at the right depict the same information for individual genebank units as for accessions in the top row of data.

Roadmap for NPGS Plan Implementation

The schedule and progress for implementing the NPGS Plan depend on support by the Administration and budgetary increases appropriated by Congress (Components 1, 2). The following implementation roadmap assumes that ARS can fully control how budgetary increases are applied. If the Plan were not fully funded, not funded according to the proposed schedule, or if Congress assigned appropriations to specific genebank units or crops, the Plan's strategies and roadmap would be adjusted accordingly (Fig. 13.2; *the costs to implement this Plan are estimated and do not constitute a USDA request for funding*).

Permanent increases in annual, recurrent base funding to total $29.7 million over the 10-year period are needed to fully implement the Plan; incremental increases of $17.45 million are needed during the first 5 years and an additional $12.25 million for the second 5 years of the Plan to expand NPGS operational capacities and support research to develop new PGR maintenance methods and apply them to reduce and avoid PGR maintenance backlogs across all NPGS genebank units (Fig. 13.2). During the 10-year Plan period, an increase in annual, recurrent base funding of $25 million is needed to develop new PGR phenotypic evaluation methods, including high-throughput phenomic approaches, and to greatly expand PGR evaluation capacities and programs with university, NGO, Tribal Nation, and private-sector collaborators. An additional increase in annual, recurrent base funding ($1.8 million) is needed to manage, analyze, and deliver the higher volumes of data generated by the expanded phenotypic evaluation and genotypic characterization programs. Genotypic characterization of the NPGS PGR accessions would be funded by a total "one-time" funding of $57.17 million during the 10-year Plan, according to the 5-phase schedule described in greater depth in Component 10.

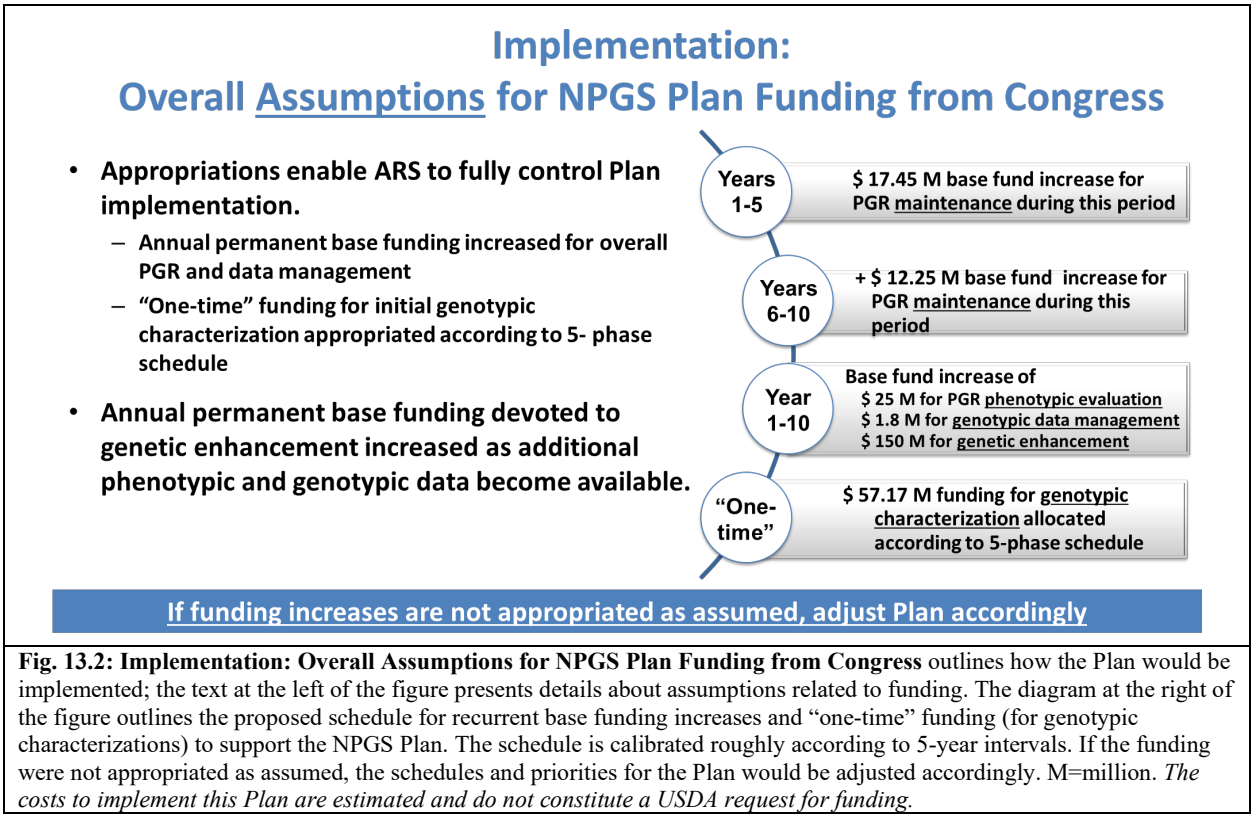


Fig. 13.2: Implementation: Overall Assumptions for NPGS Plan Funding from Congress outlines how the Plan would be implemented; the text at the left of the figure presents details about assumptions related to funding. The diagram at the right of the figure outlines the proposed schedule for recurrent base funding increases and "one-time" funding (for genotypic characterizations) to support the NPGS Plan. The schedule is calibrated roughly according to 5-year intervals. If the funding were not appropriated as assumed, the schedules and priorities for the Plan would be adjusted accordingly. M=million. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*

Based on experience managing current genetic enhancement projects, including those for maize (GEM), hemp and coffee, an increase in recurrent annual base funding of $500,000 to $1.5 M (depending on specific features of the crop) would be needed to operate a new genetic enhancement project for a particular crop (Component 12). If new genetic enhancement projects that include university, NGO, Tribal Nation, and private-sector cooperators were conducted for 100 priority crops of the almost 200 crops managed by the NPGS, increases between $50M and $150M (Component 12, Fig. 13.2) in recurrent annual base funding would be needed. It is envisioned that such projects would begin during the later phases of the 10-year Plan period once sufficient phenotypic evaluation and genotypic characterization capacity and data were available for a specific crop to identify the optimal starting or source PGR and to guide the progress of the genetic enhancement project.

If Administration and Congressional annual budget processes indicated that funding to initiate the NPGS Plan would begin in the subsequent fiscal year, the NPGS would convene meetings of USDA/ARS staff beforehand to develop and refine detailed implementation strategies for the initial stages of the Plan (Fig. 13.3). High-level working groups and technical steering groups composed of ARS staff would be assembled for Plan oversight, implementation, and guidance. NPGS staff, CGCs, the NGRAC, and other customers/stakeholders would be consulted to refine crop-specific priorities for PGR management and genetic enhancement.

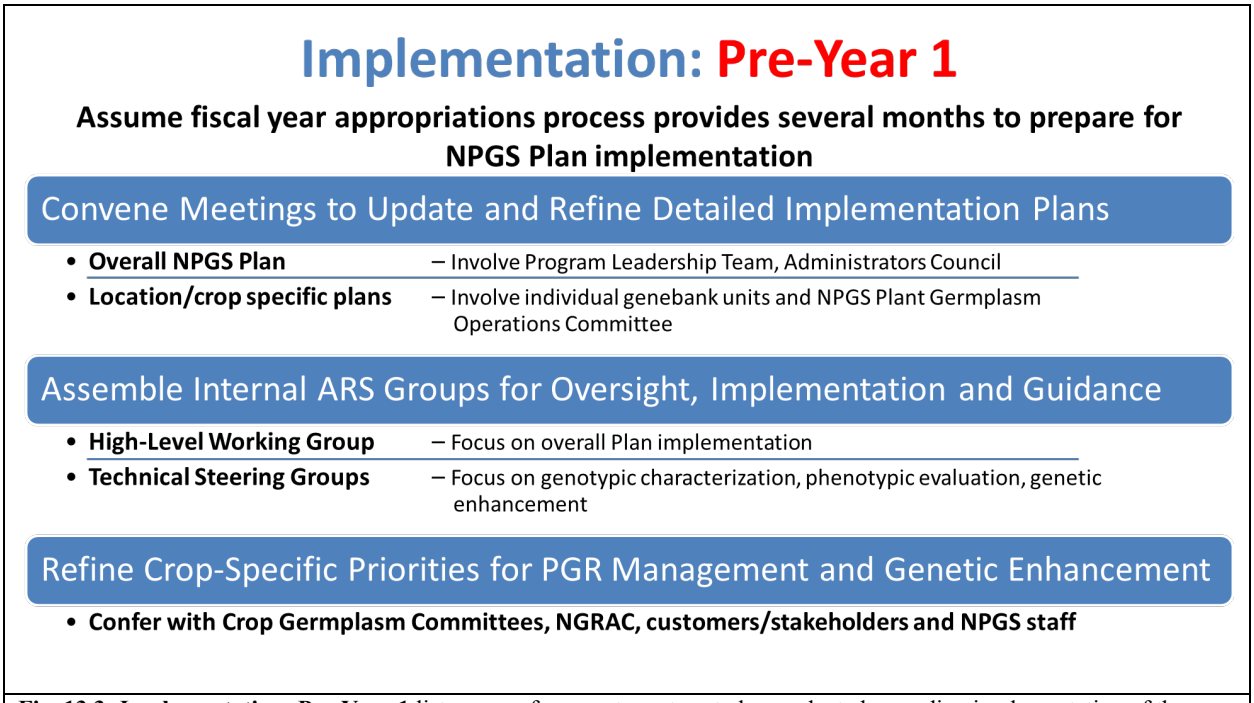


Fig. 13.3: Implementation: Pre-Year 1 lists some of preparatory steps to be conducted preceding implementation of the NPGS Plan. Internal ARS working groups will be assembled to review and refine the Plan; develop procedures for oversight and guidance of Plan implementation; and refine crop-specific priorities for implementing the Plan. ARS will confer extensively with the NGRAC, Crop Germplasm Committees, other customers/stakeholders, and the NPGS staff during this key period for implementing the Plan.

During the first year of Plan funding, NPGS staff will focus on the priority outcomes of improving and expanding infrastructure and its energy efficiency, procuring needed equipment, and hiring and training additional staff (Fig. 13.4). NPGS staff would begin conducting research to devise optimal PGR and data management methods; expand in-house core facilities or establish contracts with fee-based genotyping services; and establish cooperative research agreements with university, NGO, Tribal Nation, and private-sector cooperators for methods development, genotypic characterizations, phenotypic evaluations, and initiating genetic enhancement projects (Fig. 13.4). During Year 2, the Plan implementation would be adjusted according to experience gained in Year 1 and the available funding (Fig. 13.5).

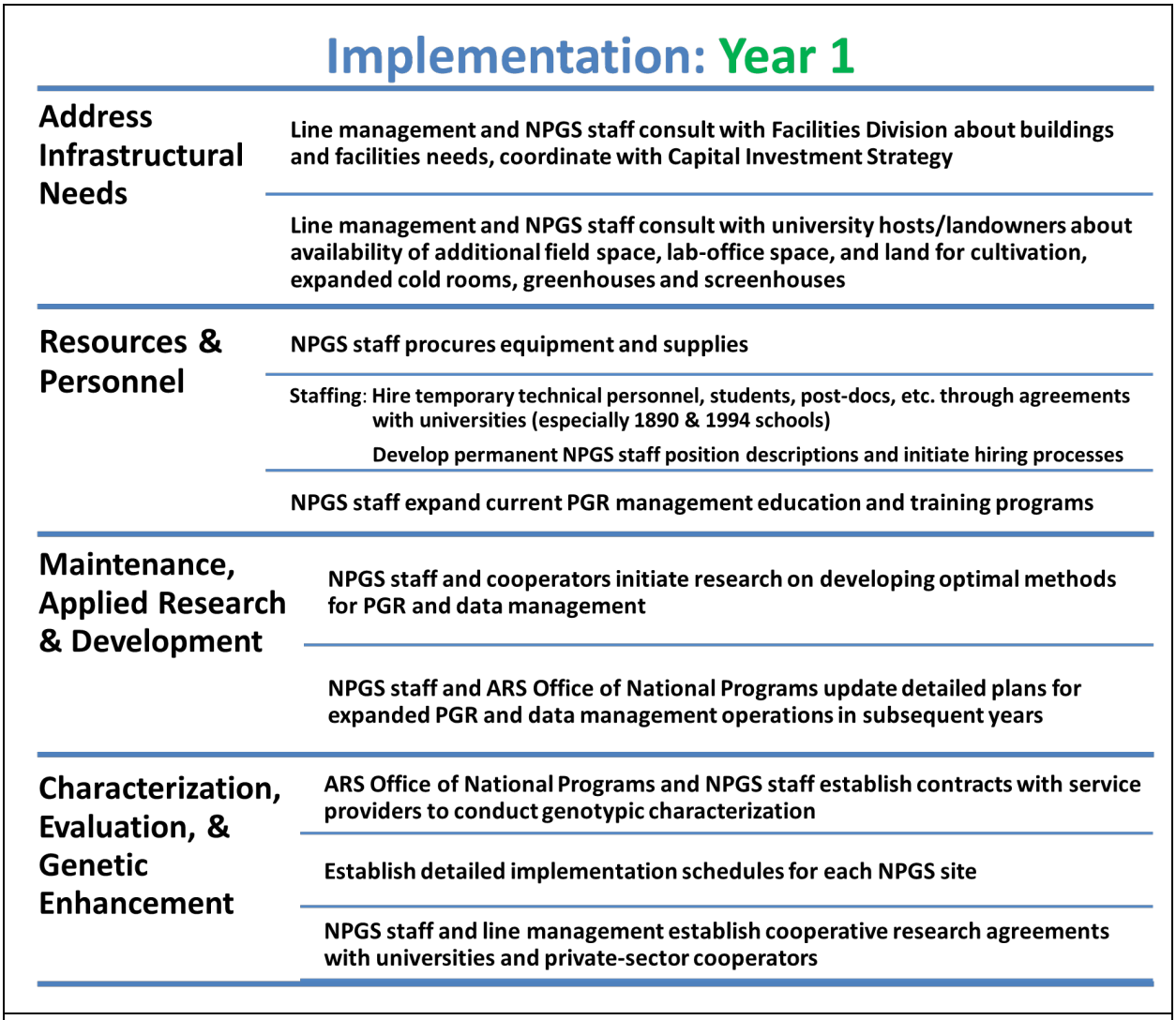


Fig. 13.4: Implementation: Year 1 in the top half (first two sections) lists details for two major priorities of the NPGS Plan in Year 1 of Implementation: 1) addressing NPGS infrastructural needs and 2) procuring equipment, supplies, and training and hiring personnel for the NPGS. Extensive consultation with building and facilities experts, customers/stakeholders, and university partners will be necessary in Year 1 of the Plan implementation.

The lower half (last two sections) lists details for two additional major priorities of the NPGS Plan in Year 1 of implementation: 1) beginning to conduct applied research for optimal PGR and data management methods and 2) formulating detailed implementation schedules for initiating genotypic characterizations, phenotypic evaluations, and genetic enhancement projects. Addressing these priorities will involve establishing numerous contracts with service providers, and cooperative research agreements with government, universities and private-sector collaborators.

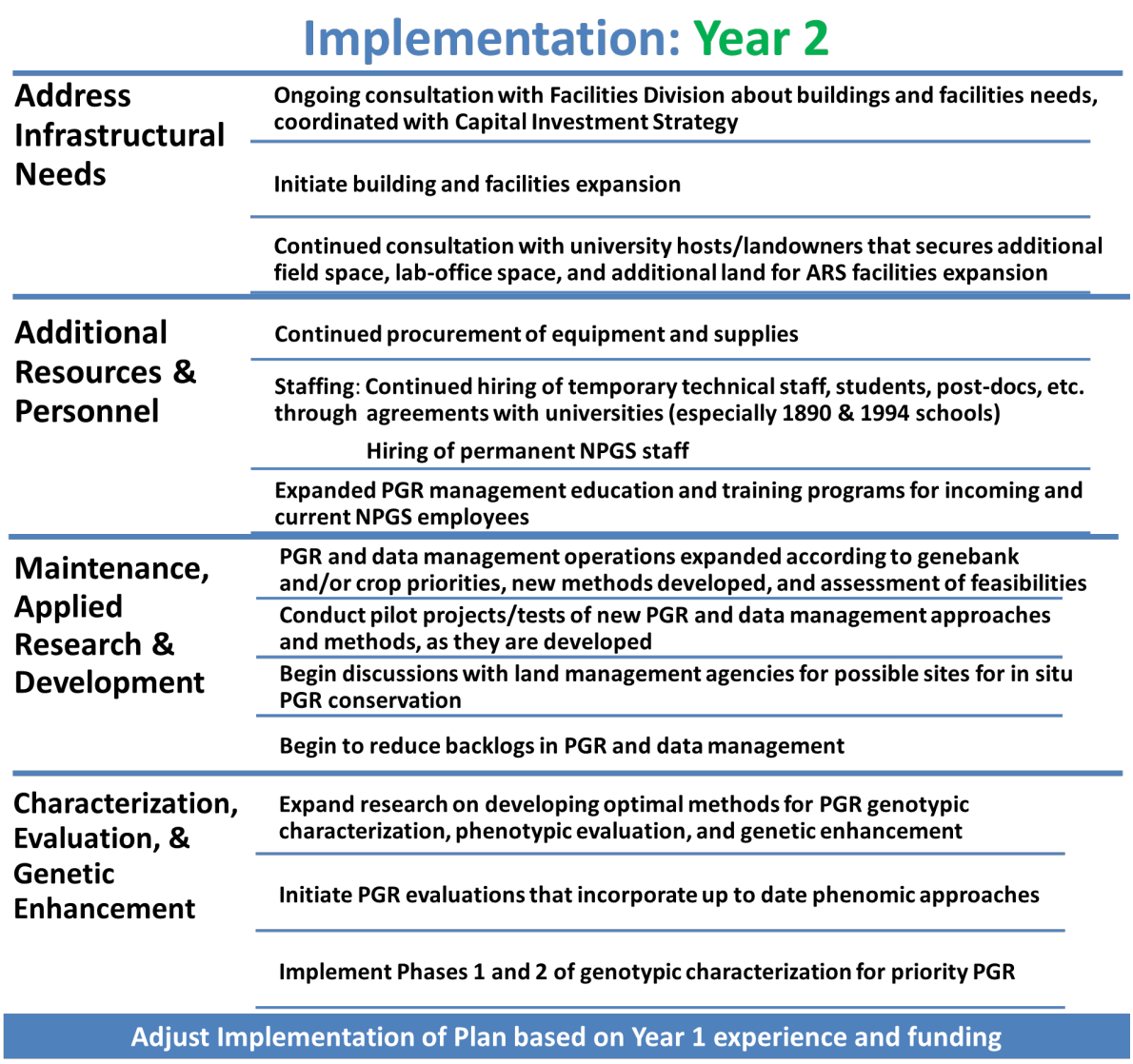


Fig. 13.5: Implementation: Year 2, in the top half (first two sections) shows how implementation of the two major priorities of the Plan will continue in Year 2: 1) addressing infrastructural needs and 2) procuring equipment, supplies, and training and hiring personnel. Expansion of NPGS buildings and facilities will begin. More staff will be hired and trained, and more equipment and supplies procured. Extensive consultation with ARS building and facilities experts, customers/stakeholders, and university partners will continue. The implementation of the Plan will be adjusted according to available funding and accumulated experience from Year 1.

The lower half (last two sections) shows how implementation of the two additional major priorities of the Plan will continue in Year 2: 1) PGR and data management operations will be expanded according to information gained with initial applied research; pilot projects will be conducted; possible in situ conservation sites will be investigated; backlogs in PGR and data management within the NPGS will begin to be reduced and 2) the initial phases of the genotypic characterization projects will be conducted; phenotypic evaluations incorporating phenomic approaches will begin; and applied research to develop optimal genotypic characterization, phenotypic evaluation and genetic enhancement methods will continue.

During Years 3-5 of the Plan implementation (Fig. 13.6), much of the requisite additional infrastructure, equipment, and supplies should be in place, and additional NPGS staff should be hired and trained. Applied research should begin to deliver superior new PGR management methods, and the expanded PGR operational capacities should begin to reduce backlogs. The first two phases of the genotypic characterization program should be near completion for some

crops. The expanded phenotypic evaluation program will have generated new phenomic-based approaches and have begun to identify priority accessions and traits for genetic enhancement and breeding programs. The greatly expanded volumes of genotypic and phenotypic data that will be available for NPGS PGR will accelerate the progress of multi-year genetic enhancement projects for priority crops.

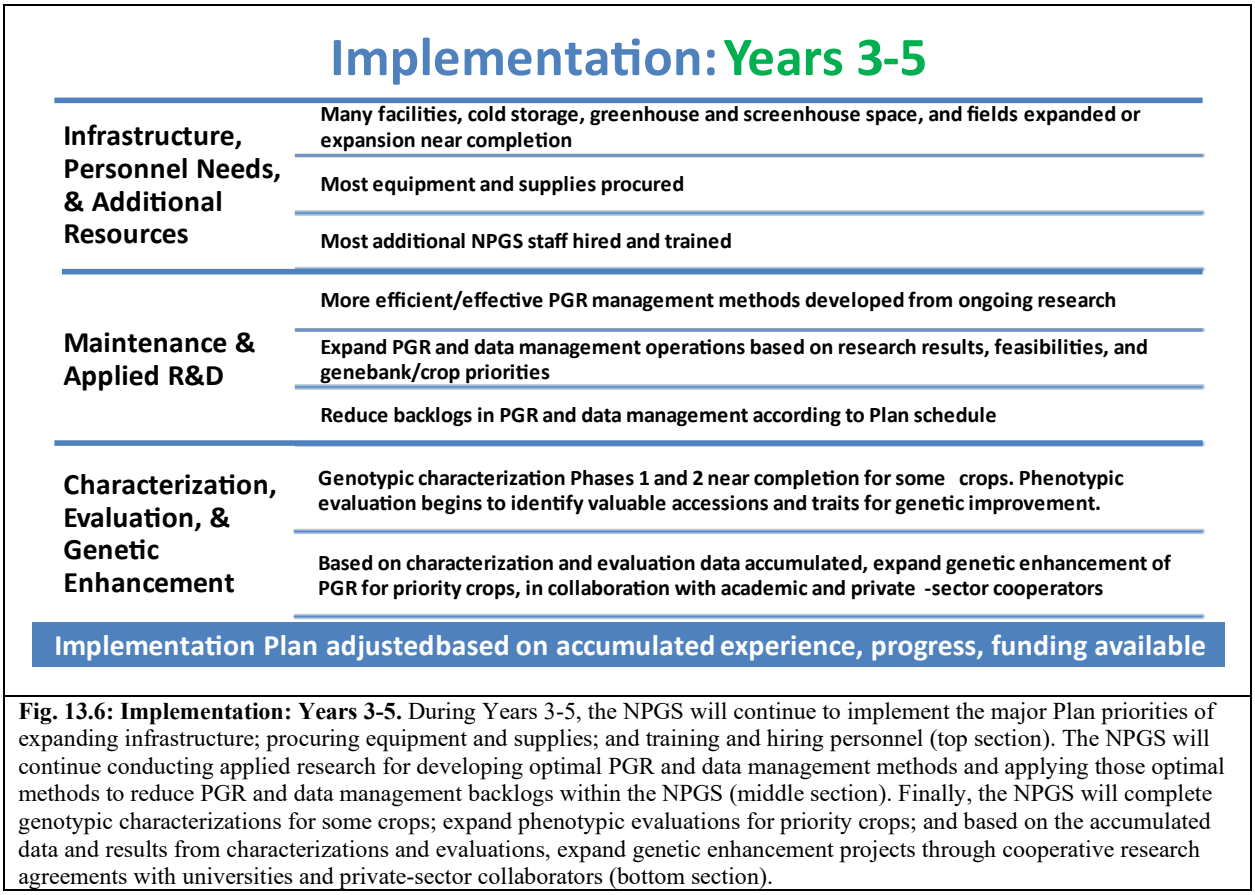


Fig. 13.6: Implementation: Years 3-5. During Years 3-5, the NPGS will continue to implement the major Plan priorities of expanding infrastructure; procuring equipment and supplies; and training and hiring personnel (top section). The NPGS will continue conducting applied research for developing optimal PGR and data management methods and applying those optimal methods to reduce PGR and data management backlogs within the NPGS (middle section). Finally, the NPGS will complete genotypic characterizations for some crops; expand phenotypic evaluations for priority crops; and based on the accumulated data and results from characterizations and evaluations, expand genetic enhancement projects through cooperative research agreements with universities and private-sector collaborators (bottom section).

