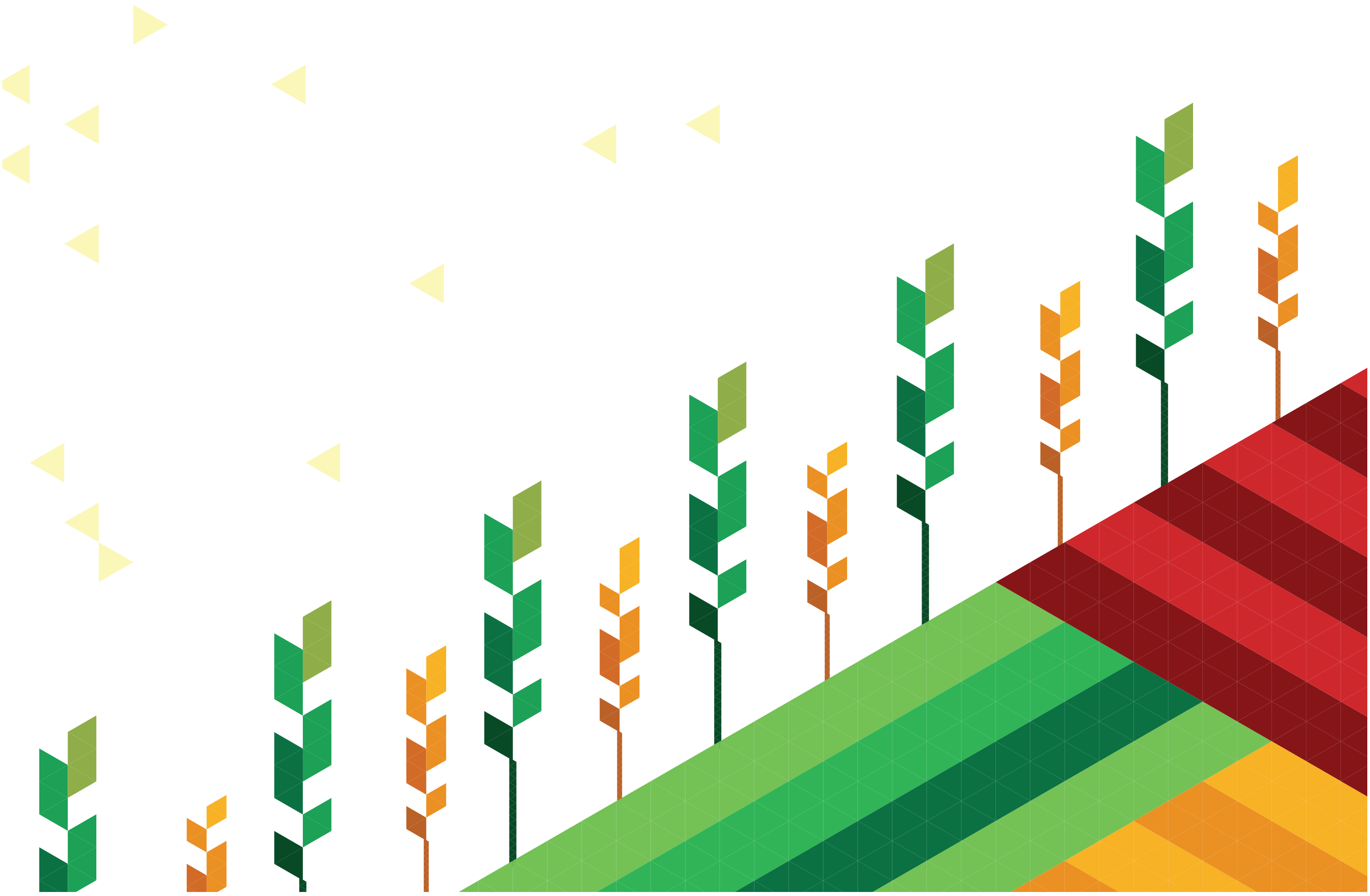
CROP TRUST

PATRON: HRH, THE PRINCE OF WALES

CGIAR

Genebank Platform

Proposal 31 March 2016



Genebanks of the CGIAR

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1. Rationale and Scope

CGIAR genebanks safeguard some of the largest and most widely used collections of crop diversity in the world, critical to attaining global development goals to end hunger and improve food and nutrition security, which arguably gives their stewardship an imperative and prominence unsurpassed by any other single undertaking in CGIAR. The genebanks, as a key driver of international exchange of plant genetic resources for food and agriculture (PGRFA), are fundamental to delivering the CGIAR Strategy and Results Framework (SRF) and three System Level Outcomes (SLO) of reduced poverty, improved food and nutrition security, and improved natural resources systems and ecosystem services. Most directly, the genebanks, through this Platform, will ensure increased conservation and use of genetic resources (sub-Intermediate Development Outcome (sub-IDO) 4.4.) and contribute to achieving Targets 2.5 and 2.a of the UN Sustainable Development Goals (Box 1).

Box 1. Global targets and outcomes for the Genebank Platform

SUSTAINABLE DEVELOPMENT GOAL 2: "End hunger, achieve food security and improve nutrition and promote sustainable agriculture"

Target 2.5: by 2020 maintain genetic diversity of seeds, cultivated plants, farmed and domesticated animals and their related wild species, including through soundly managed and diversified seed and plant banks at national, regional and international levels, and promote access to and fair and equitable sharing of benefits arising from the utilization of genetic resources and associated traditional knowledge as internationally agreed.

Target 2.a: increase investment, including through enhanced international cooperation, in rural infrastructure, agricultural research and extension services, technology development, and plant and livestock gene banks in order to enhance agricultural productive capacity in developing countries, in particular in least developed countries.

CGIAR STRATEGY AND RESULTS FRAMEWORK

SYSTEM LEVEL OUTCOME "Improved food and nutrition security for health"