The progress of the Plan's implementation, achievements, and impacts will be formally assessed at Year 5 through internal ARS reviews, presentations at a public workshop or symposium devoted to the Plan's progress, and through formal reports to the Congress, Administration, the NGRAC, and customers and stakeholders (Fig. 13.7). This 5-year assessment will be in addition to ARS's regular annual reviews of research project performance. Based on the recommendations and directives received from the assessment and the development of technological advances, the strategies and priorities for Plan implementation will be adjusted for the second 5-year period of the Plan.

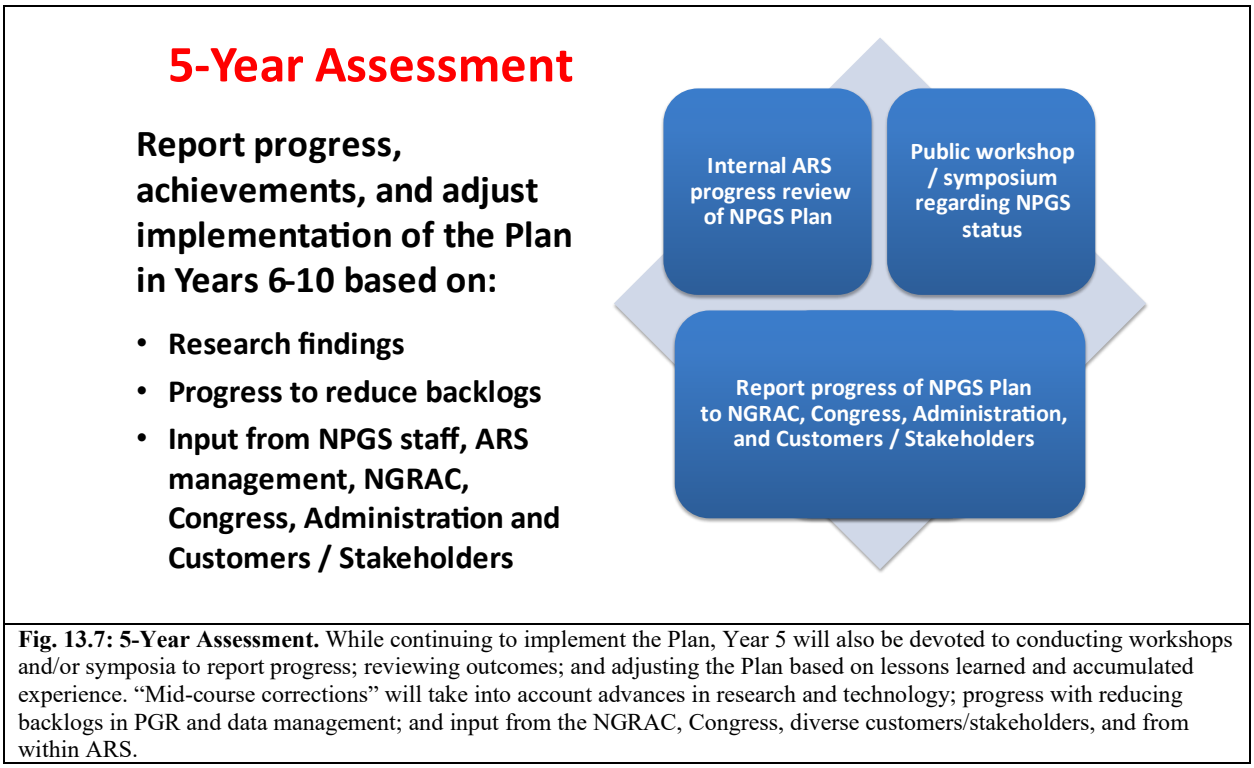


Fig. 13.7: 5-Year Assessment. While continuing to implement the Plan, Year 5 will also be devoted to conducting workshops and/or symposia to report progress; reviewing outcomes; and adjusting the Plan based on lessons learned and accumulated experience. "Mid-course corrections" will take into account advances in research and technology; progress with reducing backlogs in PGR and data management; and input from the NGRAC, Congress, diverse customers/stakeholders, and from within ARS.

During Years 6-10 (Fig. 13.8), the NPGS infrastructural and personnel expansions should be completed, and PGR management operations should be substantially improved. Applied research should deliver the outcomes of more efficient and effective PGR management methods. Operational backlogs should be reduced or eliminated; expanded PGR management capacities will enable the NPGS to avoid future backlogs. Genotypic characterizations should be complete for accessions of most crops; characterizing ca. 150,000 accessions of certain wild species and crop wild relatives would be addressed in future years. Phenomic approaches developed by NPGS researchers and collaborators should have the impact of generating large volumes of phenotypic evaluation data valuable for supporting and accelerating the progress of breeding and genetic enhancement programs. Multi-year, collaborative genetic enhancement programs should begin to deliver adapted populations with key traits derived from NPGS PGR, or new, genetically-divergent gene pools that expand the breadth of genetic diversity immediately available to safeguard national economic and food security more broadly, and as a component of the National Plant Disease Recovery System (Administration of G. W. Bush, 2004).

Similar to the Year 5 review, the NPGS Plan will be assessed at Year 10 (Fig. 13.9), focusing on new progress and results. By Year 10, the NPGS should have achieved the key outcomes of delivering more PGR, with ample associated genotypic and phenotypic data, and genetically enhanced populations or lines available for addressing rapidly changing market and environmental conditions and evolving virulent diseases and pests. By then, more genetically-engineered or genetically-edited PGR and specialized genetic stocks will require conservation by and distribution from the NPGS as well. At Year 10 of the Plan, the quality and performance of NPGS operations and applied research should be well-suited to meet future challenges to crop agriculture in the United States and globally.

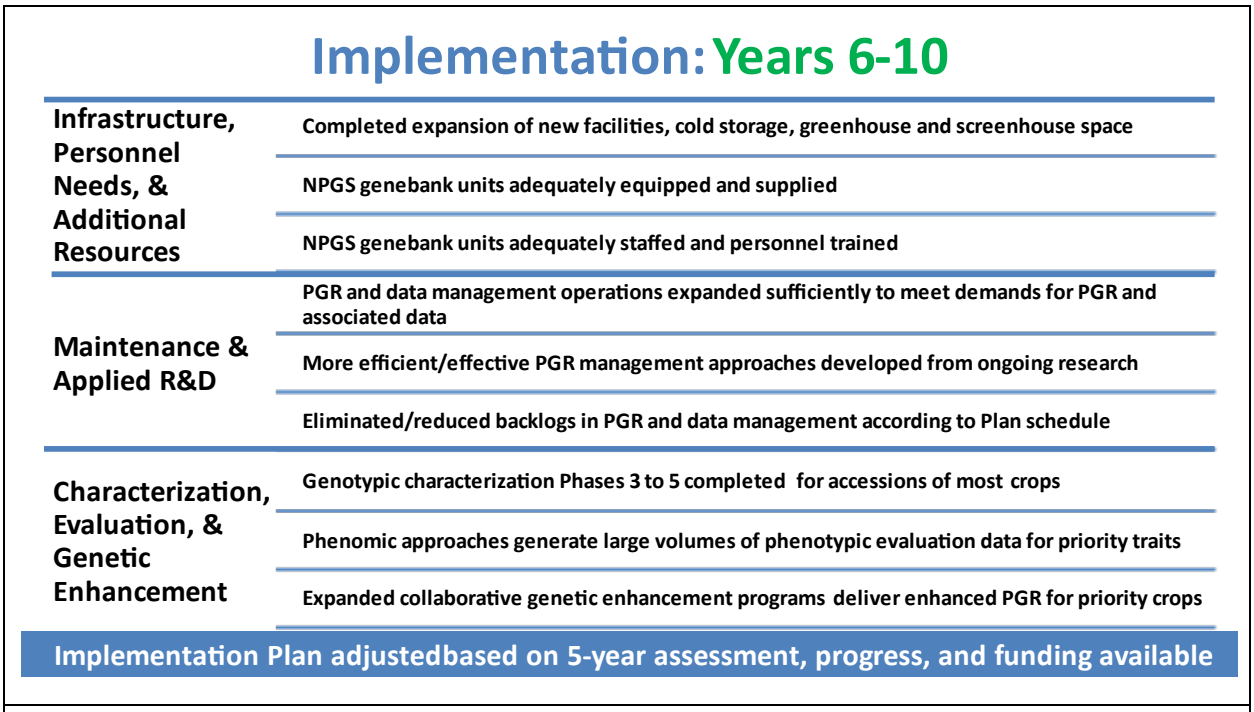


Fig. 13.8: Implementation: Years 6-10, the Plan will continue to implement its major priorities, adjusted according to accumulated experience, progress achieved, funding available, and the results of the 5-year assessment. By the end of Year 10, infrastructural expansion for the NPGS should be complete; the needed equipment and supplies should have been procured; and NPGS genebank units should be adequately staffed with trained personnel. Applied research will have developed optimal PGR and data management methods that will have been applied to reduce or eliminate PGR and data management backlogs in the NPGS. Genotypic characterizations will be complete for most crops and accessions managed by the NPGS; and phenotypic evaluations will be routinely conducted by phenomic approaches that generate large volumes of valuable data for priority crops. The expanded genetic enhancement projects, conducted through cooperative research agreements with NGO, tribal, universities, and private-sector collaborators, will have begun to deliver enhanced PGR for priority crops.

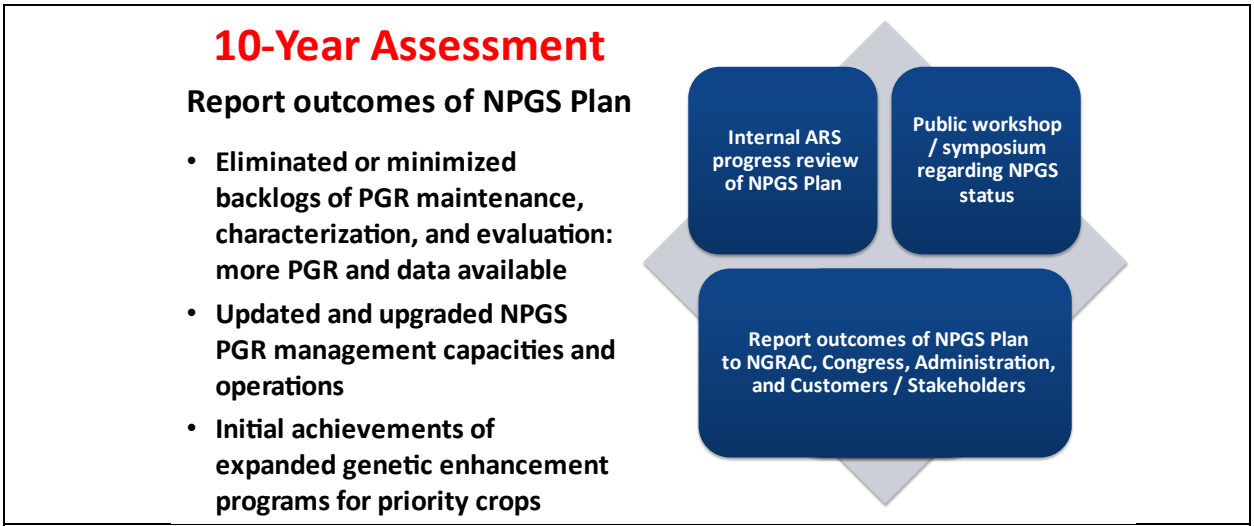


Fig. 13.9: 10-Year Assessment. The Plan will conclude at Year 10 with workshops and/or symposia to report progress and review the Plan's outcomes. If the Plan were successfully implemented, outcomes will include elimination or minimization of backlogs in PGR management; a wealth of high-quality PGR and associated information available for education, research breeding; state-of-the-art NPGS facilities, capacities, and operations; and expanded genetic enhancement programs that have released (or will release) valuable improved PGR for U. S. and global agriculture.

Acknowledgements

Sincere thanks to the National Genetic Resources Advisory Council, and these USDA/ARS personnel, listed alphabetically by surname, who played major roles in developing this Plan by providing expert advice, information, compiling and analyzing data, and drafting text:

Tomás Ayala-Silva, USDA/ARS, Tropical Agriculture Research Station (Genebank-specific information)

John Bamberg, USDA/ARS, Vegetable Crops Research Unit (Genebank-specific information)

Nahla Bassil, USDA/ARS, National Clonal Germplasm Repository, Corvallis (Genebank-specific information)

Lorie Bernhardt, USDA/ARS, Dale Bumpers National Rice Research Center (Retired, Genebank-specific information)

Harold Bockelman, USDA/ARS, Small Grains and Potato Germplasm Research Unit (Genebank-specific information)

Peter Bretting, USDA/ARS, Office of National Programs (Co-author of overall Plan; data analyses)

Edward Buckler, USDA/ARS, Plant, Soil, and Nutrition Research Unit (Component 10)

Kevin Conrad, USDA/ARS Floral and Nursery Plant Research Unit, U.S. National Arboretum (Genebank-specific information)

Clare Coyne, USDA/ARS, Plant Introduction and Testing Research Unit (Genebank-specific information)

Peter Cyr, USDA/ARS, North Central Regional Plant Introduction Station (Components 2, 10, 11)

Carolyn DeBuse, USDA/ARS, National Clonal Germplasm Repository for Tree Fruits, Nuts, & Grapes (Genebank-specific information)

Stacey Estrada, USDA/ARS, North Central Regional Plant Introduction Station (Illustrations, tables, data analyses, co-author of overall Plan)

James Frelichowski, USDA/ARS, Crop Germplasm Research Unit (Genebank-specific information)

Candice Gardner, USDA/ARS, North Central Regional Plant Introduction Station (Retired; genebank-specific information, and review of Plan)

Ricardo Goenaga, USDA/ARS, Tropical Agriculture Research Station and Subtropical Horticulture Research Station (Genebank-specific information)

Stephanie Greene, USDA/ARS, National Laboratory for Genetic Resources Preservation (Genebank-specific information, Component 3)

Ben Gutierrez, USDA/ARS, Plant Genetic Resources Research Unit (Genebank-specific information)

Mary Guttieri, USDA/ARS Hard Winter Wheat Genetic Research Unit (Text review)

Glenn Hanes, USDA/ARS, Office of National Programs (Data analyses, tables, illustrations, co-author of overall Plan)

Melanie Harrison, USDA/ARS, Plant Genetic Resources Conservation Unit (Genebank-specific information)

Claire Heinitz, USDA/ARS, National Arid Land Plant Genetic Resources Research Unit (Genebank-specific information)

Barbara Hellier, USDA/ARS, Plant Introduction and Testing Research Unit (Genebank-specific information)

Kim Hummer, USDA/ARS, National Clonal Germplasm Repository, Corvallis (Retired, Genebank-specific information)

Trevis Huggins, USDA/ARS, Dale Bumpers National Rice Research Center (Genebank-specific information)

Brian Irish, USDA/ARS, Plant Introduction and Testing Research Unit (Genebank-specific information)

Bob Jarret, USDA/ARS, Plant Genetic Resources Conservation Unit (Genebank-specific information)

Gary Kinard, USDA/ARS, National Germplasm Resources Laboratory (Component 2)

Robert Krueger, USDA/ARS, National Clonal Germplasm Repository for Citrus and Dates (Genebank-specific information)

Keith Kubenka, USDA/ARS, Crop Germplasm Research Unit (Genebank-specific information)

Joanne Labate, USDA/ARS, Plant Genetic Resources Research Unit (Retired, Genebank-specific information)

Janna Love, USDA/ARS, Crop Germplasm Research Unit (Genebank-specific information)

Adam Mahan, USDA/ARS, Soybean/Maize Germplasm, Pathology, and Genetics Research Unit (Genebank-specific information)

Tracie Matsumoto, USDA/ARS, Pacific Basin Agricultural Research Center (Genebank-specific information)

Carol Mayo Riley, USDA/ARS, Pacific Basin Agricultural Research Center (Genebank-specific information)

Anna McClung, USDA/ARS, Dale Bumpers National Rice Research Center (Genebank-specific information)

Brad Morris, USDA/ARS, Plant Genetic Resources Conservation Unit (Genebank-specific information)

Esther Peregrine, USDA/ARS, Soybean/Maize Germplasm, Pathology, and Genetics Research Unit (Retired, Genebank-specific information)

Margaret Pooler, USDA/ARS Floral and Nursery Plant Research Unit, U.S. National Arboretum (Genebank-specific information)

Mary Lou Polek, USDA/ARS, National Clonal Germplasm Repository for Citrus and Dates (Retired, Genebank-specific information)

John Preece, USDA/ARS, National Clonal Germplasm Repository for Tree Fruits, Nuts, & Grapes (Retired, genebank-specific information)

Bernard Prins, USDA/ARS, National Clonal Germplasm Repository for Tree Fruits, Nuts, & Grapes (Genebank-specific information)

Christopher Richards, USDA/ARS, National Laboratory for Genetic Resources Preservation (Component 10)

Carlos Rios, USDA/ARS, Tropical Agriculture Research Station (Retired, Genebank-specific information)

Todd Rounsaville, USDA/ARS, Floral and Nursery Plant Research Unit, U.S. National Arboretum (Genebank-specific information)

Marty Sachs, USDA/ARS, Soybean/Maize Germplasm, Pathology, and Genetics Research Unit (Genebank-specific information)

Jesse Schartner, USDA/ARS, Vegetable Crops Research Unit (Genebank-specific information)

Brian Scheffler, USDA/ARS, Genomics and Bioinformatics Research Unit (Component 10)

Melanie Schori, USDA/ARS, National Germplasm Resources Laboratory (Component 2)

Jenny Smith, USDA/ARS, National Clonal Germplasm Repository for Tree Fruits, Nuts, & Grapes (Genebank-specific information)

Zachary Stansell, USDA/ARS, Plant Genetic Resources Research Unit (Component 11)

Shyam Tallury, USDA/ARS, Plant Genetic Resources Conservation Unit (Genebank-specific information)

Lisa Taylor, USDA/ARS, Plant Introduction and Testing Research Unit (Genebank-specific information)

Joshua Udall, USDA/ARS, Crop Germplasm Research Unit (Genebank-specific information)

Gayle Volk, USDA/ARS, National Laboratory for Genetic Resources Preservation (Genebank-specific information, Components 4 and 5)

Christina Walters, USDA/ARS, National Laboratory for Genetic Resources Preservation (Co-author Components 4 and 5; data analyses; genebank-specific information)

Ming-Li Wang, USDA/ARS, Plant Genetic Resources Conservation Unit (Genebank-specific information)

Marilyn Warburton, USDA/ARS, Plant Introduction and Testing Research Unit, on temporary detail to USDA/ARS, Office of National Programs (Co-author of overall Plan)

Jacob Washburn, USDA/ARS, Plant Genetics Research Unit (Component 11)

Karen Williams, USDA/ARS, National Germplasm Resources Laboratory (Component 3)

Mike Wintersteen, USDA/ARS, Subtropical Horticulture Research Station (Genebank-specific information)

Gan-Yuan Zhong, USDA/ARS, Plant Genetic Resources Research Unit (Genebank-specific information)

Sincere thanks to the following non-USDA/ARS personnel who provided valuable concepts, information, perspectives, and drafted text:

Michael Gore, Cornell University (Component 11)

Jeffrey Haynes, USDA/AMS Plant Variety Protection Office (Component 3)

Colin Khoury, San Diego Botanical Garden, formerly USDA/ARS, National Laboratory for Genetic Resources Preservation (Component 3)

Jonathan Lynch, Penn State University (Component 11)

Seth Murray, Texas A & M University (Component 11)

Moira Sheehan, Breeding Insight, Cornell University (Components 10, 11)

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Appendix A

Explanations and Definitions for Metrics or Variables Analyzed for This Plan

The PGR managers at NPGS genebank units completed in extensive Excel spreadsheets (not shown) that recorded crop, CWR, and genebank unit-specific data for the ca. 75 metrics of PGR management operations explained in this Appendix A. Some of these metrics were developed withing the NPGS and some have been applied to assess the operations of international genebanks (e.g., Lusty et al., 2021). The data received from the PGR managers were then aggregated for analysis and presentation in infographic figures. The names of some metrics in Appendix A can differ slightly from names applied to those same metrics in the figures. Plans for future PGR management operations covered in Components 2-9 were based largely on the extensive data collected for these metrics. Plans for future PGR genotypic characterization (Component 10), phenotypic evaluation (Component 11), and genetic enhancement/pre-breeding (Component 12) programs were informed by the data from these metrics and elaborated according to projections for future technological advances and operational capacities.

1) Infrastructure, Capacity, and Support for NPGS PGR and Information Management and Research

A) Collection Size and Diversity

- # of genebank taxa records the number of taxa (different species, subspecies, botanical varieties, etc.) managed by an individual NPGS genebank unit. It serves as a measure of the scales of the PGR management workload, the operational complexity, and the diverse responsibilities for a genebank unit.
- # of genebank accessions records the number of samples, termed "accessions," managed as genetically distinct elements by an individual NPGS genebank units. It also serves as a measure of the scales of the PGR management workload, the operational complexity, and the diverse responsibilities for a genebank unit.
- # of different crops records the number of crops managed by an individual NPGS genebank units. The definitions for individual "crops" have been developed by the responsible PGR managers. It also serves as a measure of the scales of the PGR management workload, the operational complexity, and the diverse responsibilities for a genebank unit.

B) Financial Support

- Annual recurrent NPGS genebank unit funding records the recurrent "base funding" annually appropriated to the ARS research projects to support the costs of all genebank operations, including salaries and benefits, equipment, travel, rent, utilities, supplies, etc. It is reported as the gross Congressional appropriations. The genebank unit actually receives 90% of that total (termed "net-to-location"); 10% is devoted to ARS-wide support functions (e.g., human resources, administration, accounting, etc.). This metric measures the primary financial resources available for all NPGS genebank operations. The four Regional Plant Introduction Station genebank units (Ames, Geneva, Griffin, and

Pullman) also receive some "off-the-top" funds allocated annually by the State Agricultural Experiment Stations (SAES) from USDA/NIFA Hatch funds.

C) Staffing

- Personnel levels (# FTEs permanent and temporary) measure, as full-time-equivalents (FTEs), the number of permanent and temporary personnel employed by a genebank unit. It is a primary measure for PGR management capacity. Approximately 90% of the permanent NPGS genebank staff are ARS employees, but the "off-the-top" funding mentioned earlier supports several permanent NPGS land-grant university employees. Depending on the genebank unit, temporary staff are ARS employees or a mixture of ARS and land-grant university employees, who are often students.

D) Physical Resources

- NPGS unit cold storage space measures in cubic feet the volume available for safeguarding PGR under refrigeration or cryostorage at a genebank unit. It is a primary measure for PGR maintenance capacity. Cold storage conditions are usually +4˚ C (41˚ F), -18˚ C (0˚ F), or ultracold (cryo) temperatures.
- NPGS genebank unit greenhouse space measures in square feet the area available for maintaining, regenerating, propagating, and/or conducting research with PGR in greenhouses/glasshouses at a genebank unit. It is an important measure for PGR management capacity.
- NPGS genebank unit screenhouse & other enclosed spaces for cultivation measures in square feet the area available at a genebank unit for maintaining, regenerating, propagating, and/or conducting research with PGR in partially enclosed structures, often without permanent water, lighting, etc. It is an important measure for PGR management capacity.
- NPGS genebank unit field space measures in acres the land area available for maintaining, regenerating, propagating, and/or conducting research with PGR at a genebank unit. It is a primary measure for PGR management capacity. If the genebank unit is co-located at a land-grant university or located nearby, the land used for genebank unit operations is frequently owned by universities and/or SAES that lease or provide it cost-free to the NPGS. Some land available for genebank unit operations is owned by ARS.

E) Information Management Capacity

- # of records in GRIN-Global (systemwide) measures the volume of data (e.g., PGR inventory, taxonomic names, genotypes, and traits) maintained and accessible via GRIN-Global. It serves as a primary measure of both NPGS information management infrastructure and capacity.
- # of gigabytes in GRIN-Global (systemwide) measures the volume of digital information maintained and accessible via GRIN-Global. It serves as a primary measure of both NPGS information management infrastructure and capacity.

- # of advanced GG users (GRIN-Global Curator Tool) users measures the number of genebank unit personnel who use the most powerful and advanced functions of GRIN-Global. It serves as an important measure for PGR information management capacity.
- # of NPGS staff working hours spent using GG (Average # of hours/day using Curator Tool, per user) measures how intensively genebank unit personnel use the most powerful and advanced functions of GRIN-Global. It also serves as an important measure for PGR information management capacity.
- # of "privileged" GRIN-Global data entry accounts measures the number of genebank unit personnel authorized to make changes to the data in GRIN-Global. It also serves as an important measure for PGR information management capacity.

F) Collaborations

- Average # of annual individual external research and PGR management collaborations serves as a valuable indirect measure of research activity and information transfer at a genebank unit. It also measures the degree to which the genebank unit participates in domestic and international PGR management networks. Here "external" usually refers to non-ARS collaborations that generally require a formal inter-institutional agreement of some sort. genebank units can define external collaborations according to their particular local contexts and conditions.

2) PGR Information Management: GRIN-Global (GG) Data and Website Usage

A) Data Volume

- # of records in GRIN-Global measures the volume of data (e.g., PGR inventory, taxonomic names, genotypes, and traits) maintained and accessible via GRIN-Global. These data are also recorded earlier under Information Management Capacity.
- # of bytes in GRIN-Global measures the volume of digital information maintained and accessible via GRIN-Global. These data are also recorded earlier under Information Management Capacity.

B) Data Usage

- # of visitors annually to GRIN-Global public web site measures the average volume of total devices that access the GRIN-Global public web site per year. This metric measures an important aspect of the demand for data associated with the NPGS and its germplasm.
- # of sessions annually for GRIN-Global public web site measures the average volume of unique devices (IDP numbers) that access the GRIN-Global public web site per year. This metric also measures an important aspect of the demand for data associated with the NPGS and its germplasm.
- # of page views for GRIN-Global public web site annually measures the average volume of individual "pages" of the GRIN-Global public web site viewed per year. This metric also measures an important aspect of the demand for data associated with the NPGS and its germplasm.

C) Document Digitization and Uploading into GRIN-Global

- # of paper records to digitize measures the volume of paper records at a genebank unit that should be scanned into digital records. It serves as an important index for the backlog of physical records in the NPGS that must be safeguarded in digital form.
- # of paper records digitized annually measures the volume of paper records at a genebank unit that are scanned into digital records per year. It is relevant for measuring the pace whereby the preceding backlog is being addressed.
- # of local digital genebank unit records requiring upload to GRIN-Global measures the volume of digital records maintained locally in a genebank unit that should be uploaded to GRIN-Global. It serves as an important index for the backlog of digital information that must be incorporated into GRIN-Global.
- # of digital genebank records uploaded to GRIN-Global annually measures the volume of digital records maintained locally in a genebank unit that are uploaded to GRIN-Global annually. It is relevant for measuring the pace whereby the preceding backlog is being addressed.
- % of digital genebank records uploaded to GRIN-Global annually measures the relative rate whereby records maintained locally in a genebank unit are uploaded to GRIN-Global annually. It is also relevant for measuring the pace whereby the preceding backlog is being addressed.

D) GRIN-Global Taxonomy

- # of species recorded in GRIN-Global measures the taxonomic diversity in the NPGS PGR collection, and the extent to which NPGS accessions have been identified to the level of species and that information has been added to GRIN-Global.
- Average # of species records added to GRIN-Global annually measures growth in the taxonomic diversity in the NPGSPGR collection, and progress with identifying NPGS accessions to the level of species and adding that information GRIN-Global.
- # of horticultural crops evaluated for crop wild relative (CWR) data measures the extent to which horticultural crops in the NPGS PGR collection have been evaluated for CWR data.
- % of taxonomy records with protologue links measures one aspect of the quality and completeness of taxonomic information for NPGS accessions.
- % of scientific names with resolved geography data measures one aspect of the quality and completeness of geographical data associated with the scientific names for NPGS accessions.

3) PGR Acquisition and In Situ Conservation

A) PGR Acquisition

- # of accessions in collection is also recorded earlier under “Collection size and diversity”. It provides primary information about the size and scale of crop collections and overall genebank unit PGR collections.

- Average # of new accessions acquired annually measures the volume whereby specific crop collections and/or overall genebank unit PGR collections expand per year. It provides primary information for measuring the growth and estimating future sizes of specific crop collections and/or overall genebank unit PGR collections.
- Annual growth rate (average % of accessions acquired annually) measures the annual growth rate of specific crop collections and/or overall genebank unit PGR collections. It provides primary information for measuring the growth and estimating future sizes of specific crop collections and/or overall genebank unit PGR collections.

B) In Situ Conservation

- # of species and/or populations conserved in situ is a valuable measure for the extent to which the PGR conserved in NPGS genebank units are also conserved via in situ conservation in reserves, usually through NPGS partnerships with land management agencies. In situ PGR conservation is meant to complement ex situ PGR conservation in NPGS genebank units.
- # of species and/or populations included in land management agency plans is also a valuable measure for the extent to which the PGR conserved in NPGS genebank units are also conserved via in situ conservation. Including particular species and populations in land management agency plans provides a valuable indication for both present and future commitments to in situ PGR conservation. In situ PGR conservation is meant to complement ex situ PGR conservation in NPGS genebank units.

4) Safeguarding PGR Through Long-Term Storage

A) Safety Duplication at NLGRP - Fort Collins, CO

- # of accessions duplicated at NLGRP Ft. Collins measures the volume of duplicate samples of accessions from PGR collections safeguarded in the NPGS "base collection" at the NLGRP Ft. Collins. It is a primary measure for the quality of long-term maintenance for NPGS PGR.
- % of accessions duplicated at NLGRP Ft. Collins measures the proportion of duplicate samples of accessions from PGR collections safeguarded in the NPGS "base collection" at the NLGRP Ft. Collins. It is also a primary measure for the quality of long-term maintenance for NPGS PGR.
- # of accessions duplicated at NLGRP Ft. Collins in LN2 measures the volume of duplicate samples of accessions from PGR collections safeguarded in the NPGS "base collection" under liquid nitrogen cryogenic conditions at the NLGRP Ft. Collins. It is a primary measure for the quality of long-term maintenance for NPGS PGR.
- % of accessions duplicated at NLGRP Ft. Collins in LN2 measures the proportion of duplicate samples of accessions from PGR collections safeguarded in the NPGS "base collection" under liquid nitrogen cryogenic conditions at the NLGRP Ft. Collins. It is also a primary measure for the quality of long-term maintenance for NPGS PGR.
- # of accessions duplicated at NLGRP Ft. Collins in vitro storage measures the volume of duplicate samples of accessions from PGR collections safeguarded in the NPGS "base

collection" in tissue culture at the NLGRP Ft. Collins. It is a primary measure for the quality of long-term maintenance for NPGS PGR.

- % of accessions duplicated at NLGRP Ft. Collins in vitro storage measures the proportion of duplicate samples of accessions from PGR collections safeguarded in the NPGS "base collection" in tissue culture at the NLGRP Ft. Collins. It is also a primary measure for the quality of long-term maintenance for NPGS PGR.
- # of accessions duplicated at NLGRP Ft. Collins under conventional reduced-temperature storage measures the volume of duplicate samples of accessions from PGR collections safeguarded in the NPGS "base collection" under conventional reduced temperatures at the NLGRP Ft. Collins. It is a primary measure for the quality of long-term maintenance for NPGS PGR.
- % of accessions duplicated at NLGRP Ft. Collins under conventional reduced-temperature storage measures the proportion of duplicate samples of accessions from PGR collections safeguarded in the NPGS "base collection" under conventional reduced temperatures at the NLGRP Ft. Collins. It is also a primary measure for the quality of long-term maintenance for NPGS PGR.
- Average # of accessions duplicated at NLGRP Ft. Collins annually measures the average volume of samples of accessions from PGR collections that are transferred to NLGRP Ft. Collins for duplication each year. It is a primary measure for NPGS PGR maintenance capacity.
- Average % of accessions duplicated at NLGRP Ft. Collins annually measures the relative rate whereby accessions from PGR collections are transferred to NLGRP Ft. Collins for duplication each year. It is a primary measure for NPGS PGR maintenance capacity.

B) Safety Back-Up at NLGRP - Ft. Collins, CO

- # of accessions backed-up at NLGRP Ft. Collins measures the volume of backed-up samples of accessions from PGR collections safeguarded in the NPGS "base collection" at the NLGRP Ft. Collins. It is a primary measure for the quality of long-term maintenance for NPGS PGR.
- % of accessions backed-up at NLGRP Ft. Collins measures the proportion of backed-up samples of accessions from PGR collections safeguarded in the NPGS "base collection" at the NLGRP Ft. Collins. It is also a primary measure for the quality of long-term maintenance for NPGS PGR.
- # of accessions backed-up at NLGRP Ft. Collins in LN2 measures the volume of backed-up samples of accessions from PGR collections safeguarded in the NPGS "base collection" under liquid nitrogen cryogenic conditions at the NLGRP Ft. Collins. It is a primary measure for the quality of long-term maintenance for NPGS PGR.
- % of accessions backed-up at NLGRP Ft. Collins in LN2 measures the proportion of backed-up samples of accessions from PGR collections safeguarded in the NPGS "base collection" under liquid nitrogen cryogenic conditions at the NLGRP Ft. Collins. It is also a primary measure for the quality of long-term maintenance for NPGS PGR.
- # of accessions backed-up at NLGRP Ft. Collins in vitro storage measures the volume of backed-up samples of accessions from PGR collections safeguarded in the NPGS "base

collection" in tissue culture at the NLGRP Ft. Collins. It is a primary measure for the quality of long-term maintenance for NPGS PGR.

- % of accessions backed-up at NLGRP Ft. Collins in vitro storage measures the proportion of backed-up samples of accessions from PGR collections safeguarded in the NPGS "base collection" in tissue culture at the NLGRP Ft. Collins. It is also a primary measure for the quality of long-term maintenance for NPGS PGR.
- # of accessions backed-up at NLGRP Ft. Collins under conventional reduced-temperature storage measures the volume of backed-up samples of accessions from PGR collections safeguarded in the NPGS "base collection" under standard reduced temperatures at the NLGRP Ft. Collins. It is a primary measure for the quality of long-term maintenance for NPGS PGR.
- % of accessions backed-up at NLGRP Ft. Collins under conventional reduced-temperature storage measures the proportion of backed-up samples of accessions from PGR collections safeguarded in the NPGS "base collection" under standard reduced temperatures at the NLGRP Ft. Collins. It is also a primary measure for the quality of long-term maintenance for NPGS PGR.

C) Time Needed to Safeguard Accessions at NLGRP - Ft. Collins, CO

- Range of # of years needed to safeguard duplicates of accessions at NLGRP-Ft. Collins provides a primary estimate for this "duplication backlog" by the number of years, expressed as a range between minima and maxima, needed to store duplicate samples of accessions at the NLGRP-Ft. Collins. It is a primary measure for NPGS PGR maintenance capacity.
- Median # of years needed to safeguard duplicates of accessions at NLGRP-Ft. Collins also provides a primary estimate for this "duplication backlog" by the number of years, expressed as a median #, median of medians, and average of medians, needed to store duplicate samples of accessions at the NLGRP-Ft. Collins. It is also a primary measure for NPGS PGR maintenance capacity.

D) Long-Term Storage at Svalbard Global Seed Vault

- # of accessions in long-term storage at Svalbard Global Seed Vault measures the volume of duplicate samples of NPGS seed-propagated accessions stored at the Svalbard Global Seed Vault, a third site for safeguarding NPGS accessions.
- % of accessions in long-term storage at Svalbard Global Seed Vault also measures the proportion of duplicate samples of NPGS seed-propagated accessions stored at the Svalbard Global Seed Vault, a third site for safeguarding NPGS accessions.

5) Germination, Viability, and Longevity Testing of NPGS PGR Accessions

- # of accessions with recent germination, viability, or longevity test data measures the volume of accessions for which data from recent (as defined by the PGR manager) germination, viability, or longevity tests are available. It is a primary measure for the quality of long-term maintenance for NPGS PGR.

- % of accessions with recent germination, viability, or longevity test data measures the proportion of accessions for which data from recent (as defined by the PGR manager) germination, viability, or longevity tests are available. It also is a primary measure for the quality of long-term maintenance for NPGS PGR.
- # of accessions requiring germination, viability, or longevity testing measures the volume of accessions requiring germination, viability, or longevity tests. It is a primary measure for the quality of long-term maintenance for NPGS PGR.
- % of accessions requiring germination, viability, or longevity testing measures the proportion of accessions requiring germination, viability, or longevity test. It is also a primary measure for the quality of long-term maintenance for NPGS PGR.
- Average # of accessions tested annually for germination, viability, or longevity measures the average volume of accessions tested each year for germination, viability, or longevity. It is a primary measure for NPGS PGR maintenance capacity.
- Average % of accessions tested annually for germination, viability, or longevity measures the relative rate whereby accessions are tested each year for germination, viability, or longevity tests. It is also a primary measure for NPGS PGR maintenance capacity.

A) Years Needed to Test Accessions That Require Germination, Viability, or Longevity Testing

- Range of # of years needed to test accessions that require germination, viability, or longevity testing estimates a backlog for needed germination, viability, or longevity tests by the number of years, expressed as a range between minima and maxima, required to test accessions that currently require germination, viability, or longevity assays. It is a primary measure for NPGS PGR maintenance capacity.
- Median # of years needed to test accessions that require germination, viability, or longevity testing estimates the backlog for needed germination, viability, or longevity tests by the number of years, expressed as a median number, median of median, and average of medians required to test accessions that currently require germination, viability, or longevity assays. It is also a primary measure for NPGS PGR maintenance capacity.

6) PGR Pathogen Testing and Clean-Up

A) Pathogen Testing

- Average # of accessions tested annually for pathogens measures the volume of accessions tested per year for presence of designated pathogens. It is a primary measure for NPGS PGR maintenance capacity.
- Average % of accessions tested annually for pathogens measures the relative rate whereby accessions are tested per year for presence of designated pathogens. It is also a primary measure for NPGS PGR maintenance capacity.
- # of accessions requiring pathogen testing measures the volume of accessions requiring testing for presence of designated pathogens. It is a primary measure for the quality of long-term maintenance for NPGS PGR.

- % of accessions requiring pathogen testing measures the proportion of accessions requiring testing for presence of designated pathogens. It also is a primary measure for the quality of long-term maintenance for NPGS PGR.

B) **Pathogen "Clean-Up"**

- Average # of accessions "cleaned up" of pathogens annually measures the volume of accessions for which designated pathogens are removed from accessions via therapy per year. It is a primary measure for NPGS PGR maintenance capacity.
- Average % of accessions "cleaned up" of pathogens annually measures the rate whereby designated pathogens are removed from accessions via therapy per year. It is also a primary measure for NPGS PGR maintenance capacity.
- # of accessions requiring pathogen clean-up measures the volume of accessions requiring therapy to remove designated pathogens. It is a primary measure for the quality of long-term maintenance for NPGS PGR.
- % of accessions requiring pathogen clean-up measures the proportion of accessions requiring therapy to remove designated pathogens. It is also a primary measure for the quality of long-term maintenance for NPGS PGR.

C) Time Needed to Reduce Backlogs of Pathogen Testing and Clean-Up for NPGS Accessions

- Range of # of years needed to test accessions that require testing for pathogens estimates the backlog for pathogen testing accessions by the number of years, expressed as a range between absolute minima and maxima, needed to test accessions that currently require testing for pathogens. It is a primary measure for NPGS PGR maintenance capacity.
- Median # of years needed to test accessions that require testing for pathogens also estimates the backlog for pathogen testing accessions by the number of years, expressed as a median #, median of medians, and average medians, needed to test accessions that currently require testing for pathogens. It is also a primary measure for NPGS PGR maintenance capacity.
- Range of # of years needed to clean-up accessions from pathogens estimates the backlog for cleaning up accessions from pathogens by the number of years, expressed as a range between absolute minima and maxima, needed to clean-up accessions that currently require clean-up from pathogens. It is a primary measure for NPGS PGR maintenance capacity.
- Median # of years needed to clean-up accessions from pathogens estimates the backlog for cleaning up accessions from pathogens by the number of years, expressed as a median #, median of medians, and average medians, needed to clean-up accessions that currently require clean-up. It is also a primary measure for NPGS PGR maintenance capacity.

7) PGR Regeneration or Repropagation

A) Overall Regeneration or Repropagation

- Average # of accessions regenerated or repropagated annually measures the volume of accessions regenerated or repropagated per year. It is a primary measure for NPGS PGR maintenance capacity.
- Average % of accessions regenerated or repropagated annually measures the relative rate whereby accessions are regenerated or repropagated per year. It is also a primary measure for NPGS PGR maintenance capacity.
- # of accessions requiring regeneration or repropagation measures the volume of accessions requiring regeneration or repropagation. It is a primary measure for the quality of maintenance for NPGS PGR.
- % of accessions requiring regeneration or repropagation measures the proportion of accessions requiring regeneration or repropagation. It is also a primary measure for the quality of maintenance for NPGS PGR.

B) Regeneration by Insect Pollination

- Average # of accessions requiring controlled insect pollination regenerated annually measures the volume of accessions regenerated by insect pollination per year. It is a primary measure for NPGS PGR maintenance capacity.
- Average % of accessions requiring controlled insect pollination regenerated annually measures the relative rate whereby accessions are regenerated by insect pollination per year. It is also a primary measure for NPGS PGR maintenance capacity.
- # of accessions requiring controlled insect pollination measures the volume of accessions requiring regeneration via this method. It is a primary measure for the quality of maintenance for NPGS PGR.
- % of accessions requiring controlled insect pollination measures the proportion of accessions requiring regeneration via this method. It is also a primary measure for the quality of maintenance for NPGS PGR.

C) Regeneration by Hand Pollination

- Average # of accessions requiring controlled hand pollination regenerated annually measures the volume of accessions regenerated by hand pollination per year. It is a primary measure for NPGS PGR maintenance capacity.
- Average % of accessions requiring controlled hand pollination regenerated annually measures the relative rate whereby accessions are regenerated by hand pollination per year. It is also a primary measure for NPGS PGR maintenance capacity.
- # of accessions requiring hand pollination measures the volume of accessions requiring regeneration via this method. It is a primary measure for the quality of maintenance for NPGS PGR.
- % of accessions requiring hand pollination measures the proportion of accessions requiring regeneration via this method. It is also a primary measure for the quality of maintenance for NPGS PGR.

D) Specialized Regeneration or Repropagation Requirements (CWR Regeneration or Repropagation Will Often be Categorized Here)

- Average # of accessions with specialized regeneration or repropagation requirements increased annually measures the volume of accessions with specialized regeneration or repropagation methods such as grafting, micropropagation, pollinator exclusion, isolation, cultivation in protected environments, etc. increased per year. It is a primary measure for NPGS PGR maintenance capacity.
- Average % of accessions with specialized regeneration or repropagation requirements increased annually measures the relative rate whereby accessions with specialized regeneration or repropagation requirements are increased per year. It is also a primary measure for NPGS PGR maintenance capacity.
- # of accessions with specialized regeneration or repropagation requirements measures the volume of accessions requiring regeneration or repropagation by methods such as grafting, micropropagation, pollinator exclusion, isolation, cultivation in protected environments, etc. It is a primary measure for the quality of long-term maintenance for NPGS PGR.
- % of accessions with specialized regeneration or repropagation requirements measures the proportion of accessions requiring regeneration or repropagation via such methods. It is also a primary measure for the quality of maintenance for NPGS PGR.

E) Time Needed to Reduce Backlogs for Regenerating or Repropagating NPGS Accessions

- Range of # of years needed to regenerate or repropagate accessions requiring regeneration or repropagation estimates the backlog by the number of years, expressed as a range between absolute minima and maxima, needed to regenerate or repropagate all accessions that currently require regeneration or repropagation, regardless of the method. It is a primary measure for NPGS PGR maintenance capacity.
- Median # of years needed to regenerate or repropagate genebank unit accessions requiring regeneration or repropagation estimates the backlog by the number of years, expressed as a median number, median of medians, and average of medians, needed to regenerate or repropagate all accessions that currently require regeneration or repropagation, regardless of the method. It is also a primary measure for NPGS PGR maintenance capacity.

8) PGR Availability and Distribution

A) Availability

- # of accessions available for distribution measures the volume of accessions available for distribution on request. It is one of the single most valuable indices for the overall NPGS PGR management quality and capacity for a NPGs crop collection and genebank unit.
- % of accessions available for distribution measures the proportion of accessions available for distribution on request. It also is one of the single most valuable indices for the overall NPGS PGR management quality and capacity for a NPGs crop collection and genebank unit.

B) Distribution

- Average # of accessions distributed annually measures the average volume of accessions distributed in a year. It serves as a valuable index for the demand for a NPGS crop collection's and genebank unit's PGR, and its capacity to meet that demand.
- Average % of accessions distributed annually measures the average proportion of accessions distributed in a year. It also serves as a valuable index for the demand for a NPGS crop collection's and genebank unit's PGR, and its capacity to meet that demand.
- Average # of seed packets or propagation units distributed annually measures the average volume of seed packets and propagation units distributed in a year. This measure complements the previous measures based on accession number. It also serves as a valuable index for the demand for a NPGS crop collection's and genebank unit's PGR, and its capacity to meet that demand.
- Average # of germplasm orders filled annually measures the average volume of germplasm orders (usually comprise multiple accessions, seed packets, and/or propagation units) filled per year. It serves as a measure of the breadth of different customers/stakeholders served by a NPGS crop collection and genebank unit. It also serves as a valuable index for the demand for a NPGS crop collection's and genebank unit's PGR, and its capacity to meet that demand.