INTERMEDIATE DEVELOPMENT OUTCOME 4 "Increased productivity"

Sub-IDO 4.4 "Increased conservation and use of genetic resources"

The importance of the collections managed by CGIAR is recognized in international policy. Through agreements[1] (Article 15) signed in 2006 between each CGIAR Center and the Governing Body of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA), Centers are obliged to make collections and associated data under their management available under the Multilateral System of Access and Benefit Sharing of the ITPGRFA. Under the same agreements, the genebanks are bound to "manage and administer these *ex situ* collections in accordance with internationally accepted standards, in particular the Genebank Standards, as endorsed by the FAO Commission on Genetic Resources for Food and Agriculture" (FAO 2014). The Governing Body of the

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[1] planttreaty.org/content/agreements-concluded-under-article-15

Treaty has emphasized the importance of the continuing support of the CGIAR Fund Council to the development of the global system for *ex situ* conservation[2]. Nine of the 11 CGIAR genebanks are also compliant with the principles and criteria of the Fund Disbursement Strategy of the Global Crop Diversity Trust (Crop Trust)[3], which allows them to receive long-term support from the endowment fund managed by the Crop Trust, which is recognized by the Governing Body of the ITPGRFA as an essential element of the Funding Strategy of the ITPGRFA.

What the CGIAR Genebanks offer

The 11 CGIAR genebanks manage 730,000 accessions in 35 collections, as seed, as plants in the field or screenhouse, in tissue culture, in cryopreservation and as DNA samples. These collections include tree species, forages, crop wild relatives, root and tuber crops, and bananas, as well as a wide range of cereals and grain legumes. CGIAR genebanks conserve, by far, the world's most genetically diverse and widely disseminated collection of germplasm available under the Multilateral System of the ITPGRFA. The associated germplasm health units (GHUs) ensure germplasm is distributed without phytosanitary risk. A summary of the work and status of each genebank and GHU is provided in Annex 1.