9) PGR Documentation

A) Provenance

- # of accessions with provenance or origin information measures the volume of accessions with basic ecogeographical information about their site of origin. It serves as a valuable measure for the quality of basic "passport data" for PGR of a NPGS crop collection and genebank unit.
- % of accessions with provenance or origin information measures the proportion of accessions with basic ecogeographical information about the site of origin. It also serves as a valuable measure for the quality of basic "passport data" for PGR of a NPGS crop collection and genebank unit.
- # of accessions with accurate geospatial data for origin measures the volume of accessions with accurate geospatial data (latitude, longitude, altitude, etc.) for their site of origin. It serves as a valuable measure for the availability of more precise locale data for PGR of a NPGS crop collection and genebank unit.
- % of accessions with accurate geospatial data for origin measures the proportion of accessions with accurate geospatial data (latitude, longitude, altitude, etc.) for their site of origin. It also serves as a valuable measure for the availability of more precise locale data for PGR of a NPGS crop collection and genebank unit.

B) Taxonomic Identity

- # of accessions assigned to a species measures the volume of accessions that have been identified to a taxonomic (scientific) species. It can function as one index for the overall value of a NPGS crop collection and genebank unit, because taxonomically identified

accessions can serve a broader spectrum of research and breeding purposes than those that are not.

- % of accessions assigned to a species measures the proportion of accessions that have been identified to a taxonomic (scientific) species. It can also function as one index for the overall value of a NPGS crop collection and genebank unit, because taxonomically identified accessions can serve a broader spectrum of research and breeding purposes than those that are not.

10) PGR Genotypic Characterization

- # of accessions with genotypic characterization data maintained within or directly linked to similar data in GRIN-Global measures the volume of accessions with genotypic characterization data (usually genetic marker data) either maintained within GRIN-Global per se, or directly linked to similar data in GRIN-Global via web connections. Notably, the number of genotypic data points available per accession is not specified, nor if that amount is sufficient, because standards for the minimum number of useful data points have not been determined. It can serve as a measure of a NPGS crop collection's and a genebank unit's PGR management capacity because ready access to genotypic characterization data significantly assists many PGR management operations. It can function as one index for the overall value of a NPGS crop collection and genebank unit, because genotypically-characterized accessions can serve a broader spectrum of research and breeding purposes than those that are not.
- % of accessions with genotypic characterization data maintained within or directly linked to similar data in GRIN-Global measures the proportion of accessions with genotypic characterization data (usually genetic marker data) either maintained within GRIN-Global per se, or directly linked to similar data in GRIN-Global via web connections. Notably, the number of genotypic data points available per accession is not specified, nor if that amount is sufficient, because the standards for minimum number of useful data points have not been determined. It can also serve as a measure of a NPGS crop collection's and a genebank unit's PGR management capacity because ready access to genotypic characterization data significantly assists many PGR management operations. It can also function as one index for the overall value of a NPGS crop collection and genebank unit, because genotypically-characterized accessions can serve a broader spectrum of research and breeding purposes than those that are not.
- Average # of genotypic characterization records per accession maintained within or directly linked to similar data in GRIN-Global measures the average degree and depth whereby a NPGS crop collection's and genebank unit's accessions have been characterized genotypically, and those data are either maintained within GRIN-Global per se, or directly linked to similar data in GRIN-Global via web connections. It can also serve as a measure of a NPGS crop collection's and a genebank unit's PGR management capacity because ready access to genotypic characterization data significantly assists many PGR management operations. It can also function as one index for the overall value of a NPGS crop collection and genebank unit, because genotypically-characterized accessions can serve a broader spectrum of research and breeding purposes than those that are not.

11) PGR Phenotypic Evaluations, Digital Imaging

A) Phenotypic Evaluations

- # of accessions with phenotypic evaluation data maintained within or directly linked to similar data in GRIN-Global measures the volume of accessions with phenotypic evaluation data either maintained within GRIN-Global per se, or directly linked to similar data in GRIN-Global via web connections. It can function as one index for the overall value of a NPGs crop collection and genebank unit, because phenotypically evaluated accessions can serve a broader spectrum of research and breeding purposes than those that are not.
- % of accessions with phenotypic evaluation data maintained within or directly linked to similar data in GRIN-Global measures the proportion of accessions with phenotypic evaluation data maintained within GRIN-Global per se, or directly linked to similar data in GRIN-Global via web connections. It also can function as one index for the overall value of a NPGs crop collection and genebank unit, because phenotypically evaluated accessions can serve a broader spectrum of research and breeding purposes than those that are not.
- Average # of phenotypic evaluation datapoints per accession maintained within or directly linked to similar data in GRIN-Global measures the average number of phenotypic evaluation datapoints per accession either maintained within GRIN-Global per se, or directly linked to similar data in GRIN-Global via web connections. It can also serve as a measure of a crop collection's and a genebank unit's PGR management capacity because ready access to certain phenotypic evaluation data can significantly assist many PGR management operations. It can also function as one index for the overall value of a NPGs crop collection and genebank unit, because phenotypically evaluated can serve a broader spectrum of research and breeding purposes than those that are not.
- Average # of accessions evaluated phenotypically annually for incorporation or direct linkage to similar data in GRIN-Global measures the average volume of accessions evaluated phenotypically per year that will be incorporated or linked to similar data in GRIN-Global via web connections. It can serve as a primary measure for a NPGS crop collection's or genebank unit's PGR management capacity.
- Average % of accessions evaluated phenotypically annually for incorporation or direct linkage to similar data in GRIN-Global measures the average proportion of accessions evaluated phenotypically per year that will be incorporated or linked to similar data in GRIN-Global via web connections. It can also serve as a primary measure for a NPGS crop collection's or genebank unit's PGR management capacity.

B) Digital Imaging

- # of accessions with digital images maintained within or directly linked to similar data in GRIN-Global measures the volume of accessions with digital images maintained within or directly linked to similar data in GRIN-Global via web connections. It can function as one index for the overall value of a NPGS crop collection and genebank unit, because accessions illustrated by digital images can serve a broader spectrum of research and breeding purposes than those that are not.

- % of accessions with digital images maintained within or directly linked to similar data in GRIN-Global measures the proportion of accessions with digital images maintained within or directly linked to similar data in GRIN-Global via web connections. It can also function as one index for the overall value of a NPGS crop collection and genebank unit, because accessions illustrated by digital images can serve a broader spectrum of research and breeding purposes than those that are not.
- Average # of accessions annually imaged digitally for incorporation or direct linkage to similar data in GRIN-Global measures the average volume of accessions for which digital images are captured per year and incorporated or directly linked to similar data in GRIN-Global via web connections. It can serve as a measure of a NPGS crop collection's and a genebank unit's information management capacity.
- Average % of accessions annually imaged digitally for incorporation or direct linkage to similar data in GRIN-Global measures the average proportion of accessions for which digital images are captured per year and incorporated or directly linked to similar data in GRIN-Global via web connections. It can also serve as a measure of a NPGS crop collection's and a genebank unit's information management capacity.

12) Genetic Enhancement/Pre-Breeding, and Breeding

- # of genetic enhancement/pre-breeding programs conducted at the genebank unit or in close, direct collaboration with the genebank unit measures the volume of genetic enhancement/pre-breeding activities associated with the NPGS genebank unit. It serves as an important measure of a NPGS genebank unit's capacity to directly facilitate the use of its PGR in research and breeding programs.
- # of breeding programs conducted at the genebank unit or in close, direct collaboration with the genebank unit measures the volume of breeding activities associated with the NPGS genebank unit. It serves as an important measure of a NPGS genebank unit's capacity to directly enlist its PGR in cultivar development and overall crop genetic improvement.

Appendix B

PGR Management Challenges, Goals, and Actions for Individual NPGS Genebank Units (Fig. B.1)

Below, Figure B.1 summarizes pictorially the major PGR management operational challenges for the NPGS and its constituent genebank units. Subsequent pages in this Appendix B provide more detailed information about challenges facing individual genebank units, listed by their geographical locations, plus the goals and actions proposed for addressing those challenges.

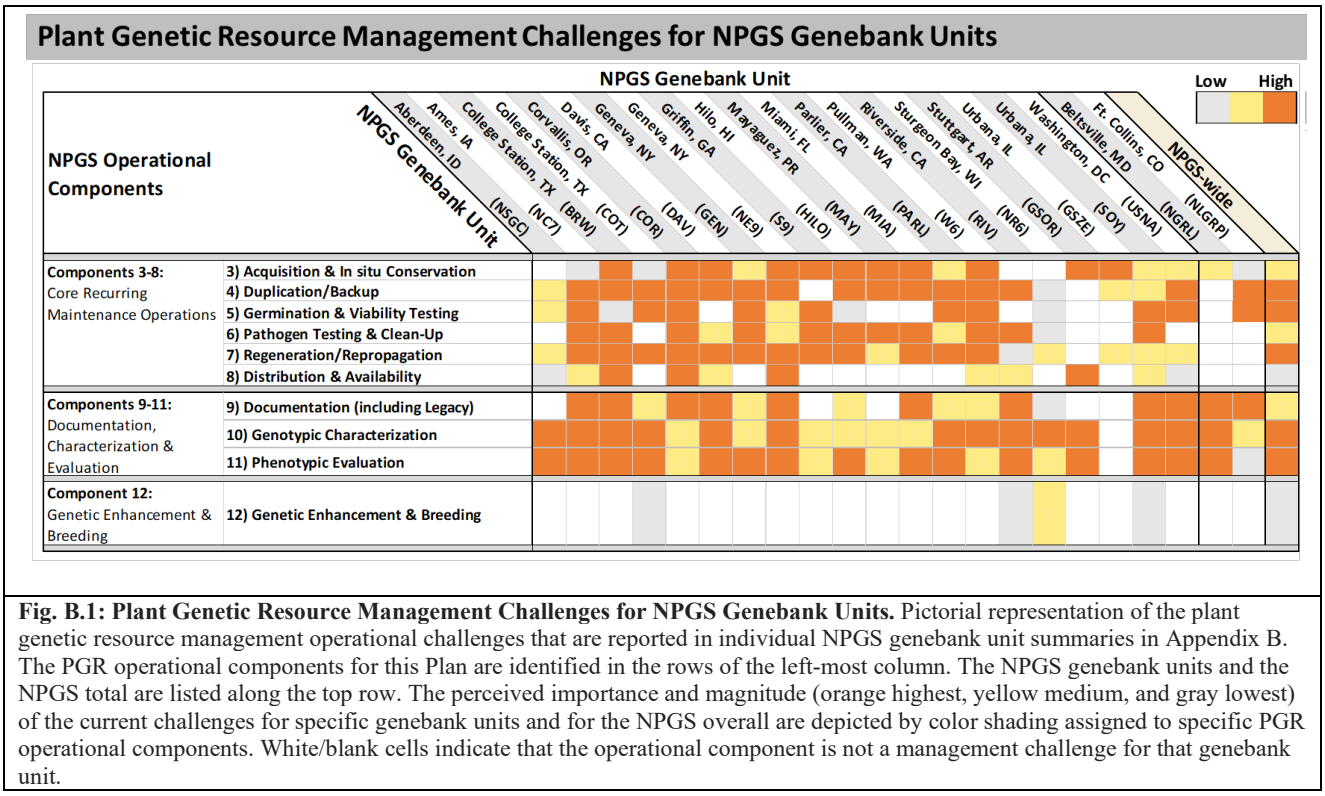

Fig. B.1: Plant Genetic Resource Management Challenges for NPGS Genebank Units. Pictorial representation of the plant genetic resource management operational challenges that are reported in individual NPGS genebank unit summaries in Appendix B. The PGR operational components for this Plan are identified in the rows of the left-most column. The NPGS genebank units and the NPGS total are listed along the top row. The perceived importance and magnitude (orange highest, yellow medium, and gray lowest) of the current challenges for specific genebank units and for the NPGS overall are depicted by color shading assigned to specific PGR operational components. White/blank cells indicate that the operational component is not a management challenge for that genebank unit.

Aberdeen, ID: National Small Grains Collection (NSGC)

Background

The USDA/ARS National Small Grain Collection (NSGC) is the oldest and largest NPGS "active site" collection (136,000+ accessions, 144+ taxa, 10 crops) whose 5 permanent and 2 temporary staff members manage PGR from predominantly homogeneous and homozygous small grains species, most of which self-pollinate. It also stores and distributes rice PGR that are regenerated, characterized, and evaluated at the Stuttgart genebank unit (GSOR). Its current annual financial support (ca. $1,400,000+) is from USDA/ARS. It operates from USDA/ARS facilities and land.

Current Challenges

The primary current challenges for the NSGC include:

- Filling critical personnel vacancies.
- Substantial backlogs in accession back-up at NLGRP for CWR and genetic stocks, primarily of oat, barley, and wheat, with few seeds per accession.
- Substantial backlogs in germination/viability testing for CWR and genetic stocks.
- Lack of methods for germination/viability testing especially for seeds of CWR and genetic stocks.
- Lack of methods for germinating some types of seeds, especially for CWR and genetic stocks.
- Substantial backlogs in accession regeneration for CWR and genetic stocks.
- No comprehensive, systematic program for genotypic characterization.
- No comprehensive, systematic program for phenotypic evaluations.
- Insufficient availability of some accessions, especially genetic stocks and CWR accessions.

Goals and Actions

The primary +5- and +10-year needs for the NSGC include increasing:

- Genebank annual budget from ca. $1,400,000+ to $1,470,000 +5 and to $1,500,000 +10 years. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*
- Greenhouse space from ca. 2,300+ ft2 to 2,500 ft2 +5 and 3,000 ft2 +10 years for regenerating CWR accessions.
- Partnerships and/or local expertise for managing genetic stock accessions, and germinating CWR taxa.

The preceding increases will expand NSGC operational capacity to achieve these outcomes:

- Reduce the backlog of accessions requiring germination/viability testing by increasing the number and percentages of accessions germinated/viability tested/year, especially for

CWR such as *Aegilops*, and genetic stocks of wheat, barley, and oats, which are represented by few seeds per accession.

- Conduct research to devise efficient and effective methods for germination/viability testing for some seeds, e.g., for genetic stocks, and CWR such as *Aegilops.*
- Conduct research to devise efficient and effective methods for germinating some types of seeds, such as CWR.
- Reduce the backlog of accession regeneration by increasing the number and percentages of accessions regenerated/year for oats, barley, and wheat CWR and genetic stocks.
- Participate in the comprehensive, systematic NPGS program for genotypic characterization.
- Participate in the comprehensive, systematic NPGS program for trait evaluation, especially in CWR, such as *Aegilops,* specifically for stem rust resistance, and drought tolerance for wheat and barley. Evaluate Fusarium head blight resistance from wheat and barley accessions, and crown rust and stem rust host-plant resistance from oat CWR.
- Increase availability of oat, barley, and wheat genetic stocks and CWR for distribution.

Ames, IA: North Central Regional Plant Introduction Station (NC7, NCRPIS)

Background

The USDA/ARS North Central Regional Plant Introduction Station (NC7, NCRPIS), one of the oldest and largest NPGS sites (53,000+ accessions, 1700+ taxa, 27 crops, 32 permanent and 22 temporary staff), manages numerous crop collections, mostly from outcrossing, heterogeneous and heterozygous species that require controlled insect or hand pollination. It also has played a major role in the ongoing development of the NPGS's GRIN-Global information management system. Its current financial support (ca. $2,900,000) is from USDA/ARS, Iowa State University (ISU), and the State Agricultural Experiment Stations of the North Central Region. It operates from USDA/ARS and ISU facilities, and farms ISU land.

Current Challenges

The primary current challenges for the NC7 include:

- Substantial backlogs in accession back-up at NLGRP (especially maize (*Zea*), medicinals, ornamentals).
- Substantial backlogs in germination/viability testing (especially pseudocereals (*Amaranthus,* and *Chenopodium*), woody landscape plants).
- Substantial backlogs in pathogen-testing and pathogen "clean-up" for some seeds, especially cucurbits (*Cucurbita, Cucumis*).
- Substantial backlogs in digitizing valuable legacy paper records.
- Lack of procedures for germination/viability testing for some seeds.
- Lack of procedures for germinating some types of seeds.
- Lack of procedures for pathogen-testing and pathogen "clean-up" for some seeds (especially cucurbits (*Cucurbita, Cucumis*).
- Substantial backlogs in accession regeneration (especially maize (*Zea*), maize CWR, pseudocereals (*Amaranthus, Chenopodium*).
- Lack of bioinformatic and programming capacity for developing algorithms and machine learning to capture data from spectral imaging.
- No comprehensive, systematic program for genotypic characterization.
- No comprehensive, systematic program for phenotypic evaluations.
- Insufficient availability of accessions (especially maize (*Zea*), ornamentals, woody landscape plants).
- Substantially increased demand projected for accessions.
- Limited in situ conservation effort for *Helianthus* and *Cucurbita pepo* CWR.

Goals and Actions

The primary +5- and +10-year needs for the NC7 include increasing:

- Genebank annual budget from ca. $2,900,000 to $4,600,000 at +5 and $5,400,000 at +10 years. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*

- Cold room space from ca. 60,000 ft3 to 86,000 ft3 at +5 years.
- Greenhouse space from ca. 8,500 ft2 to 18,000 ft2 at +5 and 27,500 ft2 at +10 years.
- Screenhouse space from ca. 3,000 ft2 to 6,000ft2 at +5 years.
- Technical staff from ca. 32 permanent and 22 temporary to 35 permanent and 22 temporary at +5, and 37 permanent and 27 temporary at +10 years.

The preceding increases will expand NC7 operational capacity to achieve these outcomes:

- Reduce the backlog in accession back-up at NLGRP (especially maize (*Zea*), medicinals, ornamentals) by increasing the number and percentages of accessions backed-up at NLGRP/year.
- Reduce the backlog of accessions requiring germination/viability testing by increasing the number and percentages of accessions germinated/viability tested/year, (especially pseudocereals (*Amaranthus, Chenopodium*), and woody landscape plants).
- Reduce the backlog of accessions requiring pathogen-testing and pathogen "clean-up" for some seeds by increasing the number and percentages of accessions with seeds pathogen-tested and "cleaned-up"/year (especially cucurbits (*Cucurbita, Cucumis*).
- Reduce the backlog of digitizing valuable legacy paper records by increasing the number and percentages of those records digitized/year.
- Reduce the backlog of accession regeneration by increasing the number and percentages of accessions regenerated/year (especially maize (*Zea*), maize CWR, pseudocereals (*Amaranthus, Chenopodium*). Partnerships will be especially important for maize (*Zea*), and maize CWR regenerations.
- Conduct research to devise efficient and effective methods for germination/viability testing for some seeds.
- Conduct research to develop efficient and effective methods for germinating some types of seeds.
- Conduct research to devise efficient and effective methods for pathogen-testing and "clean-up" for some seeds (especially cucurbits, (*Cucurbita, Cucumis*).
- Develop bioinformatic and programming capacity for devising algorithms and machine learning to capture data from spectral imaging.
- Participate in a comprehensive, systematic NPGS program for genotypic characterization.
- Participate in a comprehensive, systematic NPGS program for trait evaluation.
- Increase availability of accessions (especially maize (*Zea)*, ornamentals, woody landscape plants).
- Manage substantially increased demand projected for accessions.
- Investigate the feasibility of in situ conservation of *Helianthus* and *Cucurbita pepo* CWR on public lands.

Beltsville, MD: National Germplasm Resources Laboratory (NGRL)

Background

The USDA/ARS National Germplasm Resources Laboratory (NGRL) staff of 16.6 FTE has lead responsibilities for developing and maintaining the NPGS's GRIN-Global information management system including GRIN-Taxonomy, which is the international standard for taxonomic nomenclature for economically important plants. It also leads the NPGS's programs for plant exploration, exchange, and in situ conservation of U.S. CWR. The NGRL also includes a pathology project that supports germplasm quarantine and curation programs to minimize the risks of distributing virus-infected plant material in the U.S. and globally. Its current financial support (ca. $2,300,000) is from USDA/ARS. It operates from USDA/ARS facilities.

Current Challenges

The primary current challenges for the NGRL include:

- Lack of sufficient information management capacity to handle increasing demands for data and information for NPGS PGR delivered by GRIN-Global.
- Lack of sufficient resources needed for information technology personnel to maintain and develop GRIN-Global as the preeminent PGR information management system.
- Numerous priority U.S. CWR species are insufficiently conserved ex situ and in situ.
- GRIN-Taxonomy does not provide nomenclatural information needed for CWR of ornamentals and other crops.

Goals and Actions

The primary +5- and +10-year needs for the NGRL include increasing:

- Genebank annual budget from ca. $2,300,000+ to $4,000,000+ at +5 years and $5,100,000+ at +10 years. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*
- Technical staff from ca. 16.6 permanent FTE to 20.4 permanent FTE at +5 years.

The preceding increases will expand the NGRL operational capacity to achieve these outcomes:

- Meet the projected substantial increases in demand from researchers, breeders, producers, etc. for the data and information from GRIN-Global.
- Accelerate the rate of developing the capacities for GRIN-Global to deliver an increased number and variety of information management functions.
- Manage the projected substantial increase in the amount of data and information, especially from greatly expanded genotypic characterization and phenotypic evaluations, that GRIN-Global must maintain and deliver.
- Lead expanded programs of exploration for priority U.S. CWR for ex situ conservation and collaborative in situ conservation of U.S. CWR by communicating conservation priorities and establishing more interagency and inter-institutional agreements with land management organizations.
- Expand GRIN Taxonomy's coverage to encompass CWR of ornamentals and other crops.

College Station, TX: National Collection of *Carya* (Pecan) Genetic Resources (BRW)

Background

The staff members of the USDA/ARS National Collection of *Carya* (Pecan) Genetic Resources manage 4,100+ accessions, 23 taxa, and 2 crops comprising mostly outcrossing, heterogeneous and heterozygous long-lived trees. Its current financial support (ca. $180,000+) is from USDA/ARS. It operates from USDA/ARS facilities at College Station, TX, and manages 360 acres of orchards at College Station and 240 acres at Brownwood, TX.

Current Challenges

The primary current challenges for BRW include:

- Gaps in the collection's genetic coverage.
- Substantial backlogs in accession regeneration/repropagation, including tree removal.
- Substantial backlogs in accession back-up at NLGRP and in duplicate orchard plantings.
- Substantial backlogs in pathogen-testing and pathogen "clean-up" for *Xylella* in accessions.
- Substantial backlogs in digitizing valuable legacy paper records.
- Lack of procedures and capacity for viability testing of pollen stored in LN.
- Lack of procedures for pathogen-testing and pathogen "clean-up" for *Xylella*.
- No comprehensive, systematic program for genotypic characterization.
- No comprehensive, systematic program for phenotypic evaluations.
- No availability of accessions for distribution because of *Xylella*.
- Limited in situ conservation efforts for U.S. *Carya* populations.

Goals and Actions

The primary +5- and +10-year needs for this BRW include increasing:

- Genebank annual budget from ca. $183,000 to ca. $683,000 at +5 and $1,183,000 at +10 years. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*
- Cold room space from ca. 120 ft3 to 400 ft3 at +5 years.
- Greenhouse space from ca. 5,000 ft2 to 7,500 ft2 at +5 years.
- Staff from ca. 0.8 permanent FTE to 2.8 permanent FTE and 1 temporary FTE at +5, and 4.8 permanent FTE and 3 temporary FTE at +10 years.

The preceding increases will expand this BRW's operational capacity to achieve these outcomes:

- Fill gaps in the collection's coverage through targeted field collecting.
- Expand the number of partnerships with land management agencies and landowners to conserve U.S. *Carya* populations.
- Increase the quality and expand the size of genebank unit facilities, particularly 0˚F cold storage, and greenhouse space for growing seedlings.

- Reduce the backlog in accession back-up by increasing the number and percentages of accessions backed-up at NLGRP/year via pollen in LN and through duplicate field plantings.
- Reduce the backlog of accessions requiring pathogen-testing and pathogen "clean-up" of trees potentially infected by *Xylella* by increasing the number and percentages of accessions pathogen-tested and "cleaned-up"/year.
- Reduce the backlog of digitizing valuable legacy paper records (field records, pedigree books) by increasing the number and percentages of those records digitized/year.
- Conduct research to devise efficient and effective methods for pathogen-testing and "clean-up" of *Carya* trees from *Xylella*.
- Participate in a comprehensive, systematic NPGS program for genotypic characterization of PGR.
- Participate in a comprehensive, systematic NPGS program for phenotypic evaluation of PGR, focusing particularly on *Carya* rootstock traits.
- Enable availability of *Carya* accessions via efficient and effective methods for pathogen-testing and "clean-up" of *Carya* trees from *Xylella*.

College Station, TX: National Cotton Germplasm Collection (COT)

Background

The USDA/ARS National Cotton Germplasm Collection (COT) is the premier cotton genetic resources collection in the world with 9,800+ accessions, 39 taxa, 3 different crops. A staff of 2.4 permanent FTE employees manages this collection of facultatively annual, perennial, outcrossing or self-pollinating, heterogeneous and heterozygous species that are regenerated either by hand pollination in greenhouses, or self-pollinate in pollinator exclusion cages that protect against unwanted insect pollination. Control of flowering in many accessions is determined by daylength, necessitating cultivation in Costa Rica. Its current financial support (ca. $893,000+) is from USDA/ARS, with recurrent grant support from Cotton, Inc., especially for field regenerations. It operates from USDA/ARS facilities and farms Texas A & M land and leased land in Costa Rica.

Current Challenges

The primary current challenges for COT include:

- Insufficient information management capacity.
- No comprehensive, systematic program for genotypic characterization.
- Insufficient greenhouse space for regenerating perennial cotton CWR.
- Substantial backlogs in accession regeneration.
- Limited in situ conservation effort for native U.S. cotton CWR.
- No comprehensive, systematic program for phenotypic evaluations.
- Backlogs in accession back-up at NLGRP.
- Insufficient cold storage space, especially -18˚C.
- Substantial backlogs in germination/viability testing.
- Completing the digitization of valuable legacy paper records.

Goals and Actions

The primary +5- and +10-year needs for the COT include increasing:

- Genebank annual budget from ca. $890,000+ to $1,400,000 at +5 and $1,800,000 at +10 years. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*
- Cold room space from ca. 3,000 ft3 to 6,000 ft3 at +5 years and 9,000 ft3 at +10 years.
- Greenhouse space from ca. 8,700 ft2 to 12,000 ft2 at +5 years.
- Technical staff from ca. 2.4 permanent FTE to 4.4 permanent and 1 temporary FTE at +5, and 6.4 permanent and 3 temporary FTE at +10 years.

The preceding increases will expand COT operational capacity to achieve these outcomes:

- Characterize cotton accession via genotyping by sequencing (GBS) as part of a comprehensive, systematic NPGS program for genotypic characterization.

- Reduce the backlog of accession regeneration by increasing the number and percentages of accessions regenerated/year in TX and Costa Rica.
- Finish digitizing valuable legacy paper records by increasing the number and percentages of those records digitized/year.
- Focus phenotypic evaluations on high priority traits, incorporating digital imaging when feasible, as part of a comprehensive, systematic NPGS program for phenotypic evaluation.
- Expand genetic enhancement/pre-breeding research in collaboration with Texas A & M University and ARS-Stoneville.
- Establish agreements/arrangements with land management organizations for supporting in situ conservation of native U.S. cotton species on public lands.
- Reduce the backlog in accession back-up at NLGRP by increasing the number and percentages of accessions backed-up at NLGRP/year.
- Safeguard additional accessions on-site in -18˚C storage conditions.
- Reduce the backlog of accessions requiring germination/viability testing by increasing the number and percentages of accessions germinated/viability tested/year.

Corvallis, OR: National Clonal Germplasm Repository for Temperate Fruits and Nuts (COR)

Background

The USDA/ARS National Clonal Germplasm Repository for Temperate Fruits and Nuts (COR) staff of 10 permanent FTE and 1.5 temporary FTE manages 12,000+ accessions and 670+ taxa of 8 primarily clonally propagated, specialty crops and their crop wild relatives (CWR), developed or collected mainly from genetically heterogeneous and heterozygous species. Its current financial support (ca. $1,600,000+) is from USDA/ARS. It operates from USDA/ARS facilities, with field collections that occupy 45 acres of Federal and 10 acres of State of Oregon land. The main offices, laboratories, and greenhouses are housed in Federal buildings located on 4.169 acres of State of Oregon land.

Current Challenges

The primary current challenges for COR include:

- Substantial expansion of PGR collections of eight specialty crops and their CWR, including of hazelnuts (*Corylus*), strawberry (*Fragaria*), hops (*Humulus*), mint (*Mentha*), pear (*Pyrus*), currants/gooseberries (*Ribes*), caneberries (*Rubus*), and cranberry and blueberry (*Vaccinium*).
- Substantial backlogs in accession back-up at NLGRP for the eight specialty crops and their CWR.
- Substantial backlogs in germination/viability testing of seeds for the eight specialty crops and their CWR.
- Substantial backlogs in pathogen-testing and pathogen "clean-up" for strawberry, hops, currants/gooseberries, caneberries, and blueberry/cranberry.
- Substantial backlogs in digitizing valuable legacy paper records.
- Substantial backlogs in uploading valuable digital records to GRIN-Global.
- Lack of procedures for storing some PGR in LN at NLGRP, especially for hazelnuts, pear, caneberries, currants and gooseberries, and blueberries and their CWR.
- Increasing need of fungicidal and bactericidal sprays to protect the hazelnut collection from Eastern filbert blight, and the pear collection from fire blight.
- Substantial backlogs in accession regeneration, especially for currants, caneberries, and blueberry/cranberry, and for repropagating pear and quince on fire blight-resistant rootstocks by grafting.
- Need for expanded systematic program for genotypic characterization especially for hazelnut, hops, mints, pear, quince, currants, caneberries, and blueberry/cranberry.
- Need for expanded systematic program for phenotypic evaluations especially for nut quality and incompatibility factors for hazelnut; host-plant resistance to new disease and pests for strawberry; low temperature- and disease-resilient pear; and biochemical analyses, daylength response, and host-plant resistance for hops.
- Substantially increased distributions to meet projected demand for all crops managed.
- Limited in situ conservation effort especially for hazelnut, hops, currants, and blueberry/cranberry CWR.

Goals and Actions

The primary +5- and +10-year needs for COR include increasing:

- Genebank annual budget from ca. $1,680,000+ to $2,900,000+ at +5 years and $3,200,000 at +10 years. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*
- Cold room space from ca. 360 ft3 to 720 ft3 at +5 years.
- Greenhouse space from ca. 10,000+ ft2 to 12,000+ ft2 at +5 years and 15,000+ ft2 at +10 years.
- Screenhouse space from ca. 17,000+ ft2 to 20,000 ft2 at +5 years, and 25,000 ft2 by 10 years.
- Technical staff from 10 permanent FTE and 1.5 temporary FTE to 12 permanent FTE and 3 temporary FTE at +5 years, and 14 permanent FTE and 4 temporary FTE at +10 years.

The preceding increases will expand the COR operational capacity to achieve these outcomes:

- Manage substantially larger PGR collections of specialty crops, including U.S. CWR of hazelnuts (*Corylus*), strawberry (*Fragaria*), hops (*Humulus*), mint (*Mentha*), pear (*Pyrus*), currants/gooseberries (*Ribes*), caneberries (*Rubus*), and cranberry and blueberry (*Vaccinium*).
- Reduce the backlog in accession back-up at NLGRP through the cryopreservation techniques as mentioned in table below “tc” = “tissue culture:”

Crop	Cultivars	Species/CWR
Hazelnut	Dormant buds (DB)	Seeds (embryos), pollen in LN2
Strawberry	Meristems from tc	Seeds in LN2
Hops	Meristems from tc	Seeds in LN2
Mint	Meristems from tc	Meristems from tc
Pear	DB/ Meristems from tc	Seeds in LN2
Currants/gooseberries	DB/ Meristems from tc	Seeds in LN2
Caneberries	Meristems from tc	Seeds in LN2
Blueberries	DB/ Meristems from tc	Seeds in LN2
Cranberries	Meristems from tc	Seeds in LN2

- Reduce the backlog of accessions requiring germination/viability testing by increasing the number and percentages of accessions germinated/viability tested/year, especially CWR of hazelnut, strawberries, hops, pear, currant, caneberries, blueberries, and cranberries.
- Reduce the backlog of accessions requiring pathogen-testing and pathogen “clean-up” by increasing the number and percentages of accessions pathogen-tested and “cleaned-up”/year, especially for strawberries, hops, pear, currant, gooseberries, caneberries, blueberries, and cranberries.
- Reduce the backlog of accession regeneration and repropagation by increasing the number and percentages of accessions regenerated or repropagated/year, especially

repropagating pear and quince on fire blight-resistant rootstocks by grafting; currants, caneberries, and blueberry/cranberry.

- Reduce the backlog of digitizing valuable legacy paper records by increasing the number and percentages of those records digitized/year.
- Reduce the backlog of uploading valuable digital records to GRIN-Global by increasing the number and percentages of those records uploaded/year, especially for strawberry.
- Conduct research to devise efficient and effective methods for storing some PGR in LN at NLGRP, especially pear and caneberries.
- Conduct research to devise efficient and effective methods for regenerating by seeds pear and CWR of most of the crops.
- Conduct research to devise efficient and effective methods for eliminating the fire blight pathogen from pear and quince.
- Expand local genetic marker program for hazelnut, hops, mints, pear, currants, caneberries, blueberry/cranberry, and quince via participation in a comprehensive, systematic NPGS program for genotypic characterization.
- Participate in a comprehensive, systematic NPGS program for phenotypic evaluation. Local phenotypic evaluations will focus on nut quality and incompatibility factors for hazelnut; host-plant resistance to new disease and pests for strawberry; temperature- and disease resilient pear; and biochemical analyses, daylength response, and host-plant resistance for hops; and host-plant resistance to new disease (virus) and pests for blueberry.
- Manage substantially increased demand from breeders and researchers for PGR of most of the major fruit and nut crops at the genebank unit.
- Investigate the feasibility of in situ conservation for CWR of hazelnut, strawberries, hops, currants, caneberries, and blueberry/cranberry on public lands.

Addendum: Corvallis (COR) Buildings and Facilities

The Corvallis National Clonal Germplasm Repository (COR) is in Priority Group 6 of the USDA/ARS 2012 Capital Investment Strategy (CIS). In FY 2020, $13.5 million was appropriated for renovation and construction of the greenhouses as part of the CIS. With this funding a 10% increase of screenhouse and greenhouse space is expected and will meet the +5 year goal for expanded screenhouse and greenhouse space.

Davis, CA: National Clonal Germplasm Repository (DAV)

Background

The staff (8.8 permanent FTE) of the USDA/ARS National Clonal Germplasm Repository at Davis, CA (DAV) safeguards 6,900+ accessions and 225 taxa of 14 major tree fruit, tree nut, and vine crops, adapted to Mediterranean climates, that are clonally maintained and propagated in field orchards and screenhouse plantings. The accessions are mainly derived from outcrossing, heterogeneous and heterozygous species. Its current financial support (ca. $1,300,000) is from USDA/ARS. It operates from USDA/ARS and University of California-Davis (UC-D) facilities and cultivates UC-D land.

Current Challenges

The primary current challenges for the DAV include:

- Insufficient orchard and vineyard space for maintaining PGR collections.
- Insufficient irrigation water from field wells.
- Long-term inadequacy of operational capacity.
- For most crops, lack of knowledge or technology for backing-up in LN at NLGRP.
- Substantial backlogs for backing-up most crops at NLGRP because of the lack of effective methods and operational capacity to implement such methods if they were available.
- Substantial backlogs in digitizing valuable legacy paper records.
- Substantial backlogs in accession repropagation for some crops.
- Lack of provenance data for many legacy accessions.
- No comprehensive, systematic program for genotypic characterization.
- No comprehensive, systematic program for phenotypic evaluations.
- Lack of digital images for many accessions.
- Insufficient availability of accessions for some crops, e.g., kiwifruit.
- Projected substantially increased demand for accessions of some crops.
- Limited in situ conservation effort for CWR, e.g., of walnut and grape.

Goals and Actions

The primary +5- and +10-year needs for the DAV include increasing:

- Genebank annual budget from ca. $1,300,000 to $2,300,000 at +5 years. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*
- Volume and quality of irrigation water for field PGR collections as soon as possible.
- Field space for orchard and vineyard plantings to 100 acres at +5 years.
- Technical staff from ca. 8.8 permanent FTE to 12.8 permanent and 1 temporary FTE at +5 years.

The preceding increases will expand DAV operational capacity to achieve these outcomes:

- Manage a substantial increase (35%+) in the overall size of the genebank collection, especially for walnut, grapes, *Prunus*, and crop wild relatives (CWR), to fill genetic gaps.
- Expand the orchard and vineyard space to rotate crops.
- Conduct research in conjunction with NLGRP to devise efficient and effective methods for cryopreserving in LN vegetative tissues of most NCGR-Davis crops and *Prunus* pollen and seeds.
- Reduce the backlog in accession back-up at NLGRP for most crops by increasing the number and percentages of accessions backed-up at NLGRP/year.
- Reduce the backlog of digitizing numerous valuable legacy paper records by increasing the number and percentages of those records digitized/year.
- Re-propagate entire crop collections (e.g., pistachio, walnuts, almonds, cherries, and plums) on superior rootstocks and/or in different orchard locations.
- Investigate historical information and apply genotypic data to enhance the provenance information for legacy accessions.
- Participate in a comprehensive, systematic NPGS program for genotypic characterization, with local efforts focused on walnut, pistachio, almond, and grape.
- Evaluate accessions for new traits, e.g., rootstock quality, host-plant resistance to pathogens and abiotic stresses, as part of a comprehensive, systematic NPGS program for phenotypic evaluation.
- Substantially increase the proportion of accessions digitally imaged.
- Increase availability of accessions for crops such as pistachio, walnut, mulberry, persimmon, figs.
- Manage substantially increased demand for accessions of crops such as pistachio, walnut, fig, persimmon, and grape.
- Investigate the feasibility of in situ conservation of native walnuts and grapes on public lands.

Addendum: Availability of adequate field space

The Davis genebank unit maintains its PGR collections in orchards and vineyards located on land leased from the University of California-Davis (UC-D), which is insufficient for maintaining current collections and for the expansions projected for +5 and +10 years. Furthermore, well water for irrigating field PGR collections is insufficient for current and future needs. At present, the additional land needed is not available from the UC-D. Furthermore, the UC-D has shortened the duration of land leases to 5 years, which can be problematic for long-term (20 year+) orchard or vineyard PGR plantings. Consequently, securing adequate irrigation water and field space, either through long-term lease or purchase, is a crucial need for this genebank unit. Should sufficient irrigation water and land not be available, the PGR collections and genebank unit might require relocation to an alternative ARS site.

Fort Collins, CO: National Laboratory for Genetic Resources Preservation (NLGRP)

Background

The USDA/ARS National Laboratory for Genetic Resources Preservation (NLGRP) is one of the world's largest and preeminent genebanks for secure, long-term storage of PGR collections. The NLGRP currently preserves 1.2 million accessions at low temperatures; 400,000+ of those are duplicated accessions from NPGS genebank units that manage PGR of ca. 200 crops. The remaining accessions are duplicates from international and other national PGR collections safeguarded at the NLGRP. Its 25 FTE permanent and 7 FTE temporary staff members operate this technologically advanced storage facility, and also conduct critical research on PGR cryopreservation, viability/quality testing, genomic tools supporting genebank operations, and interfaces between ex situ and in situ conservation. The NLGRP's broad experience with all the individual NPGS genebank units and most of the NPGS crops affords it a unique and inclusive perspective for supporting the NPGS's overall PGR maintenance and genetic diversity conservation program. Its current annual financial support (ca. $5,047,000) is from USDA/ARS. The NLGRP operates as a USDA/ARS facility on the Colorado State University campus in Fort Collins, CO.

Current Challenges

The primary current challenges for the NLGRP include:

- Substantial backlogs in backing-up accessions because too few propagules are available for appropriate back-up protection.
- Backlogs in developing effective methods for long-term storage of some PGR create backlogs in safety duplication at NLGRP. Without the capacity to conduct extensive experimentation to develop methods that increase survival, some PGR can be fatally damaged from initial exposure to long-term storage conditions.
- Lack of knowledge for why some propagules retrieved from storage cannot be grown into normal plants and, for other propagules, whether normal growth and development even are possible.
- Substantial backlogs for testing propagule quality puts all accessions (especially CWR) at risk from deterioration or death in storage, as "expiration dates" (when propagules die from aging) for stored PGR are unknown.
- Operational inefficiencies and risks that critical data at the NLGRP are not preserved because specialized data management needs currently are not met by the GRIN-Global database.
- Safeguarding at the NLGRP accessions and entire collections that are not curated elsewhere and lack an identifiable stakeholder.
- Lack of genomic data needed to conserve PGR genetic diversity efficiently and effectively, and to inform managerial decisions--genetically heterogeneous accessions (e.g., CWR) specifically pose major conservation challenges.
- Plant-microbiomes in PGR have not been characterized; consequently their positive and negative effects for plant health are unknown, as is the need to remove them before storage, or to store them within plant propagules.

- Large volumes of phenotypic data from the extensive PGR testing program at the NLGRP are currently inaccessible or incompatible with GRIN-Global, reducing the quantity of valuable data available through GRIN-Global.
- Lack of a comprehensive, systematic program for training current and future NPGS personnel in ex situ PGR preservation and genetic diversity management.
- Lack of a coordinated NPGS program to acquire and preserve genetic diversity of U.S. CWR species.
- NLGRP facility infrastructure requires modernization.

Goals and Actions

The primary +5- and +10 years needs for the NLGRP include increasing:

- Genebank annual budget from ca. $5,047,000 to $8,900,000+ at +5 years and $12,100,000 at +10 years. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*
- Cold room space from ca. 193,527 ft3 to 253,000+ ft3 at +10 years.
- Technical staff from 25 permanent FTE and 7 temporary FTE to 45 permanent FTE and 19 temporary FTE at +5 years.

The preceding increases will expand the NLGRP's operational capacity to achieve these outcomes:

- Reduce the current backlog in duplicating and backing-up NPGS PGR by expanding processing capacities when preservation protocols exist; reducing processing time through more efficient propagule acquisition methods; and collaborating with the other genebank units to acquire sufficient numbers of propagules during the growing season and consolidate information about accession growth traits.
- Expand cryopreservation capacities by developing new methods to protect or repair propagules that are damaged during cryoexposure, including improved cryoprotectant applications; use of plants' natural abilities to acclimate to cold and low water stress; and therapies that mitigate pathological metabolism. Develop cryopreservation approaches when freezer storage is ineffective.
- Further safeguard NPGS PGR from viability loss or genetic erosion by ensuring that the accessions stored at NLGRP meet standards for quantity and quality (i.e., they are true back-ups of the genebank units' accessions). Reexamine acceptable risks of loss and how current genebank standards mitigate the risks. Update standards for propagule numbers, viability, and testing frequency by incorporating new technologies that improve the sensitivity and reliability of predicting survival during storage.
- Apply the most cost-effective PGR preservation methods, as identified from revised risk estimates that balance the relative operational costs of long-term storage methods with quality and quantity standards for backing-up accessions.
- Reduce the current backlog of NPGS accessions requiring germination/viability monitoring tests by implementing more efficient workflows and procedures; expanding testing capacities; adjusting monitoring frequencies with reliable estimates of aging rates; and collaborating with other genebank units to gain insights about growth factors

affecting storage behavior, longevity during medium-term storage, as well as identifying growth or germination requirements.

- Streamline NLGRP raw data entry into GRIN-Global to ensure that the data are safeguarded, available in analyzable form, and that records of deviations from prescribed storage conditions (i.e., moisture and temperature) are archived.
- Develop improved protocols to recover propagules from storage and achieve normal plant development by applying biotechnologies that incorporate microculture, as well as experimentation, to identify cues that induce germination in dormant seeds.
- Transfer knowledge and methods for PGR management of CWR to other genebank units, land management agencies, and botanical gardens that supply seeds of CWR and other wild taxa. This goal will be achieved by enhanced characterization of morphological traits of seeds in the accessions; testing germination under a range of temperature conditions; and genotyping multiple individuals within the accessions.
- Index and identify microbes that are undetected in PGR until recovery of cryoexposed propagules occurs and that apparently interfere with that recovery.
- Conduct research to implement automation, multispectral scanning, and machine learning technologies to confirm taxonomic identifications of seeds; measure seed size and morphology; generate insights related to seed composition; and count out seeds for viability testing.
- Co-lead a comprehensive, systematic multi-institutional program for training NPGS personnel and students, especially in new methods for long-term PGR preservation.
- Expand NLGRP's statistical genetics, population genetics, and genetic marker program to encompass additional priority PGR and to develop additional analytical applications. Participate in a comprehensive, systematic, multi-genebank unit NPGS program for genotypic characterization in order to improve PGR management through application of that genotypic characterization information.
- Continue and expand interagency and inter-institutional collaborations and agreements for in situ conservation with land management organizations and conservation groups and apply ex situ PGR management knowledge to support conservation of CWR species.

Addendum: Fort Collins (NLGRP) Buildings and Facilities

The NLGRP plays a unique role within the NPGS; consequently its infrastructural needs are unique. Much of this facility, constructed in 1992, is nearing the end of its expected life span and will require major renovations. Furthermore, since 1992, the workflows for processing and storing PGR have changed. The NLGRP needs extensive, but well-planned, repairs to ensure it can continue to provide critical protection for U.S. and global agriculture. Initial efforts to rectify critical, time-sensitive building problems (e.g., roof, HVAC, and seed vault) have been mostly addressed, and a facility retrofit/recommissioning study is underway with funding from ARS Facilities Division. The energy costs of maintaining -18˚C in the large cold-storage vaults continues to increase, underscoring the need for alternative energy options. Seed driers are aged and need replacement. The cryovats used to store cryopreserved PGR have 30-year lifespans. Two to three new cryovats should be purchased per year to house accessions from the expanding NPGS PGR collection and to maintain an even age distribution among current cryovats, as a means of avoiding potentially catastrophic losses if many old tanks were to fail concurrently.

Geneva, NY: Plant Genetic Resources Research Unit, National Clonal Germplasm Repository for Apple, Cold-Hardy Grape, and Tart Cherry (GEN)

Background

The USDA/ARS Plant Genetic Resources Research Unit, National Clonal Germplasm Repository for Apple, Cold-hardy Grape, and Tart Cherry (GEN) staff of 6.7 permanent FTE and 1 temporary FTE manages 7,600+ accessions, 98 taxa, and three crops of primarily outcrossing, heterogeneous and heterozygous species that are either clonally propagated or regenerated by controlled pollination. Its current financial support (ca. $1,300,000) is from USDA/ARS and the State Agricultural Experiment Stations of the Northeastern Region. It operates from USDA/ARS and Cornell AgriTech facilities and maintains PGR in orchards on Cornell land.