The CGIAR is responsible for 94% of the reported distributions of germplasm under the ITPGRFA[4]. Between 2012 and 2014, the genebanks distributed more than 380,000 samples in response to requests, of which more than a third was received by users outside CGIAR in 120 countries (Figures 1 to 5). The value of each of these accessions and the unique knowledge provided by the collection curators to germplasm requestors is difficult to quantify, largely because of the challenge of tracing back and attributing impact to such upstream contributions. While new improved varieties, (e.g. scuba rice, drought-tolerant maize, rust-resistant wheat) include genebank accessions in their pedigrees, the specific contribution of genebanks to economic returns has generally been too challenging to quantify. Only a few studies have formally linked impact back to genebanks (see Box 2).

Box 2. Some examples of impact of genebanks

- IRRI studied pedigree data in 2011 (McCouch et al., 2012) and discovered that:
  - of 4317 released rice varieties, 90% of non-IRRI varieties and 100% of IRRI varieties had at least one accession from the genebank in its pedigree;
  - the 12 most popular IRRI genebank accessions have been used in more than 1000 crosses each;
  - around 11% of the collection has been used in at least one cross.
- A study of the use of the CIAT genebank (Johnson, Pachico and Wortmann, 2003) revealed that 60% of the 411 bean varieties released since 1976 contain material from CIAT's collection.
- Pigeonpea accession ICP 8863 collected from a farmer's field and conserved in the ICRISAT genebank, was found to have promising resistance to *Fusarium* wilt, a fungus disease devastating yields in India. The purified line was released as 'Maruthi' in 1986. The impact of this genebank accession was estimated to be US$ 61.7 million in 1996, with a 65% internal rate of return (Bantilan and Joshi, 1996).
- The CGIAR Standing Panel on Impact Assessment commissioned a study (Robinson & Srinivasan, 2013) to assess the impact of two improved varieties released in Asia, which were developed using germplasm that could be clearly traced back to CGIAR genebanks. The study estimated that the aggregate economic benefits accruing from the adoption of Kasetsart 50 (cv. KU 50), an improved

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[2] planttreaty.org/content/resolution-82015-policy-guidance-global-crop-diversity-trust

[3] croptrust.org/wp-content/uploads/2014/12/Crop-Trust-Fund-Disbursement-Strategy.pdf

[4] planttreaty.org/sites/default/files/gb6w20e.pdf

cassava variety, exceed US$ 44 million in Thailand and US$ 53 million in Vietnam (at adoption levels of 60% and 75%, respectively). Cv. CMC 76, a key parent in the pedigree of KU 50, came from the CIAT genebank after being collected in Venezuela in 1967, and was selected by CIAT cassava breeders during the evaluation of genebank accessions.

- Similarly, the germplasm used in the evaluations and crosses to create cv. Cooperation 88 (C88), a blight resistant potato variety now spreading rapidly in China, was derived from the CIP genebank. Harboring diversity from the center of origin of the potato in the Andes, the collection contributed essential diversity to broaden the genetic basis of the potato in China. C88 is calculated to have accrued economic benefits of US$ 350 million, increasing to US$ 465 million per year if farm-level adoption continues to increase.

The 11 genebanks, strategically located in centers of crop diversity, ensure that germplasm acquisitions and distributions are comprehensively global, with a diverse partner and user base (Figure 5). Distribution figures reported from the genebanks since 2012 illustrate that every genebank has a truly global outreach (Figure 2). This is also reflected in an analysis of genebank distributions that illustrates the degree to which CGIAR is contributing to germplasm exchange worldwide, underpinning the interdependence among countries for diversity in these major staple crops. Figure 3 traces the movement of genebank materials of different geographical origins to all regions of the world. Some of the largest national genebanks, such as those of USDA and the Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK) in Germany, exhibit germplasm flows that are strongly influenced by their geographical location, whereas the CGIAR Centers are facilitating a busy, global exchange of germplasm of diverse geographical origins. Given such a wide outreach, the potential for further growth in distributions is substantial.

There is a reasonable basis to expect increased demand for germplasm from CGIAR genebanks. Present-day technologies for disease indexing, high-throughput sequencing and phenotyping and screening data have the potential to create a dramatic increase in value and demand for diversity (McCouch et al. 2012). Most Centers report an overall increase in distribution in recent years and, given a supportive policy framework, this can be expected to continue. The annual rate of distribution between 1985 and 2009 for nine CGIAR genebanks was 39,970 samples, according to Galluzzi et al (2015). Between 2012 and 2014, the same nine genebanks reported an annual average distribution of 91,973 samples[5].

What the Platform offers

In addition to the Centers' individual achievements, the collaboration among the CGIAR genebanks over several decades, through the Systemwide Program on Genetic Resources and the Genebanks CRP strengthened what has come to be called a "Global System" for the *ex situ* conservation and sustainable use of PGRFA at a global level.[6] Specific achievements include:

- critical contributions to the negotiation of the FAO *In Trust* Agreements, the ITPGRFA, the Standard Material Transfer Agreement (SMTA) used for all germplasm exchange, and the agreements concluded under Article 15 of the ITPGRFA, which covers the *in trust* collections;
- major contributions to the development of the Global Plan of Action[7], The State of the World's Plant Genetic Resources for Food and Agriculture[8] and the FAO Genebank Standards[9];

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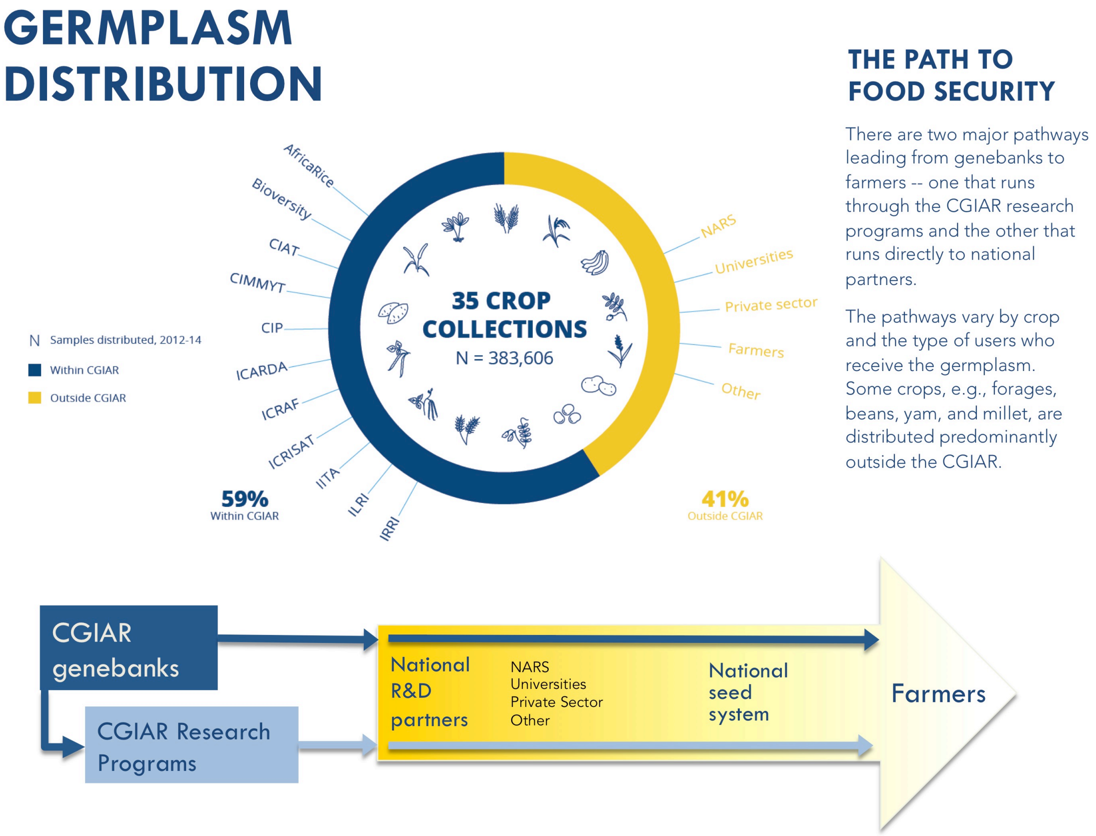
[5] Reports in the CRP online reporting tool (grants.croptrust.org/ltg).