Current Challenges

The primary current challenges for GEN include:

- Expanding genetic coverage of tart cherry (*Prunus*), grape (*Vitis*) and apple (*Malus*) CWR.
- Substantial backlogs in accession back-up at NLGRP, especially for grape (*Vitis)*.
- Lack of efficient and effective methods for cryopreservation of grape (*Vitis*).
- Substantial backlogs in germination/viability testing, especially for apple (*Malus*) and grape (*Vitis*) CWR accessions.
- Substantial backlogs in pathogen-testing for grape (*Vitis*) and tart cherry (*Prunus*) accessions.
- Need to repropagate the entire apple (*Malus*) PGR collection on new rootstocks for controlling diseases and developing a new cultivation system for high density planting on additional land.
- Need to develop new theories and methodologies for prioritizing apple (*Malus*) accessions for PGR management operations.
- Unknown taxonomic identity of some grape (*Vitis*) hybrids.
- Backlog of SNP genotype data for apple (*Malus*) and GBS data for tart cherry (*Prunus*) to be uploaded to GRIN-Global or Genome Database for Rosaceae (GDR).
- No ongoing comprehensive, systematic program for genotypic characterization.
- No comprehensive, systematic program for phenotypic evaluations, especially for cultivars of apple (*Malus*).
- Limited in situ conservation effort for North American grape (*Vitis)* CWR.

Goals and Actions

The primary +5- and +10-year needs for the GEN include increasing:

- Genebank annual budget from ca. $1,300,000 to $1,800,000 at +5 years and $2,500,000 at +10 years. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*
- Cold room space from ca. 280 ft3 to 300 ft3 at +5 years and 320 ft3 at +10 years.

- Greenhouse space from 0 now (destroyed by fire) to 2,000 ft2 at +5 years and 2,500 ft2 at +10 years.
- Orchard acreage from 50 acres to 60 acres at +5 years.
- Technical staff from ca. 6.7 permanent FTE and 1 temporary FTE to 9 permanent FTE and 4 temporary FTE at +5 years, and 12 permanent FTE and 6 temporary FTE at +10 years.

The preceding increases will expand the GEN operational capacity to achieve these outcomes:

- Manage expanded PGR collections of tart cherry (*Prunus*), grape (*Vitis*), and apple (*Malus*) CWR.
- Reduce the backlog in accession back-up at NLGRP for grape (*Vitis*) by increasing the number and percentages of accessions backed-up at NLGRP/year.
- Reduce the backlog of apple (*Malus*) and grape (*Vitis*) CWR accessions in the form of seeds requiring germination/viability testing, seedling evaluations, and new selections for accessions.
- Reduce the backlog of grape (*Vitis*) and tart cherry (*Prunus*) accessions requiring pathogen-testing by increasing the number and percentages of accessions pathogen-tested/year.
- Repropagate the entire apple (*Malus*) PGR collection on new rootstocks on additional land.
- Develop new theories and methodologies for prioritizing apple (*Malus*) accessions for PGR management operations.
- Determine the genetic identity of grape (*Vitis*) hybrids and assign a descriptive classification.
- Conduct research to devise efficient and effective methods for cryopreservation of tart cherry (*Prunus*).
- Make available extant SNP genotype data for apple (*Malus*) and GBS data for tart cherry (*Prunus*); conduct genotypic characterization of grape (*Vitis*) via VitisGen and Breeding Insight; participate in a comprehensive, systematic NPGS program for genotypic characterization.
- Participate in a comprehensive, systematic NPGS program for phenotypic evaluation, especially focusing on cultivars of apple (*Malus*).
- Investigate the feasibility of in situ conservation of North American grape (*Vitis)* CWR on public lands.

Addendum: Geneva (GEN) New Grape Research Facility

Federal funding of $68.9 million was secured in FY 2019 to build a new facility for the ARS Grape Genetics Research Unit (GGRU) at Cornell AgriTech in Geneva. Planning for construction of the new facility is underway. The facility will meet critical operational needs not only for the GGRU but will also house the PGRU grape PGR manager. Expanded greenhouse and cold room space in the new facility will be devoted to maintaining grape PGR. Nonetheless, expanded office and laboratory space for apple and tart cherry PGR management must be secured in another facility.

Geneva, NY: Plant Genetic Resources Research Unit, Northeast Regional Plant Introduction Station (NE9)

Background

The USDA/ARS Plant Genetic Resources Research Unit (PGRU), Northeast Regional Plant Introduction Station (NE9) manages genetic resources of vegetables. The 11.8 FTE permanent and 1 FTE temporary staff members of the vegetable crop genebank unit manage 12,700+ accessions of approximately 200 taxa within 13 major domestic vegetable crops. The annual and biennial PGR managed encompass outcrossing, heterogeneous and heterozygous species or inbreeding, homogeneous, and homozygous species. Most of the PGR at this genebank unit require highly labor-intensive controlled pollinations via various pollen exclusion techniques. Additionally, this genebank unit recently assumed responsibility for establishing and maintaining a national hemp PGR collection, requiring substantial upgrades in security infrastructure and seed production and storage capacity. The current financial support (ca. $1,590,000) for the project is from USDA/ARS and the State Agricultural Experiment Stations of the Northeastern Region. The PGRU operates from USDA/ARS and Cornell facilities and conducts field PGR regenerations on Cornell land.

Current Challenges

The primary current challenges for the NE9 vegetable crops project at Geneva include:

- Rejuvenating several vegetable PGR collections from which many legacy accessions have been lost.
- Substantial expansion of the genebank unit's PGR collections, especially for hemp (*Cannabis*) and most of the vegetable crops.
- Scaling the capacity to increase and distribute regulatory compliant hemp (*Cannabis*) accessions requires substantial modification of security, seed production, and storage infrastructure.
- Poor adaptation of some crops (e.g., artichoke *Cynara*) and accessions to field regeneration at Geneva.
- Substantial backlogs in accession duplication and back-up at NLGRP especially for onions (*Allium)*, *Asparagus*, *Brassica*, and *Physalis.*
- Substantial backlogs in germination/viability testing for onion (*Allium),* celery (*Apium), Asparagus, Benincasa*, *Brassica*, *Physalis*, radish (*Raphanus*)*,* and *Trichosanthes*.
- Substantial backlogs in pathogen-testing for seeds of tomato (*Solanum)*.
- Substantial backlogs in accession regeneration for onions (*Allium*), celery (*Apium*), *Asparagus*, *Benincasa*, *Brassica*, *Cucurbita*, *Physalis*, and *Trichosanthes* collections.
- Substantial backlogs in digitizing legacy paper records.
- Substantial backlogs in uploading digital records to GRIN-Global.
- Lack of procedures for efficient and effective long-term storage of accessions via cryopreservation (e.g., onion (*Allium*), hemp (*Cannabis*), and other long-term storage methods (e.g., artichoke (*Cynara*)
- Lack of procedures for regenerating some accessions, especially onion (*Allium*)*,* artichokes (*Cynara*), and hemp (*Cannabis*).

- No comprehensive, systematic program for genotypic characterization.
- No comprehensive, systematic program for phenotypic evaluations.
- Substantially increased demand projected for accessions of most hemp and vegetable crops.

Goals and Actions

The primary +5- and +10-year needs for NE9 include increasing:

- Genebank annual budget from ca. $1,590,000 to $2,700,000+ at +5 years and $3,000,000+ at +10 years. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*
- Cold room space from 7,100 ft^3 to 14,000 ft^3 at +5 years.
- Greenhouse space from 7,500+ ft^2 to 12,000 ft^2 at +5 years and 15,000 ft^2 at +10 years. This will involve reconstructing greenhouse facilities recently destroyed by fire.
- Screenhouse space from 0 ft^2 to 2,500 ft^2 at +5 years.
- Field space from 30 acres to 45 acres at +5 years.
- Technical staff from approximately 11.8 permanent and 1 temporary FTE to 17 permanent and 4 temporary FTE at +5 years, and 20 permanent and 6 temporary FTE at +10 years.

The preceding increases will expand NE9's operational capacity to achieve these outcomes:

- Re-acquire genetic diversity lost from legacy accessions of numerous vegetable crops e.g., celery (*Apium*), *Asparagus,* buckwheat (*Fagopyrum*), radish *(Raphanus*), and *Trichosanthes*.
- Investigate relocating selected vegetable PGR collections (e.g., artichoke (*Cynara*) to other genebank units, such as Parlier or Pullman.
- Manage substantially larger PGR collections, including hemp (*Cannabis*) and most of the vegetable crops.
- Reduce the backlog in accession duplication/back-up at NLGRP (especially for onion (*Allium*), *Asparagus*, *Brassica*, *Physalis*, and tomato (*Solanum*) by increasing the number and percentages of accessions backed-up at NLGRP/year.
- Increase the annual number and percent of accessions germinated and viability tested for onions (*Allium*), celery (*Apium*), *Asparagus*, *Benincasa*, *Brassica*, *Physalis*, radish (*Raphanus*), and *Trichosanthes* to reduce backlogs in testing.
- Increasing the number and percentages of accessions pathogen-tested/year for tomato (*Solanum*) to reduce backlogs in testing.
- Increase the annual rate of accessions regenerated for onion (*Allium*), celery (*Apium*), *Asparagus*, *Benincasa*, *Brassica*, *Cucurbita*, *Physalis*, and *Trichosanthes* to reduce backlogs in regeneration.
- Increase number and percent of valuable legacy paper records digitized by increasing the number and percentages of those records digitized/year.

- Reduce the substantial backlog of uploading digital records to GRIN-Global by increasing the number and percentages of those records uploaded annually.
- Conduct research to devise efficient and effective methods for long-term storage of accessions at the NLGRP via cryopreservation (e.g., onion (*Allium*)) and other reduced temperature methods (e.g., artichoke (*Cynara*)).
- Conduct research to devise efficient and effective methods for regenerating problematic accessions, especially for onion (*Allium*) artichoke (*Cynara*).
- Participate in a comprehensive, systematic NPGS program for genotypic characterization.
- Participate in a comprehensive, systematic NPGS program for trait evaluation. Test new trait evaluation methods to increase data collection capabilities for GRIN-Global.
- Manage substantially increased demand for accessions of onion (*Allium*), celery (*Apium*), *Brassica*, *Cucurbita*, buckwheat (*Fagopyrum*), radishes (*Raphanus*), and tomato (*Solanum)*.

Addendum: Geneva (NE9) Buildings and Facilities

The greenhouse, administrative, and security infrastructure, recently destroyed by fire, must be rebuilt and expanded to maintain the substantial increases projected for the sizes of the vegetable and hemp PGR collections. Similarly, cold room and screenhouse space require substantial expansion. Local PGR managers are formulating plans for facility expansion and will confer with ARS Building and Facilities Division regarding those needs.

Griffin, GA: Southern Regional Plant Introduction Station (termed S9, SRPIS and also USDA/ARS Plant Genetic Resources Conservation Unit)

Background

The staff of 24 permanent FTE and 1.5 temporary FTE at the USDA/ARS Southern Regional Plant Introduction Station (SRPIS, S9), one of the oldest and largest NPGS genebank units, manages a large PGR collection: 100,000+ accessions, 1,600+ taxa, and 28 major crop groups. Some accessions are of self-pollinating, homogeneous and homozygous species; others are of outcrossing, heterogeneous and heterozygous species that require controlled insect or hand pollination; and some are clonally propagated accessions maintained in vitro. Its current financial support (ca. $2,900,000+) is from USDA/ARS, University of Georgia (UGA) and the State Agricultural Experiment Stations of the Southern Region. It operates from USDA/ARS and UGA facilities, and farms UGA land in Griffin, GA, and USDA/ARS land at Byron, GA.

Current Challenges

The primary current challenges for S9 include:

- Expanded collections of *Sorghum*, millets (*Panicum* and *Pennisetum*), clover (*Trifolium*), switchgrass (*Panicum*), and little bluestem (*Schizachyrium*).
- Substantial backlogs in germination/viability testing, especially for wing bean (*Psophocarpus*), warm season grasses, sweet potato (*Ipomoea*) CWR, gourds (*Lagenaria, Momordica*), and peanut (*Arachis*) CWR, associated with the need to regenerate accessions with low seed numbers.
- Substantial backlogs in pathogen-testing and pathogen "clean-up", especially chiles (*Capsicum*) for viruses, squash mosaic virus in *Cucurbita*, watermelon (*Citrullus*), and peanuts (*Arachis*, for which quarantine capacity is needed).
- Substantial backlogs in accession regeneration, especially for *Hibiscus*, winged bean (*Psophocarpus*), warm season grasses, *Cucurbita,* eggplant (*Solanum*), gourd (*Lagenaria, Momordica*), *Luffa*, okra (*Abelmoschus*), chiles (*Capsicum*--perhaps from single-selfed plants), and Bambara groundnut (*Vigna*).
- Lack of procedures for pathogen-testing and pathogen "clean-up", especially for peanut (*Arachis*).
- Lack of procedures for effectively regenerating some accessions, especially for *Cucurbita*.
- Relatively few genotypic characterizations for most crops. No comprehensive, systematic program for genotypic characterization.
- Need for additional phenotypic evaluations for most crops. No comprehensive, systematic program for phenotypic evaluations.
- Limited in situ conservation effort for some taxa, such as *Ipomoea* CWR.

Goals and Actions

The primary +5- and +10-year needs for S9 include increasing:

- Genebank annual budget from ca. $2,900,000 to $4,000,000 at +5 years and $4,200,000 at +10 years. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*
- Cold room space from ca. 33,000+ ft3 to 85,000 ft3 at +5 years.
- Greenhouse space from ca. 16,000+ ft2 to 32,000 ft2 at +5 years.
- Field space from 40 acres to 80 acres at +5 years.
- Technical staff from 24 permanent FTE and 1.5 temporary FTE to 31 permanent FTE and 3.5 temporary FTE at +5 years.

The preceding increases will expand S9's operational capacity to achieve these outcomes:

- Manage expanded collections of *Sorghum* and millets (*Panicum* and *Pennisetum*), clover (*Trifolium*), switchgrass (*Panicum*), and little bluestem (*Schizachyrium*).
- Reduce the backlog of accessions requiring germination/viability testing by increasing the number and percentages of accessions germinated/viability tested/year, especially for wing bean (*Psophocarpus*), warm season grasses, sweet potato (*Ipomoea*) CWR, gourds (*Lagenaria, Momordica*), and peanut (*Arachis*) CWR, following regeneration of accessions with low seed numbers.
- Reduce the backlog of accessions requiring pathogen-testing and pathogen "clean-up" by increasing the number and percentages of accessions with seeds pathogen-tested and "cleaned-up"/year, especially for chiles (*Capsicum*) for viruses, squash mosaic virus in *Cucurbita*, watermelon (*Citrullus*), and peanuts (*Arachis*).
- Reduce the backlog of accession regeneration by increasing the number and percentages of accessions regenerated/year, especially for *Hibiscus*, warm season grasses, wing bean (*Psophocarpus*), millets, *Cucurbita*, eggplant (*Solanum*), gourd (*Lagenaria*, *Momordica*), *Luffa*, okra (*Abelmoschus*), chiles (*Capsicum*, perhaps from single-selfed plants), and Bambara groundnut (*Vigna*).
- Secure quarantine capacity for peanut (*Arachis*) at another site.
- Conduct research to devise efficient and effective methods for pathogen-testing and "clean-up" for some seeds, especially of peanut (*Arachis*).
- Conduct research to determine the factors inducing flowering in *Cucurbita* and with that information devise efficient and effective methods of regeneration.
- Conduct research on the efficacy of physical buffers (e.g., barrier plantings) for preventing cross-pollination among specialty legumes, castor (*Ricinus*), *Sesamum*, and other crops.
- Expand genotypic characterizations, especially for *Sorghum*, millets, castor (*Ricinus*), *Cucurbita*, eggplant (*Solanum*), okra (*Abelmoschus*), watermelon (*Citrullus*), peanut (*Arachis*), Bambara ground nut (*Vigna*), cowpea (*Vigna*), mung bean (*Vigna*), and *Vigna* CWR. Participate in a comprehensive, systematic NPGS program for genotypic characterization for all crops.

- Expand current phenotypic evaluations for some crops, such as *Hibiscus,* sesame (S*esamum*), and jute (*Corchorus capsularis* and *C. olitorius*) for food traits; specialty legumes for phytochemical traits; *Sorghum* for agronomic traits; chiles (*Capsicum*), *Cucurbita,* and eggplant (*Solanum*) for fruit traits; gourd (*Lagenaria*, *Momordica*), okra (*Abelmoschus*) for host-plant resistance; and Bambara groundnut (*Vigna*). Participate in a comprehensive, systematic NPGS program for phenotypic evaluation and digital imaging.
- Investigate the feasibility of in situ conservation of sweet potato (*Ipomoea*) CWR on public lands.

Addendum: Griffin (S9) Buildings and Facilities

Heating and cooling systems in the USDA/ARS headhouse were recently replaced with a high efficiency system that features expanded control functions. Two USDA/ARS greenhouses will be renovated, and all the glass panels replaced. An addition to the USDA/ARS seed processing building is being designed to include a new walk-in cold room and freezer for PGR storage that will replace the current cold room and freezer that have exceeded their life spans. The remaining facilities at the Griffin genebank unit that have also exceeded their life span are scattered across the UGA-Griffin campus, and consequently are challenging to manage. A proposal to design and build a new facility to house all operations of the Griffin genebank has been submitted for consideration by the USDA/ARS Infrastructure Initiative.

Hilo, HI: National Clonal Germplasm Repository for Tropical Fruit and Nut Crops (HILO)

Background

The 12.7 FTE permanent and 1.3 temporary FTE staff members of the USDA/ARS National Clonal Germplasm Repository for Tropical Fruit and Nut Crops (HILO) in Hilo, HI, conserve 1,100+ accessions, 30+ taxa, and 18 crops of mainly clonally propagated, outcrossing, heterogeneous and heterozygous subtropical and tropical tree fruit and nut crops. It also safeguards duplicate plantings of crops from the Miami and Mayagüez genebank units. Its current financial support (ca. $2,100,000+) is from USDA/ARS. It operates from USDA/ARS facilities and fields located on land leased from the University of Hawaii, Waiakea State Agricultural Experiment Station.

Current Challenges

The primary current challenges for the HILO include:

- Substantially expanded PGR collection size, including new crop collections, such as coffee.
- Substantial backlogs in accession back-up at NLGRP for numerous crops.
- Backlogs in germination/viability testing for papaya seeds.
- Substantial backlogs in pathogen-testing and pathogen "clean-up" for macadamia, avocado, and cacao.
- Substantial backlogs in digitizing valuable legacy paper records for pineapple.
- Backlogs in accession regeneration for papaya, and repropagation for macadamia.
- Need for revision of taxonomic information for dragonfruit.
- Lack of efficient and effective methods for backing-up numerous crops in reduced temperature storage at NLGRP.
- Lack of efficient and effective methods for repropagating some crops.
- Lack of efficient and effective methods for pathogen-testing for some crops, e.g., viruses in coffee.
- No comprehensive, systematic program for genotypic characterization in-house, although some ad hoc genotypic characterizations have been conducted by cooperators.
- No comprehensive, systematic program for phenotypic evaluations.
- Backlog in digital imaging for some crops, such as papaya.

Goals and Actions

The primary +5- and +10-year needs for HILO include increasing:

- Genebank annual budget from ca. $2,100,000+ to $2,600,000+ at +5 years and $3,500,000+ at +10 years. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*
- Cold room space from ca. 220+ ft3 to 410+ ft3 at +5 years and 610+ ft3 at +10 years.
- Greenhouse space from ca. 6,300+ ft2 to 10,300+ ft2 at +5 and 13,800 ft2 at +10 years. A quarantine greenhouse should be built to enable PGR importation.

- Screenhouse space from ca. 13,300+ ft2 to 17,300 ft2 at +5 years and 21,600 ft2 at +10 years.
- Field space from ca. 40 acres to 45 acres at +5 years and 60 acres at +10 years.
- Technical staff from ca. 12.7 permanent FTE and 1.3 temporary FTE to 13.7 permanent FTE and 1.5 temporary FTE at +5 years, and 15.7 permanent FTE and 1.5 temporary FTE at +10 years.

The preceding increases will expand HILO's operational capacity to achieve these outcomes:

- Manage substantially more PGR accessions, with new collections of five different crops, including coffee, and expanded safety duplicate plantings of cacao and avocado.
- Collaborate with Australian cooperators to expand genetic coverage of macadamia collection.
- Reduce the backlog in accession back-up at NLGRP (e.g., pineapple) by increasing the number and percentages of accessions backed-up at NLGRP/year.
- Reduce the backlog of papaya accessions requiring germination/viability testing by increasing the number and percentages of accessions germinated/viability tested/year.
- Reduce the backlog of accessions requiring pathogen-testing by increasing the number and percentages of accessions pathogen-tested/year (e.g., macadamia for quick decline, avocado sunblotch, CSSV in cacao).
- Reduce the backlog of papaya regeneration by increasing the number and percentages of accessions regenerated/year.
- Reduce the backlog of accession repropagation by increasing the number and percentages of macadamia accessions repropagated into a new field.
- Reduce the backlog of digitizing valuable pineapple legacy paper records by increasing the number and percentages of those records digitized/year.
- Reduce the backlog of digital imaging PGR by increasing the number and percentages of accessions imaged/year for several crops (e.g., papaya).
- Conduct research to revise taxonomic data for dragonfruit.
- Conduct research in collaboration with NLGRP to devise efficient and effective methods for backing-up numerous crops (e.g., breadfruit, coffee, durian, guava, litchi, longan, macadamia, papaya, pili nut, pulasan).
- Conduct research to devise efficient and effective methods for propagating pili nut.
- Conduct research to devise efficient and effective methods for pathogen-testing and "clean-up" for some crops, especially viruses in coffee.
- Participate in a comprehensive, systematic NPGS program for genotypic characterization; continue to collaborate with Sustainable Perennial Crops Laboratory in Beltsville for genotypic characterizations of crops such as breadfruit, litchi, longan, durian, and peach palm and to identify gaps in the litchi collection. Continue genotypic characterization of macadamia PGR in cooperation with Australia and with the University of Illinois for genotypic characterization of some crops.
- Participate in a comprehensive, systematic NPGS program for phenotypic evaluation, with local emphasis on fruit and nut quality of numerous crops; flowering behavior and plant architecture in litchi, longan, pulasan.

Mayagüez, PR: Tropical Agricultural Research Station and St. Croix, VI Worksite (MAY)

Background

The USDA/ARS Tropical Agricultural Research Station (TARS) at Mayagüez, PR (MAY), one of the oldest NPGS genebank units (founded in the early 1900s), manages 1200+ accessions of 40+ taxa from 12 major crops. Its staff of 13.5 permanent and 2 temporary FTE manages mainly PGR of tropical and subtropical tree fruit crops that are maintained in orchard plantings. It also safeguards backup plantings of tropical crops from the Hilo and Miami genebank units. Its current financial support (ca. $2,000,000+) is from USDA/ARS. It operates from USDA/ARS facilities and land at Mayagüez, Isabela, and Corozal, PR. It also operates a quarantine grow-out/regeneration site on St. Croix, USVI.

Current Challenges

The primary current challenges for MAY include:

- Expanding size of crop collections, such as cacao and tropical tree fruits (e.g., Spanish lime, *Annona*, *Pouteria*, *Manilkara*, *Garcinia*).
- Backlogs in pathogen-testing for some crops, such as banana and plantain.
- Backlogs in accession back-up of cacao and other crops at the NLGRP, and via duplicate plantings at Hilo genebank unit.
- Backlogs in accession re-propagation for expanding collections, e.g., cacao.
- Lack of methods for grafting certain crops, e.g., *Manilkara* and *Garcinia*.
- Lack of methods for backing up of accessions of several crops in reduced temperature storage at the NLGRP.
- No comprehensive, systematic program for genotypic characterization of some PGR accessions.
- No comprehensive, systematic program for phenotypic evaluations for some PGR accessions.