[6] There are different understandings of the term "global system". Here we refer to the worldwide community of genebanks and institutes, which are working together and individually to conserve and use PGRFA, and the policy instruments and global action plans that bind them together and support their work. CGIAR genebanks, given the size and diversity of their collections, their global mandate, and extensiveness of their partnerships form the central pillar to this system.

[7] fao.org/agriculture/crops/thematic-sitemap/theme/seeds-pgr/gpa/en/

- commitment to the building of the backup collections in the Svalbard Global Seed Vault (SGSV), underpinning its awareness-raising success ;
- development of Genesys[10], the global portal through which the research community may now access information on more than 2.7 million accessions, and the Systemwide Information Network on Genetic Resources (SINGER) before it;
- development of a genebank quality management system (QMS), based on a history of sharing best practices, protocols and guidelines.



There are two major pathways leading from genebanks to farmers -- one that runs through the CGIAR research programs and the other that runs directly to national partners.

The pathways vary by crop and the type of users who receive the germplasm. Some crops, e.g., forages, beans, yam, and millet, are distributed predominantly outside the CGIAR.

Figure 1. Distribution of germplasm from the CGIAR genebanks (2012 - 2014)

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[8] fao.org/agriculture/crops/thematic-sitemap/theme/seeds-pgr/sow/en/

[9] fao.org/agriculture/crops/thematic-sitemap/theme/seeds-pgr/gbs/en/

[10] www.genesys-pgr.org

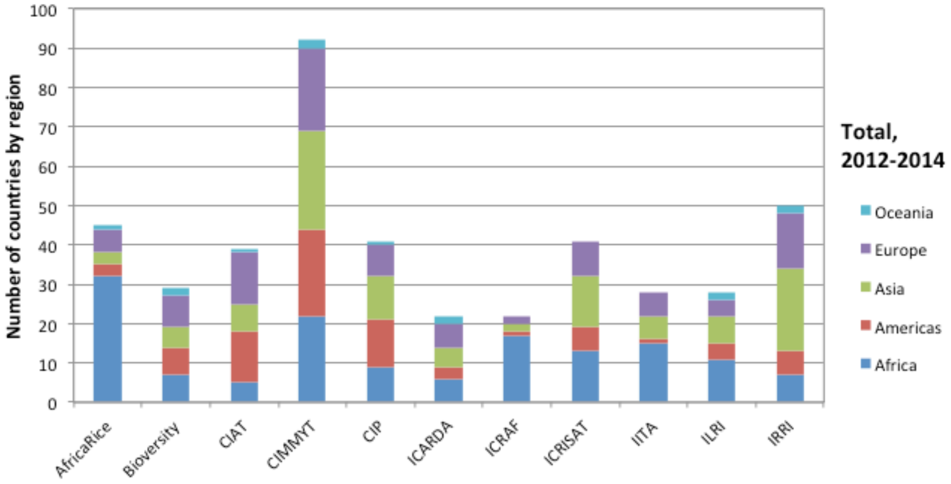
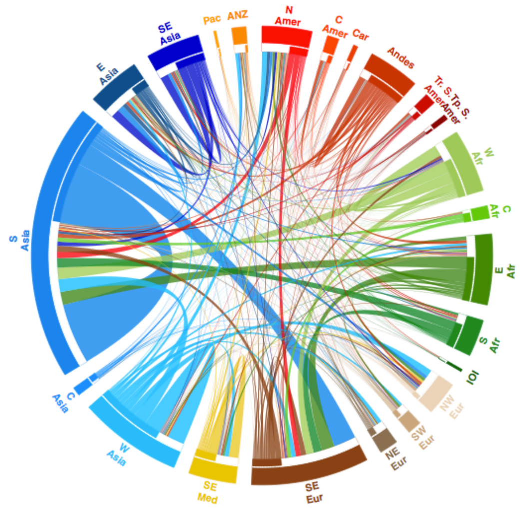


Figure 2. Number of countries and regions receiving germplasm from individual Centers (2012 – 2014)

CGIAR



USDA

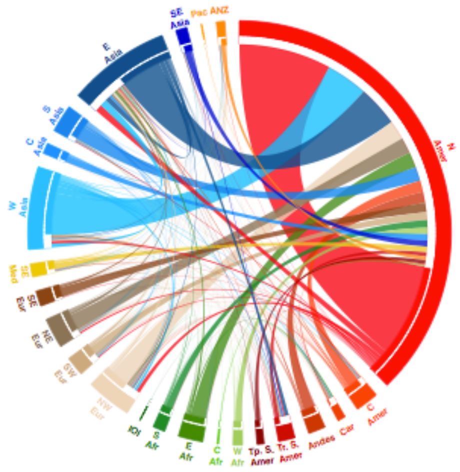
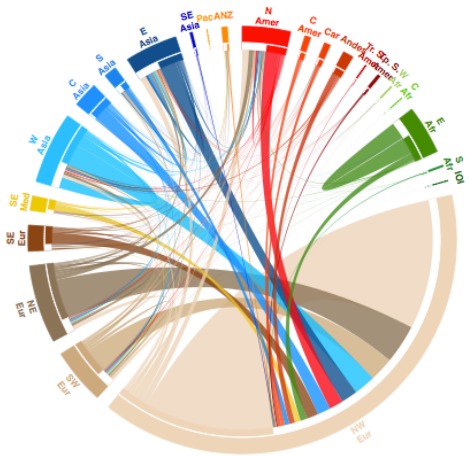


Figure 3. Comparison of germplasm distributions of CGIAR (1985–2009) genebanks and the national genebanks of the USA (2005–2015) and Germany (2007–2015). Each geographical region has a unique color. Germplasm flows are represented by a line from the region from which the germplasm originates to the region of the recipient. Thus, a light blue line represents material originating from West Asia and distributed by the genebank to different locations around the world. The width of the line depicts the relative number of distributions over the stated period. Source: Khoury, 2016.

IPK, Germany



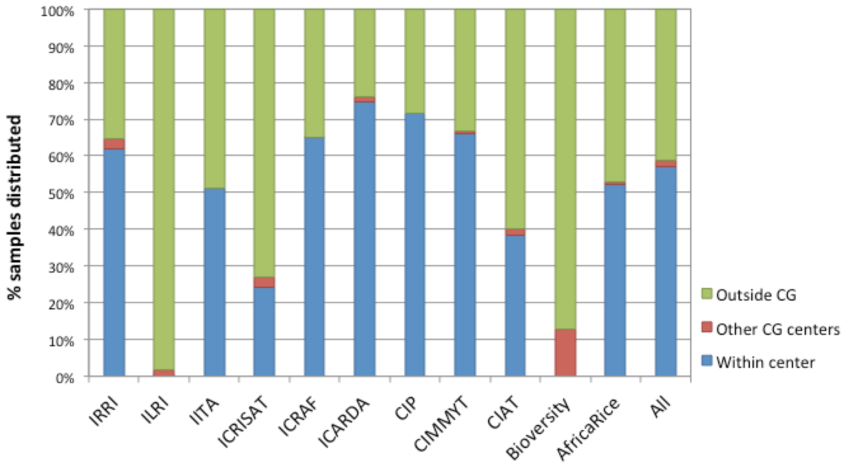


Figure 4. Distribution of samples inside and outside the CGIAR from individual Centers based on reported figures (2012 – 2014)