Goals and Actions

The primary +5- and +10-year needs for the MAY include increasing:

- Genebank annual budget from ca. $2,000,000+ to $2,300,000+ at +5 and $2,500,000+ at +10 years. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*
- Screenhouse space from ca. 17,200 ft2 to 21,000 ft2 at +5 years.
- Staff from ca. 13.5 permanent and 2 temporary FTE to 15.5 permanent and 4 temporary FTE at +5 years, and 16.5 permanent and 6 temporary FTE at +10 years.

The preceding increases will expand MAY's operational capacity to achieve these outcomes:

- Manage successfully the expanded field collections of labor-intensive PGR, including new back-up plantings of coffee, sugarcane, mango, and litchi, plus additional accessions

of cacao and tropical tree fruits (e.g., Spanish lime, *Annona*, *Pouteria*, *Manilkara*, *Garcinia*).

- Reduce the backlog in accession back-up of cacao and other crops by increasing the number and percentages of accessions backed-up at NLGRP and HILO genebank units/year. Backing-up at the NLGRP will require additional staffing there.
- Reduce the backlog of accessions of cacao requiring pathogen-testing by increasing the number and percentages of accessions pathogen-tested/year (with University of Arizona collaborator).
- Reduce backlogs in pathogen testing, especially for banana streak virus.
- Conduct research to improve grafting methods for crops such as *Manilkara* and *Garcinia.*
- Conduct research to devise efficient and effective methods for backing-up accessions in LN at the NLGRP (e.g., Spanish lime, *Annona*, *Pouteria*).
- Increase the number of accessions repropagated periodically for expanded collections (especially cacao).
- Participate in a comprehensive, systematic NPGS program for genotypic characterization of accessions, and continue to collaborate with the USDA/ARS Sustainable Perennial Crop Laboratory for genotypic characterizations.
- Participate in a comprehensive, systematic NPGS program for phenotypic evaluation of accessions, focusing locally on yield, fruit morphology and quality (e.g., Spanish lime, breadfruit), tree architecture (*Annona*, breadfruit), host-plant resistance to diseases (e.g., black pod in cacao, anthracnose in mango), and collaborative evaluations with Miami and Hilo genebank units for pulasan, breadfruit, mango, and litchi.

Addendum: Additional Information for St. Croix Worksite

For decades, the NPGS worksite at St. Croix, VI managed by the NPGS MAY genebank at Mayagüez, has served a unique role as a site where maize and sorghum PGR imported from Asia could be cultivated under quarantine and inspected for occurrence of downy mildew and other diseases currently absent from the Americas. The buildings and facilities at St. Croix were severely damaged by Hurricane Maria. The state historical preservation office's regulations have impeded the repair and/or rebuilding of those structures. Furthermore, long-term NPGS technical staff at St. Croix have either retired or resigned and hiring capable and reliable technical staff has proven problematic. Finally, USDA/APHIS has hesitated to renew Departmental Permit PDEP-11-00279 to grow quarantine sorghum, pearl millet, and maize in the field at St. Croix until a new protocol for testing seed for viruses is established by ARS. If this permit were not renewed, continued field operations at St. Croix would be infeasible.

In conjunction with ARS leadership and ARS Buildings and Facilities staff, USDA/APHIS, local governments in PR and VI, and industry/customers stakeholders, Mayagüez genebank staff are assessing the feasibility and desirability of rebuilding operational capacity at St. Croix, as compared to relocating operations to a Puerto Rico field location managed by MAY staff, where seed regenerations might be conducted at the Isabela Research Farm with potentially greater efficiency.

Miami, FL: Subtropical Horticulture Research Station (MIA)

Background

The 11.7 FTE permanent and 2 FTE temporary staff of the USDA/ARS Subtropical Horticulture Research Station in Miami (MIA), one of the oldest NPGS genebank sites, manages 1500+ accessions, 370+ taxa, and 11 crops that are mostly outcrossing, heterogeneous and heterozygous, perennial subtropical and tropical species maintained and propagated vegetatively/clonally. It also maintains duplicate, back-up plantings for crops managed primarily by the Hilo and Mayagüez genebank sites. Its current financial support (ca. $2,100,000+) is from USDA/ARS. It operates from USDA/ARS facilities on 200 acres of land near Miami, FL.

Current Challenges

The primary current challenges for the MIA include:

- Handling five new crops and more accessions of several major crops managed at MIA.
- Substantial backlogs in accession back-up at NLGRP (especially *Saccharum* (sugarcane), *Mangifera* (mango), and *Persea* (avocado)).
- Substantial backlogs in pathogen-testing and pathogen "clean-up" (especially *Saccharum* (sugarcane).
- Substantial backlogs in accession repropagation (especially for *Plumeria*).
- Substantial backlogs in digitizing valuable legacy paper records (especially for *Tripsacum*).
- Lack of efficient and effective methods for backing-up crops such as *Mangifera* (mango), *Persea* (avocado), and *Lagerstroemia* (crape myrtle) in cryostorage at the NLGRP.
- Although some genotypic characterization data exist for *Mangifera* (mango) and *Persea* (avocado), there is no comprehensive, systematic program for genotypic characterization.
- No comprehensive, systematic program for phenotypic evaluations.

Goals and Actions

The primary +5- and +10-year needs for MIA include increasing:

- Genebank annual budget from ca. $2,100,000+ to $2,300,000+ at +5 years and $2,400,000 + at +10 years. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*
- Cold room space from ca. 950+ ft3 to 1,000 ft3 at +5 years and 1,100 ft3 at +10 years.
- Greenhouse space from ca. 15,000+ ft2 to 16,000+ft2 at +10 years.
- Technical staff from ca.11.7 permanent and 2 temporary FTE to 12.7 permanent and 4 temporary FTE at +5 years.

The preceding increases will expand the MIA's operational capacity to achieve these outcomes:

- Manage PGR of five new crops (including grasses such as *Miscanthus* and *Panicum* (switchgrass)) and more accessions of crops such as *Persea* (avocado), *Psidium* (guava), and *Mangifera* (mango).

- Reduce the backlog in accession back-up at NLGRP (especially *Saccharum* (sugarcane), *Mangifera* (mango), *Persea* (avocado)) by increasing the number and percentages of accessions backed-up at NLGRP/year, once effective methods for cryostorage are developed.
- Reduce the backlog of accessions requiring pathogen-testing and pathogen "clean-up" by increasing the number and percentages of accessions pathogen-tested and "cleaned-up" according to schedule, especially *Persea* (avocado) for avocado sunblotch virus, and *Saccharum* (sugarcane).
- Reduce the backlog of accession repropagation by increasing the number and percentages of accessions regenerated according to schedule (especially for *Plumeria* accessions damaged by a recent hurricane).
- Reduce the backlog of digitizing valuable legacy paper records (e.g., for *Tripsacum*) by increasing the number and percentages of those records digitized/year.
- Reduce the backlog of incorporating digital records (e.g., for *Persea* (avocado) genotypes) into GRIN-Global by increasing the number and percentages of those records incorporated into GRIN-Global/year.
- Conduct research with NLGRP staff to devise efficient and effective methods for backing-up crops such as *Mangifera* (mango), *Persea* (avocado), and *Lagerstroemia* (crape myrtle) in cryostorage, and *Saccharum* (sugarcane) at reduced temperature storage.
- Participate in a comprehensive, systematic NPGS program for genotypic characterization.
- Participate in a comprehensive, systematic NPGS program for phenotypic evaluation.

Addendum: Miami (MIA) Greenhouse and Shade House Facilities

Two greenhouses which suffered significant damage from Hurricane Irma in 2017 were demolished. Construction of a state-of-the art plant quarantine complex, comprising a plant science greenhouse and an entomology quarantine facility, is ongoing. The headhouse next to the demolished greenhouses also suffered damage from the hurricane and is being repaired. Additionally, Hurricane Irma significantly damaged the roof and overall structural components of two screenhouses. Both facilities were repaired and are being used by the ornamental genetic resource management and research project.

Parlier, CA: National Arid Land Plant Genetic Resources Unit (PARL)

Background

The USDA/ARS National Arid Land Plant Genetic Resources Unit (PARL) at Parlier, CA, the most recently established NPGS genebank unit, plays a unique role. Its 3.2 FTE permanent and 0.5 temporary FTE staff manages 1,100+ accessions of 118 taxa and 7 crops that are mainly adapted to arid environments, and are mostly outcrossing, heterogeneous and heterozygous species. Some of the PGR are maintained as seeds and regenerated via controlled insect pollination; an equivalent number are maintained in clonal plantings. In addition, PARL regenerates accessions of numerous seed-propagated crops from other NPGS genebank units that are poorly adapted to growth in the latter sites and maintains back-up plantings of some clonally propagated accessions from the Corvallis genebank unit. The service accession regeneration and back-up PGR conservation components of PARL's operations are not covered by the summary immediately below but rather are discussed in the subsequent addendum. The PARL's current financial support (ca. $576,000) is from USDA/ARS. It operates from facilities and cultivates PGR on land at the USDA/ARS San Joaquin Valley Agricultural Sciences Center.

Current Challenges

The primary current challenges for PARL include:

- Substantial backlogs in accession back-up at NLGRP for taxa such as *Opuntia, Simmondsia*, and *Parthenium*.
- Substantial backlogs in germination/viability testing (especially for lesquerella, *Simmondsia*, *Limnanthes*, and *Cucurbita*).
- Substantial backlogs in pathogen-testing and pathogen "clean-up" for taxa such as *Opuntia*.
- Substantial backlogs in digitizing valuable legacy paper records.
- Lack of procedures for germination/viability testing for some seeds.
- Lack of procedures for pathogen-testing and pathogen "clean-up" for some taxa, such as *Opuntia*.
- Substantial backlogs in accession regeneration (especially for *Limnanthes* and *Opuntia*).
- No comprehensive, systematic program for genotypic characterization.
- No comprehensive, systematic program for phenotypic evaluations.

Goals and Actions

The primary +5- and +10-year needs for the PARL include increasing:

- Genebank annual budget from ca. $576,000 to $680,000 at +5 and $736,000 at +10 years. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*
- Technical staff from ca. 3.2 permanent and 0.5 temporary FTE to 4.4 permanent and 1 temporary FTE at +5 years. Should PARL responsibilities expand, increase staff to 5.4 or 6.4 FTE at +5 years.

- Field space from 23 to 33 acres at +10 years or to 40 acres, should PARL responsibilities expand; see Addendum below.
- -18˚C freezer capacity.

The preceding increases will expand PARL's operational capacity to achieve these outcomes:

- Manage ca. 20% more accessions and eight additional taxa, particularly of *Agave* and *Parthenium*.
- Reduce the backlog in accession back-up at NLGRP or by duplicate plantings (especially for *Opuntia*, *Simmondsia*, and *Parthenium*) by increasing the number and percentages of accessions backed-up/year.
- Reduce the backlog of accessions requiring germination/viability testing by increasing the number and percentages of accessions germinated/viability tested/year, (especially for lesquerella, *Simmondsia*, *Limnanthes*, and *Cucurbita)*.
- Reduce the backlog of accessions requiring pathogen-testing, especially for *Opuntia*, by increasing the number and percentages of accessions pathogen-tested and "cleaned-up"/year.
- Reduce the backlog of accession regeneration by increasing the number and percentages of accessions regenerated/year (especially for *Limnanthe*s), and repropagating the entire *Opuntia* collection.
- Reduce the backlog of digitizing valuable legacy paper records by increasing the number and percentages of those records digitized/year.
- Conduct research to devise efficient and effective methods for germination/viability testing for seeds of some taxa.
- Conduct research to devise efficient and effective methods for in vitro back-up of *Opuntia* at the NLGRP, and optimal back-up strategies for *Simmondsia* and other crops.
- Conduct research to devise efficient and effective methods for pathogen-testing and "clean-up" for *Opuntia*.
- Participate in a comprehensive, systematic NPGS program for genotypic characterization.
- Participate in a comprehensive, systematic NPGS program for phenotypic evaluation.

Addendum: Parlier (PARL)

Potential expansion of PARL operations to regenerate more PGR,
and to serve as the primary management site for selected NPGS PGR.

In addition to serving as the primary management site for the 1,100+ accessions of 118 taxa and 7 crops discussed above, the PARL also regenerates accessions of numerous seed-propagated crops from other NPGS genebank units that require a long, dry growing season. It also maintains back-up plantings of some clonally propagated accessions from the Corvallis (COR, hazelnut) and Pullman (W6, short-term garlic back-ups) genebank units.

Other NPGS genebank units have expressed interest in increasing the volume of accessions regenerated at the PARL or even transferring partial or total management responsibility for some crops to the PARL. As the effort to reduce the substantial NPGS PGR maintenance backlogs unfolds during the next +5 years, the feasibility and desirability of expanding the PARL's PGR management role will be reviewed with respect to the potential changes below. The needs for additional personnel, equipment, and land for the PARL also would be reviewed concurrently.

- Expand the volume of accessions currently regenerated at the PARL for other NPGS genebank units:
    - Double the number of *Vigna* accessions regenerated for the Griffin (S9) genebank unit.
    - Increase the number of cucurbit accessions regenerated for the Griffin (S9) genebank unit.
    - Increase the number of Asteraceae, Brassicaceae, and flax accessions regenerated for the Ames (NC7) genebank unit.
- Expand the volume of accessions currently backed-up at the PARL for other NPGS genebank units.
- Assume partial or total management responsibilities by the PARL for accessions and/or crops currently managed at other NPGS genebank units:
    - Assume management responsibilities for newly acquired additional grape accessions (20 taxa, ca. 2,000 accessions), especially of grape CWR.
- Transfer management responsibilities for selected vegetable crops (# of taxa and accessions to be determined) from the Geneva (NE9) and Griffin (S9) genebank units to the PARL. Accessions and/or taxa might include selected cucurbits from Geneva (NE9) and Griffin (S9), and artichoke and other vegetable crops from Geneva (NE9).

Pullman, WA Western Regional Plant Introduction Station (W6, also termed WRPIS and the USDA/ARS Plant Germplasm Introduction and Testing Research Unit)

Background

The 29.5 permanent FTE and 8 temporary FTE staff of the USDA/ARS Western Regional Plant Introduction Station (WRPIS, W6), one of the oldest and largest NPGS genebank units, manages 100,000+ accessions and 5,200+ taxa of ca. 24 major primarily seed-propagated crops, some that are inbreeding, homogeneous, and homozygous; and others that are outcrossing, heterogeneous and heterozygous species that require controlled pollination. Its current financial support (ca. $3,200,000+) is from USDA/ARS, Washington State University (WSU) and the State Agricultural Experiment Stations of the Western Region. It operates from USDA/ARS and WSU facilities in Pullman, Prosser, and Central Ferry, WA. It farms WSU land at Pullman and Prosser, and Army Corps of Engineers land at Central Ferry.

Current Challenges

The primary current challenges for W6 include:

- Increased size of its collection, especially for faba bean (*Vicia*), and CWR and other wild species from the U.S. through the Seeds of Success program.
- Substantial backlogs in accession back-up at NLGRP, especially for alfalfa (*Medicago*), *Allium*, clover (*Trifolium*), faba bean (*Vicia*), cool season grasses, *Lathyrus*, lettuce (*Lactuca*), *Lupinus*, pea (*Pisum*), bean (*Phaseolus*), beet (*Beta*), trefoil (*Lotus*), vetch (*Vicia*).
- Substantial backlogs in germination/viability testing, especially for alfalfa (*Medicago*), *Allium*, chickpea (*Cicer*), clover (*Trifolium*), faba bean (*Vicia*), cool season grasses, *Lathyrus*, lentils (*Lens*), lettuce (*Lactuca*), *Lupinus*, medic (*Medicago*), pea (*Pisum*), bean (*Phaseolus*), beet (*Beta*), trefoil (*Lotus*), vetch (*Vicia*), and Seeds of Success).
- Substantial backlogs in pathogen-testing and pathogen "clean-up" (especially for *Allium* (viruses, fungi, nematodes), chickpea (*Cicer—Ascochyta* blight on seeds), lentils (*Lens*—pea seedborne mosaic virus), lettuce (*Lactuca*—lettuce mosaic virus), pea (*Pisum*—pea seedborne mosaic virus), bean (*Phaseolus*—bean common mosaic virus), and vetch (*Vicia*)).
- Substantial backlogs in accession regeneration, especially for alfalfa (*Medicago*), *Allium,* clover (*Trifolium*), faba bean (*Vicia*), cool season grasses, *Lathyrus,* lettuce (*Lactuca*), *Lupinus,* medic (*Medicago*), bean (*Phaseolus*), beet (*Beta*), trefoil (*Lotus*), vetch (*Vicia*), and Seeds of Success).
- Lack of procedures for germination/viability testing, especially for some accessions from Seeds of Success.
- Lack of procedures for germinating some types of seed, especially for some accessions from Seeds of Success.
- Lack of procedures for efficient and effective regeneration of accessions, especially for CWR of clover (*Trifolium*) and many other crops, and species from Seeds of Success.
- No comprehensive, systematic program for genotypic characterization of most crops.

- Expanding current local program for phenotypic evaluations for most crops.
- Insufficient availability of accessions for lettuce (*Lactuca*) CWR and beet (*Beta*).
- Limited *in situ* conservation efforts for *Allium,* cool season grasses, *Phaseolus polystachios,* and U.S. CWR.

Goals and Actions

The primary +5- and +10-year needs for W6 include increasing:

- Genebank annual budget from ca. $3,200,000+ to $4,600,000+ at +5 years and $6,400,000+ at +10 years. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*
- Cold room space from ca. 25,000 ft^3 to 50,000 ft^3 at +5 years, and 70,000 ft^3 at +10 years.
- Greenhouse space from ca. 29,000+ ft^2 to 42,000+ ft^2 at +5 years and 55,000 ft^2 at +10 years.
- Screenhouse space from ca. 6,200+ ft^2 to 9,200 ft^2 at +5 years and 12,200 ft^2 at +10 years.
- Field space from 134+ acres to 210 acres at +5 years and 360 acres at +10 years.
- Technical staff from ca. 29.5 permanent FTE and 8 temporary FTE to 42 permanent FTE and 32 temporary FTE at +5 years, and 53 permanent FTE and 58 temporary FTE at +10 years.

The preceding increases will expand W6's operational capacity to achieve these outcomes:

- Manage the increased number of accessions of faba bean (*Vicia*), CWR and other wild species from the U.S. through the Seeds of Success program.
- Reduce the backlog in accession back-up at NLGRP, especially for alfalfa (*Medicago*), *Allium*, clover (*Trifolium*), faba bean (*Vicia*), cool season grasses, *Lathyrus*, lettuce (*Lactuca*), *Lupinus*, pea (*Pisum*), bean (*Phaseolus*), beet (*Beta*), trefoil (*Lotus*), vetch (*Vicia*), and Seeds of Success, by increasing the number and percentages of accessions backed-up at NLGRP/year.
- Reduce the backlog of accessions requiring germination/viability testing by increasing the number and percentages of accessions germinated/viability tested/year, especially for alfalfa (*Medicago*), *Allium*, chickpea (*Cicer*), clover (*Trifolium*), faba bean (*Vicia*), cool season grasses, *Lathyrus*, lentils (*Lens*), lettuce (*Lactuca*), *Lupinus*, medic (*Medicago*), pea (*Pisum*), bean (*Phaseolus*), beet (*Beta*), trefoil (*Lotus*), vetch (*Vicia*), and Seeds of Success.
- Reduce the backlog of accessions requiring pathogen-testing and pathogen "clean-up" by increasing the number and percentages of accessions pathogen-tested and "cleaned-up"/year. especially for *Allium* (viruses, fungi, nematodes), chickpea (*Cicer—Ascochyta* blight on seeds), lentils (*Lens*—pea seedborne mosaic virus), lettuce (*Lactuca*—lettuce mosaic virus), pea (*Pisum*—pea seedborne mosaic virus), bean (*Phaseolus*—bean common mosaic virus), and vetch (*Vicia*).

- Reduce the backlog of accession regeneration by increasing the number and percentages of accessions regenerated/year, especially for alfalfa (*Medicago*), *Allium*, clover (*Trifolium*), faba bean (*Vicia*), cool season grasses, *Lathyrus*, lettuce (*Lactuca*), *Lupinus*, medic (*Medicago*), bean (*Phaseolus*), beet (*Beta*), trefoil (*Lotus*), vetch (*Vicia*), and Seeds of Success.
- Conduct research to devise efficient and effective methods for germination/viability testing, especially for Seeds of Success.
- Conduct research to devise efficient and effective methods for germinating some types of seeds, especially for Seeds of Success.
- Conduct research to devise efficient and effective methods for regenerating accessions (especially for clover (*Trifolium*—pollination biology) and Seeds of Success—reproductive modes).
- Participate in a comprehensive, systematic NPGS program of genotypic characterization for alfalfa (*Medicago*), *Allium*, chickpea (*Cicer*), clover (*Trifolium*), faba bean (*Vicia*), cool season grasses, *Lathyrus*, lentils (*Lens*), lettuce (*Lactuca*), *Lupinus*, medic (*Medicago*), pea (*Pisum*), bean (*Phaseolus*), safflower (*Carthamus*), beet (*Beta*), trefoil (*Lotus*), vetch (*Vicia*), and Seeds of Success.
- Expand current extensive phenotypic evaluation effort for alfalfa (*Medicago*), *Allium,* chickpea (*Cicer*), clover (*Trifolium*), faba bean (*Vicia*—seed traits), cool season grasses, lentils (*Lens*), lettuce (*Lactuca*), *Lupinus*, medic (*Medicago*), pea (*Pisum*—seed traits for plant protein), bean (*Phaseolus*—seed traits), safflower (*Carthamus*), beet (*Beta*), trefoil (*Lotus*), and vetch (*Vicia*). Expand digital imaging effort for all crops. Participate in a comprehensive, systematic NPGS program for phenotypic evaluation.
- Increase availability of accessions, especially for lettuce (*Lactuca*) CWR and beet (*Beta*).
- Investigate the feasibility of in situ conservation of *Allium,* cool season grasses, *Phaseolus polystachios*, and CWR of selected crops on public lands.

Addendum: W6 Buildings and Facilities

Current plans for the new ARS building at the Pullman location include 2000 ft^2 dedicated to W6 seed storage, that would need to triple in size to hold the greater number of accessions that is projected. The current seed storage building could be remodeled to a -18˚C vault, and/or expanded and equipped with moveable shelves. Additional laboratory space could be built on existing ARS land footprints on the WSU Pullman campus by increasing the number of stories in the buildings. Additional buildings and facilities will also be needed to house the projected large (100%) increase in W6 staff. Some of the new staff could occupy either new buildings or renovated structures at the W6 Pullman farm location. Some of the additional personnel could be located in additional office space at the Central Ferry and Prosser sites, both of which have room for strategic expansion, not only for offices, but also for substantial increase in greenhouse and screenhouse space for accessions of *Phaseolus*, cool season grasses, and native CWR and wild species that are difficult to cultivate. Additional greenhouse space also could occupy the area between two current large ARS greenhouses on the Pullman campus. A previous WSU Master Plan to relocate many WSU/USDA greenhouses to an eastern area of the WSU campus should be revisited.

Riverside, CA: National Clonal Germplasm Repository for Citrus and Dates (RIV)

Background

The USDA/ARS National Clonal Germplasm Repository for Citrus and Dates (RIV) manages 1600+ accessions, 125 taxa, and 2 crop groups, citrus and date. Its 7.5 permanent staff members manage these taxa primarily in the form of cultivated trees in protective structures (greenhouses and screenhouses) and in field plantings. Most of the taxa are outcrossing, heterogeneous and heterozygous species. Cultivars are managed and propagated as clones, whereas accessions of some citrus wild relatives are regenerated by seeds. Maintaining the citrus collection involves extensive periodic testing for diseases of quarantine importance. Its current annual financial support (ca. $1,700,000+) is from USDA/ARS. It operates from USDA/ARS facilities on land leased from the University of California, Riverside (UCR), and maintains citrus orchard plantings on UCR land, and palms at the UCR Coachella Valley Agricultural Research Station in Thermal, CA. Some citrus wild relatives are maintained at the UC South Coast Research and Extension Center in Irvine, CA.

Current Challenges

The primary current challenges for RIV include:

- Completing the ongoing expansion of the protective screen house used to maintain sanitized genotypes.
- Renovating a portion of the preceding protective screen house that was recently breached.
- Substantial backlogs in citrus and date palm accession back-up at NLGRP.
- Substantial backlogs in pathogen-testing and pathogen “clean-up” for citrus PGR.
- Substantial backlogs in documentation and information management tasks.
- Lack of procedures for pathogen-testing and pathogen “clean-up” for citrus CWR.
- Substantial changes in the scientific taxonomic nomenclature for *Citrus*.
- Potential threat to date palm field plantings from emerging diseases.
- No comprehensive, systematic program for genotypic characterization.
- No comprehensive, systematic program for phenotypic evaluations.

Goals and Actions

The primary +5- and +10-year needs for RIV include increasing:

- Genebank annual budget from ca. $1,700,000+ to $2,700,000+ at +10 years. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*
- Greenhouse space from ca. 13,000+ ft2 to 19,000+ ft2 at +10 years.
- Screenhouse space from ca. 16,000+ ft2 to 22,000+ ft2 at +5 years, and 28,000ft2 at +10 years.
- Technical staff from ca. 7.5 permanent to 8 permanent and 2 temporary FTE at +5 years, and 10 permanent and 2 temporary FTE at +10 years, to add expertise and capacity for PGR management, citrus genetics/breeding, data management, and date palm tissue culture.

The preceding increases will expand RIV's operational capacity to achieve these outcomes:

- Reduce the backlog in accession back-up at NLGRP by increasing the number and percentages of citrus and date palm accessions backed-up at NLGRP/year.
- Reduce the backlog of citrus and date palm accessions requiring pathogen-testing and pathogen "clean-up" by increasing the number and percentages of accessions pathogen-tested and "cleaned-up"/year.
- By +10 years, repropagate numerous data palm accessions, beginning from plantlets in tissue culture.
- Apply revised taxonomic nomenclature for *Citrus* to records in GRIN-Global and maintained locally in collaboration with NGRL staff.
- Conduct research to devise efficient and effective methods for backing-up date palm accessions at the NLGRP.
- Conduct research to devise efficient and effective methods for pathogen-testing of citrus CWR.
- Participate in a comprehensive, systematic NPGS program for genotypic characterization of accessions.
- Participate in a comprehensive, systematic NPGS program for phenotypic evaluation of accessions.
- Conduct citrus and date palm genetic enhancement/breeding research.

Sturgeon Bay/Madison, WI: U.S. National Potato Genebank (NR6)

Background

The 6.5 FTE permanent and 0.8 temporary FTE staff of the USDA/ARS National Potato Genebank (NR6) manage 5,800+ accessions of 90 taxa of potato and related species. Most of the accessions are from outcrossing, heterogeneous and heterozygous species that require controlled hand pollination and are maintained as seed; but ca. 800 potato cultivars are maintained clonally in vitro. Its current financial support (ca. $799,000) is from USDA/ARS. It operates from University of Wisconsin Peninsula Agricultural Research Station facilities and land.

Current Challenges

The primary current challenges for the NR6 include:

- Need for more efficient and effective methods for in vitro maintenance of potato cultivars.
- No comprehensive, systematic program for genotypic characterization.
- Modest program for phenotypic evaluations.

Goals and Actions

The primary +5- and +10-year needs for the NR6 include increasing:

- Genebank annual budget from ca. $799,000 to $920,000 at +5 years and $960,000 at +10 years. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*

The preceding increases will expand NR6 operational capacity to achieve these outcomes:

- Conduct research in collaboration with NLGRP to devise more efficient and effective methods for in vitro maintenance of potato cultivars.
- Participate in a comprehensive, systematic NPGS program for genotypic characterization.
- Participate in a comprehensive, systematic NPGS program for phenotypic evaluation.

Stuttgart, AR: National Rice Genetic Stock Center (GSOR)

Background

The staff of 3 permanent FTE at the USDA/ARS National Rice Genetic Stock Center (NRGSC, GSOR) manages 38,000+ accessions and 10 taxa of primarily inbreeding, homozygous and homogeneous rice genetic stocks. Its current financial support (ca. $397,000) is from USDA/ARS. It operates from facilities of the USDA/ARS Dale Bumpers National Rice Research Center, and on land rented from the adjacent Arkansas Agricultural Experiment Station Rice Research and Extension Center.

Current Challenges

The primary current challenges for GSOR include:

- Substantial projected increase (5%+) in the size of the collection over +10 years.
- Gaps in genetic coverage of the genus *Oryza*, especially of CWR; difficulties with securing needed germplasm from international sources.
- No comprehensive, systematic program for genotypic characterization.
- Current and projected substantial demand for accessions, especially for the "diversity panel."

Goals and Actions

The primary +5- and +10-year needs for the GSOR include increasing:

- Genebank annual budget from ca. $397,000 to $420,000 at +5 and $440,000 at +10 years. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*
- Cold room space from ca. 2,800+ ft3 to 3,000 ft3 at +5 years, and 3,200 ft3 at +10 years.
- Technical staff from ca. 3 permanent FTE to 3 permanent and 1 temporary FTE a+5, and at +10 years.

The preceding increases will expand GSOR operational capacity to achieve these outcomes:

- Investigate the feasibility of acquiring rice CWR and other rice species from international sources to fill genetic gaps in the collection.
- Participate in a comprehensive, systematic NPGS program for genotypic characterization.
- Participate in a comprehensive, systematic NPGS program for phenotypic evaluation; expand extensive local evaluations to include the traits of salt tolerance, drought tolerance, and plant architecture; assay anthocyanin and phenol content and nutritional value for colored-bran rice.
- Manage substantial demand for accessions, especially for the "diversity panel."

Urbana, IL: Maize Genetic Stock Center (GSZE)

Background

The USDA/ARS Maize Genetic Stock Center (GSZE) is the premier genetic stock collection for maize in the world, composed of 42,000+ accessions, 8,500 of which are considered part of the "permanent collection." Its 3.85 FTE permanent staff manages accessions of outcrossing, homogeneous and largely homozygous maize accessions that require controlled hand pollination. Its current financial support (ca. $576,000+) is from USDA/ARS. It operates from University of Illinois (UI) facilities and cultivates the stocks on UI land.

Current Challenges

The primary current challenges for the GSZE include:

- Developing increased capacity to handle more accessions.
- Backlogs in accession regeneration
- Backlogs in accession duplication/back-up at NLGRP.

Goals and Actions

The primary +5- and +10-year needs for GSZE include increasing:

- Genebank annual budget from ca. $576,000+ to ca. $775,000+ at +5 years and ca. $975,000+ at +10 years. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*
- Cold room space from ca. 2,000 ft3 to 2,500 ft3 at +5 years, and to 3,000 ft3 at +10 years.
- Technical staff from ca. 3.85 permanent FTE to 4.85 permanent FTE at +5 years, and to 5.85 permanent FTE at +10 years.

The preceding increases will expand GSZE's operational capacity to achieve these outcomes:

- Manage a substantial increase projected for the number of genetic stocks, many generated by new genetic engineering approaches.
- Reduce the backlog in accession duplication/back-up at NLGRP by increasing the number and percentages of accessions backed-up at NLGRP/year.
- Reduce the backlog of accession regeneration by increasing the number and percentages of accessions regenerated/year.

Urbana, IL and Stoneville, MS: National Soybean Germplasm Collection (SOY)

Background

The USDA/ARS National Soybean Germplasm Collection (SOY) is the most comprehensive PGR collection for this crop in the world (22,000+ accessions, 2+ taxa, 2 crops-- perennial soybean CWR are managed as a separate crop). 7.2 FTE permanent and 0.75 FTE temporary staff at Urbana and 3 FTE permanent staff at Stoneville manage the numerous mainly homozygous and homogeneous accessions that mainly are self-pollinated. Accessions of the soybean CWR *Glycine soja* are regenerated in field cages to protect against insect damage. Field cages are required for soybean regeneration in Urbana, but not in Stoneville. Accessions of perennial *Glycine* are regenerated and evaluated exclusively under controlled greenhouse conditions. The current annual financial support (ca. $1,000,000+ at Urbana; $300,000+ at Stoneville) for *Glycine* PGR management is from USDA/ARS. The *Glycine* PGR management projects operate from USDA/ARS facilities. *Glycine* PGR are cultivated on University of Illinois land in Urbana, and USDA/ARS land in Stoneville.

Current Challenges

The primary current challenges for the SOY include:

- Aged facilities at Urbana that require renovation or replacement, and the need for additional workspace (see more extensive discussion below).
- Inadequate cold room facilities: maintained at 10°C and 40% humidity, ideal is 4°C and 25% humidity.
- Annually 10% of the soybean collection requires seed replenishment. This would be greatly reduced with the addition of -18°C storage.
- Handling projected increased numbers of accessions in SOY in the future including many with Roundup Ready and other GE traits.
- Improving the seed quality of accessions duplicated and backed-up at NLGRP.
- Substantial backlogs in germination/viability testing.
- Substantial backlogs in pathogen-testing for mottle virus for the entire collection, and for adventitious presence of Round-up Ready transgenes.
- Lack of procedures for pathogen-testing and pathogen “clean-up” for some potentially “unknown” pathogens.
- Substantial backlogs in digitizing valuable legacy paper records.
- No comprehensive systematic effort for genotypic characterization of perennial CWR.
- No comprehensive, systematic program for phenotypic evaluations or digital imaging.
- Handling high demand for PGR, especially for soybean breeding stock with genes introgressed from perennial CWR, and for genetic stocks generated by genomic research projects.

Goals and Actions

The primary +5- and +10-year needs for the SOY include increasing:

- Genebank annual budget at Urbana from ca. $1,000,000+ to $1,500,000+ at +5 years and $1,800,000 at +10 years; at Stoneville from ca. $320,000+ to $380,000+ at +5 years and $440,000+ at +10 years. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*
- Cold room space at Urbana from ca. 8,500 ft3 to 12,000 ft3 at +5 years.
- Greenhouse space from ca. 700 ft2 to 1,400 ft2 at +5 years and 3,000 ft2 at +10 years at Urbana.
- New screenhouse space at Urbana to ca. 5,000 ft2 at +5 years.
- Technical staff at Urbana from ca. 7.2 FTE permanent and 0.75 FTE temporary to 9.2 FTE permanent and 3 FTE temporary at +5 year, and 9.26 FTE permanent and 4 FTE temporary at +10 years; technical staff at Stoneville from ca. 2.5 FTE permanent to 3 FTE permanent at +5 and +10 years.

The preceding increases will expand the SOY operational capacity to achieve these outcomes:

- Reduce the backlog in accession back-up at NLGRP by increasing the number and percentages of accessions backed-up at NLGRP/year and by improving the quality of the seeds in long-term storage.
- Reduce the backlog of accessions requiring germination/viability testing by increasing the number and percentages of accessions germinated/viability tested/year.
- Reduce the backlog of accessions requiring pathogen-testing for viruses and pathogen "clean-up" by increasing the number and percentages of accessions with seeds pathogen-tested.
- Reduce the large backlog of digitizing valuable legacy paper records by increasing the number and percentages of those records digitized/year.
- Increase the number and percentages of accessions regenerated/year in insect exclusion cages.
- Increase the capacity to maintain perennial CWR in greenhouses.
- With collaborators, conduct research to devise efficient and effective methods for pathogen-testing for priority pathogens, e.g., viruses.
- Participate in a comprehensive, systematic program of genotypic characterization by external collaborators, and as part the NPGS-wide effort.
- Conduct a comprehensive, systematic phenotypic evaluation effort for host-plant resistance to pathogens and insects.
- Conduct a comprehensive, systematic program of digitally imaging accessions.
- Continue and refine local program to transfer valuable genes from perennial CWR to soybean breeding stock.
- Manage substantially increased demand for accessions.

Addendum: Urbana (SOY) Buildings and Facilities

Cold-storage, seed processing, and workspace at the Urbana soybean genebank are currently housed in a prefabricated building that is decades older than its forecast lifespan. Personnel at

that genebank unit have conferred with ARS management and with ARS Buildings and Facilities Division regarding the cost of renovating key features of that building. Nevertheless, the renovations would not expand the total workspace, and the building would still be past its useable lifespan. The expense of constructing a new, larger building should be compared to the alternative of relocating the soybean PGR collection and staff to the Ames genebank. Such a relocation would require increased funding for expanded field space, cold-storage, and seed-processing facilities at the Ames (NC7) genebank, plus possibly Congressional action enabling permanent transfer of funds from Urbana to Ames, and/or requisite expansion of the operating budget at Ames. Such a move to Ames would also require consideration for growing season length for late maturity group III and IV soybeans. Group IV (4470 accessions) makes up nearly 20% of the soybean collection.

Washington, DC: U.S. National Arboretum Woody Landscape Plant Germplasm Repository (USNA)

Background

The USDA/ARS U.S. National Arboretum Woody Landscape Plant Germplasm Repository (USNA-WLPGR) is the NPGS site devoted to conserving PGR for over 220 woody plant genera of commercial and ecological importance. Current holdings of the repository include 8,300+ accessions encompassing 2,300+ taxa. Its 4 FTE permanent and 2 FTE temporary staff manage a taxonomically and functionally diverse germplasm collection, mainly composed of outcrossing, heterogeneous and heterozygous species that are managed as trees, shrubs, and lianas in field plantings, herbaria vouchers, and stored seeds. Its operations are closely coordinated with other botanical gardens via a partnership with the American Public Gardens Association. Its current financial support (ca. $1,300,000+) is from USDA/ARS. It operates from USDA/ARS facilities and land at Beltsville, MD and at the U.S. National Arboretum in Washington, DC.

Current Challenges

The primary current challenges for the USNA include:

- Substantial backlogs in accession back-up at NLGRP, or at collaborating botanical gardens.
- Substantial backlogs in germination/viability testing often caused by accessions with too few seeds.
- Majority of accessions are woody plants that can take decades to regenerate.
- Lack of procedures for successfully storing some types of seeds at low temperatures.
- Lack of procedures for germination/viability testing for some types of seeds.
- Lack of procedures for germinating some types of seeds.
- Substantial backlogs in digitizing valuable legacy paper records.
- Multiple information systems for managing PGR data.
- No comprehensive, systematic program for genotypic characterization.
- No comprehensive, systematic program of phenotypic evaluations for priority traits such as adaptation to changing climates and tolerance of urban environments.
- Limited in situ conservation efforts for priority genera.

Goals and Actions

The primary +5 years and +10 years needs for the USNA include increasing:

- Genebank annual budget from ca. $1,300,000+ to $1,600,000+ at +5 years, and $1,800,000+ at +10 years. *The costs to implement this Plan are estimated and do not constitute a USDA request for funding.*
- Cold room space from ca. 360 ft3 to 423 ft3 at +5 years, and 504 ft3 at +10 years.
- Technical staff from ca. 4 FTE permanent and 2 FTE temporary to 4 FTE permanent and 3 FTE temporary at +5 years.

The preceding increases will expand USNA's operational capacity to achieve these outcomes:

- Increase the 0˚F cold storage capacity to safeguard more accessions as seeds.
- Increase information management capacity, especially for data in GRIN-Global.
- Reduce the backlog in safety duplication by increasing the number and percentages of accessions distributed to other botanical gardens/year.
- Reduce the backlog of accessions requiring germination/viability testing and field monitoring by increasing the number and percentages of accessions germinated/viability tested and monitored/year.
- Reduce the backlog of digitizing valuable legacy paper records by increasing the number and percentages of those records digitized/year and uploading them and other digital records to GRIN-Global.
- Reduce the backlog of accession regeneration by increasing the number and percentages of accessions regenerated/year and increasing seed supplies by recollecting rather than regenerating the accessions.
- Conduct research to devise efficient and effective methods for storing accessions of some poorly studied genera in liquid nitrogen or 0˚F.
- Conduct research to devise efficient and effective methods for germination/viability testing for some seeds.
- Conduct research to devise efficient and effective methods for germinating some types of seeds.
- Conduct research to devise efficient and effective methods for regenerating accessions received as small numbers of seeds.
- Participate in collaborative genotypic characterizations for priority genera such as sassafras, hydrangeas, boxwood, *Magnolia*, and *Cladrastis* and also in comprehensive, systematic NPGS programs for genotypic characterization.
- Focus phenotypic evaluations on priority genera, e.g., *Fothergilla*, *Lindera*, hydrangea, oaks, boxwood, and *Magnolia*.
- Investigate the feasibility of in situ conservation of priority genera on public and private lands.

Appendix C:

Component 10: Technical Details and Cost Calculations for Genotypic Characterization of NPGS PGR

This appendix provides additional technical details and cost calculations for Component 10: Genotypic Characterization of this Plan.

Technical Details and Costs for Creating Reference Genomes:

A reference genome sequence at the scaffold level is the minimum depth preferred for enabling further genomics research. A scaffold is a portion of the total genome sequence reconstructed from the alignment of numerous smaller pieces of nucleotide sequences. Creating a high-quality reference genome sequence for a species involves generating nucleotide sequences that span all chromosomes, without gaps and errors, preferably through very long "sequence reads". When DNA is read in very long unbroken sequences, errors decrease and alignment is improved, as it is easier to assemble fewer and longer sequences than many shorter ones. Following alignment, the NCBI pipeline can be used for automated annotation and initial gene prediction (the basic exon-intron architecture of a gene). The tools and computing resources of USDA/ARS's high-performance computing system SCINet can be enlisted as well.

The Earth Biogenome Project (EBP, https://www.earthbiogenome.org/) resembles the comprehensive NPGS genotypic characterization plan described herein. The EBP reports that reference genome sequences each cost $2,500 to generate, including bioinformatic support, but the low cost suggests that the EBP plans to generate only draft sequences; high quality finished genome sequences could cost as much as twice that amount. The EBP and the ARS-led Ag100Pest consortium, an ongoing effort to generate reference genome sequences for 100 agriculturally important insect species, will be consulted regarding cost effective protocols and possibly cross-project interactions and support. Generating reference genome sequences for all of the 13,000+ different plant species within the NPGS could cost $40,000,000 to $80,000,000 at today's prices. These costs could decrease as technology evolves, and as more reference genome sequences become available from ongoing research.

Technical Details and Costs Associated with Polyploidy:

Crop species with genomes containing multiple copies of chromosomes (e.g., hexaploid sweet potato with six copies of each chromosome) will be more expensive to skim sequence if 10-20X coverage is the minimal threshold for effective SNP marker discovery. The literature and experts will be consulted to ascertain whether that threshold of genome coverage can be reduced for each species; if not, the costs will be estimated as averages across crop species, although crops with large genomes will skew the actual cost estimates higher. As sequencing technology is constantly improving, the same or higher quality data might soon be available at lower costs. As Phase 2 of the plan begins, the costs of all available sequencing technology will be re-examined closely. At present, a skim sequence of 95 NPGS accessions at 10-20X coverage (including DNA extraction) would cost $12,750.

Technical Details and Costs for KASP SNP Markers:

As the most basic, easily identified, and readily analyzable form of nucleotide sequence variation, SNP markers are in many cases optimal for genotypic characterization. Nevertheless, accessions of polyploid species and, to a lesser extent, highly heterozygous outcrossing species, may not be amenable to genotyping via KASP SNP markers, or at the least will require more SNP markers to ascertain alleles accurately. Analyses for such species could even require several closely linked markers to define haplotypes with multiple alleles. These haplotypes would be more easily generated via sequencing rather than KASP SNP assays. For most diploid crops, KASP SNP genotyping for PGR management purposes can be conducted at an NPGS genebank unit or by collaborators. When genotyping capacity is lacking, or for crops with more complicated genomes requiring more extensive sequencing, service providers will be sought to extract DNA, perform assays, and rapidly deliver data and bioinformatic tools or services to visualize the data.

The estimated costs associated with KASP SNP marker assays include the cost to create a KASP assay for each SNP marker, which is currently $180 (with validation). Creation of a set of 200 KASP assays would thus cost $36,000. Genotyping each SNP marker with the KASP assays currently costs $1.60 for DNA extraction per sample + $0.05 per KASP SNP marker genotype. Genotyping 94 samples for 200 SNP markers with KASP assays would thus cost $160. KASP SNP assays created and conducted by the Intertek company are recommended by Breeding Insight, a Cornell University and USDA/ARS collaborative crop genotyping and phenotyping project, because of their rapid analyses, good service, and discounts for analyzing large volumes of samples. Breeding Insight, the Excellence in Breeding program, and the DArT and Intertek companies likely could provide the large-scale genotyping services needed for genotypic characterization of the NPGS accessions. These decisions will be revisited periodically as new genotyping platforms and genotyping service companies become available.

Technical Details and Costs for Genotypic Characterization of Wild Species:

Of the total ca. 600,000 NPGS accessions, 150,000 are from species that are not closely related to the 200 crops covered in the genotypic characterization plan outlined in Component 10 Genotypic Characterization. Those 150,000 NPGS accessions are nonetheless potentially valuable for future agricultural production or for ecosystem maintenance, restoration, or augmentation. For the most part, those species lack even partial genome sequence assemblies and/or a sufficiently high-quality reference genome sequence to enable development of numerous SNP markers for adequate coverage of the genome. The basic genomic research to develop such reference sequences might be conducted by other genomic research programs, such as the Earth Biogenome Project (https://www.earthbiogenome.org/), with the resulting data maintained in public genome databases or other specialized databases when such exist. If accessions from the NPGS were to contribute to the development of the reference genome sequences for such species, then genomic data from those NPGS accessions could be maintained and accessed through the NCBI. Once ample genomic sequencing information for those species were developed, other resources, such as subsets of SNP markers (KASP or sequence based), can be identified to enable the degree of genotypic characterization of NPGS accessions described

earlier in this Plan. These 150,000 species would be studied after genotypic characterizations of the initial 450,000 NPGS accessions are completed, probably 10 – 15 years after the overall effort begins. Costs will resemble those described earlier in this plan or will be less expensive, because newer and more cost-efficient genotyping platforms should have been developed by then.

Technical Details and Costs for Storage of Genotypic Characterization Data:

The GRIN-Global Development Team is currently incorporating the open-source BrAPI (Breeding Application Programming Interface) web services into the GRIN-Global system. BrAPI is a globally recognized community-of-practice that establishes a standard for database interoperability (enabling one computer system to "speak" to another without files being manually transferred by users) and to ensure data meets FAIR data policies. FAIR data are those that meet principles of Findability, Accessibility, Interoperability, and Reusability. Currently, 170+ web-service endpoints in the BrAPI standard interface enable real-time accession, phenotype, and genotype queries that return response data on-the-fly. The GRIN-Global Development Team will develop new interface endpoints in-house as needed and submit these enhancements as proposed BrAPI additions to the consortium of public and private stakeholders that maintains the BrAPI standard. Becoming BrAPI-compliant enables a secure and error-free method for GRIN-Global to share data to other BrAPI-compliant systems including mobile phenotyping apps such Field Book from Kansas State University, phenotypic database systems like BMS and BreedBase of the Excellence in Breeding (EiB) program of the Consultative Group on International Agriculture Research, genetic database systems such as the Genomic and Open-source Breeding informatics initiative (GOBii, from EiB and Cornell University), software with PGR management tools such as Germinate (James Hutton Institute), and many more applications. Through BrAPI, users can customize their data collection, curation, analyses, and reporting by connecting any compliant software that meets their needs.