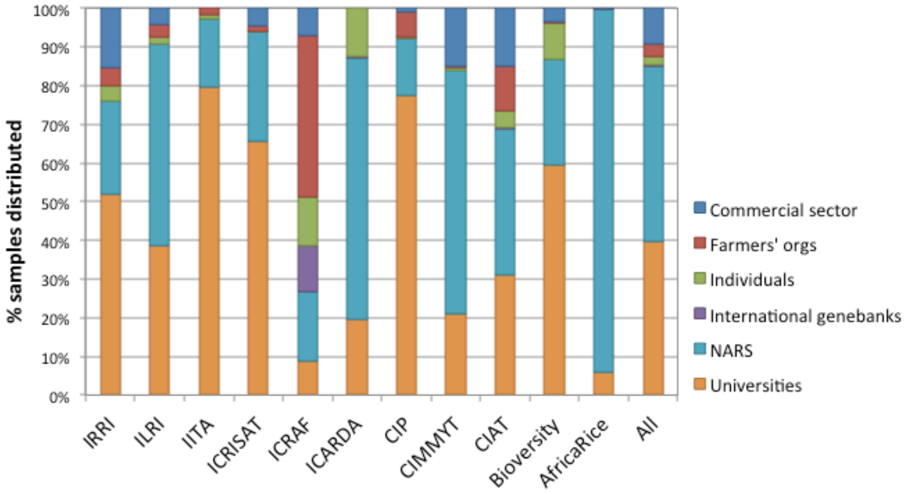


Figure 5. Proportion of external distributions received by different user types (2012–2014).

Since 2012, the genebanks have been working together under the independent oversight of the Crop Trust in the Genebank CRP. This has brought about stronger monitoring, evaluation, reporting and learning, and has ensured a tighter cohesion towards shared targets and quality management. For the first time, the CGIAR genebanks are able to report their status and progress at a system level using common metrics. The development and adoption of improved and common data management tools has also accelerated. Following in the footsteps of the CRP, this Platform will provide a strengthened governance structure and continue to improve integration and cohesion across Centers and crops. This is important in the current context, where the genebanks have different levels of experience and resources, but together are recognized under one brand – CGIAR – which is widely taken to symbolize the highest standards of operation. Shared approaches will bring about greater efficiency, more powerful tools and resources to access collections, alignment of standards, and stronger trust and transparency, not only among the CGIAR genebanks but also beyond. The term “platform” symbolizes the solid, systemwide strength of the genebanks in providing the cohesion and grounding, together with the other Platforms, by which the Agri-food System CRPs (AFS-CRPs) will modernize their breeding programs and deliver genetic gains and increased productivity.

Global Challenges

At present, the CGIAR genebanks employ around 400 skilled staff, undertaking a range of operations to monitor, test, germinate, multiply, clean, culture, document and package germplasm, under high scientific standards of operation. In the three-year period between 2012 and 2014, these staff regenerated more than 200,000 accessions, sub-cultured more than 100,000 tissue-culture samples, health-tested more than 140,000 accessions and acquired more than 30,000 new accessions. Given the threats faced by plant species and habitats[11] and the decline in occurrence of traditional landraces in many parts of the world (Brush, S. 2004), CGIAR genebanks' primary role in ensuring the conservation of crop genetic resources is vital for supporting the SRF and for future generations to have access to the genetic diversity that is no longer found in farmers' fields or wild habitats.

Key to increasing the value of these resources is developing a deeper understanding of their potential use. Large-scale genetic and phenotypic characterization of collections is triggering an explosion in our scientific understanding, with the potential to effect tremendous change in productivity, sustainability and resilience of improved crop varieties. A vision of CGIAR genebanks providing a complete guide to the collections in terms of taxonomic, geographic, genotypic and phenotypic attributes of accessions is no longer science fiction, but neither is it realistically attainable within the scope of this Platform. What is proposed here puts priority on long-term conservation, and takes a significant step towards the "complete characterization" of the collections. The length of this step depends on the outputs of collaboration with primary users, and the capacity of the genebanks to complement these outputs with their own efforts to characterize those collections that are not currently the focus of breeder or user attention.

In aiming for increase in both conservation and use of PGRFA, the Platform will address three major challenges:

- **CGIAR must do more for less.** New technologies, knowledge and processes offer the possibility of further raising standards to become more efficient and more effective. The genebanks must work strategically, both individually and together within the global system, to exploit new opportunities, conserve more diversity and respond to more demands while controlling costs. Furthermore, they must achieve all these without compromising their obligation to ensure the long-term conservation of the materials in their care.
- **CGIAR must, in aiming for increased genetic gain, respond better to breeders' needs for genetic diversity and specific traits.** The genebanks must align their operations towards more targeted use and exploitation of the collections. This they can do by enriching the data associated with them. In particular, genebanks should exploit the tools and data resulting from the large-scale genotyping and phenotyping initiatives of the AFS-CRPs and other CGIAR Platforms. Stronger integration and two-way flow of information between the genebanks and the rest of the CGIAR portfolio are critical to achieving this aim.
- **CGIAR must comply with its legal obligations and engage in shaping international genetic resources agreements.** CGIAR's acquisition, development and dissemination of genetic resources and data are directly affected by international agreements. If those agreements fail, or if they are implemented in ways that do not reflect the realities of agricultural research and development, the CGIAR's mission will be undermined. The CGIAR must proactively engage in the development of these processes to ensure that they create a supportive policy environment for CGIAR genebanks, breeding programs and national partners.

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[11] iucnredlist.org/

2. Platform structure and modules

To respond to these three challenges, the Platform is structured into three modules:

Conservation Module: Support and improve essential genebank operations

At the core of the Platform, and by far its largest component, is the sustained and improved operation of the 11 genebanks and GHUs, the routine work that is essential to ensure that the germplasm in the collections is healthy, viable, free of important pests and pathogens, and available for distribution. A much clearer picture of the status of the collections has been revealed as a result of the Genebank CRP. Most notably, of the 734 000 accessions held by CGIAR in 2014, 529 000 (72%) were available for distribution and 413 000 (59%) were safety duplicated. In order to reach agreed performance targets of 90% availability and safety duplication, the genebanks will regenerate and GHUs will carry out phytosanitary cleaning of accessions that are currently not safe to distribute. Special attention is needed to improve the status of collections of clonal crops, wild species and trees. This involves research to develop effective phytosanitary diagnostics, optimize cryopreservation and storage protocols, eliminate redundancies in collections, and determine more strategic methods of conservation and curation of costly-to-conserve taxa. For collections processing large numbers of accessions, automation of germination, seed sorting and handling processes also has the potential to bring about significant efficiencies. Through increased efficiency, critical review, and more strategic curation, the genebanks will be able to improve operations while controlling costs by 2022.

These elements of work are focused on improving the status and use of the CGIAR genebanks and GHUs for the benefit of existing and new users throughout CGIAR and beyond. All activities are carried out within the context of a rational global system. Genebanks (inside or outside CGIAR) holding the same or similar crops must collaborate more to avoid duplication of activities and benefit from each other’s skills and facilities. Conservation priorities are described in individual global crop conservation strategies, which were developed in 2006–2012. These strategies are gradually being revisited by the communities that developed them, and, where appropriate, more formal “Crop User Groups” are being established to provide a means for better communication and to feed into the prioritization of activities in the CGIAR genebanks. Through these communities, every opportunity will be taken to strengthen capacity both internally and externally to the CGIAR. Workshops on QMS and data management, and initiatives to improve seed conservation methods and phytosanitary procedures will involve national partners, and most particularly collecting efforts and diversity gap analysis will be carried out in collaboration with national partners who manage major collections or are located in hotspots of crop diversity.

Use Module: Empower effective us of plant genetic resources

The key for genebanks to enable smarter and more targeted use of diversity is closer collaboration with their primary users. Through the Platform, the genebanks will foster stronger flows of information, tools and skills between genebanks and genebank users. Coordinated approaches to genotyping and phenotyping, and standardization of methods and tools, through the Genetic Gains Platform, as well as initiatives beyond the CGIAR, such as DivSeek[12] and the ITPGRFA’s Global Information System (GLIS[13]), will empower the Use Module to ensure that big data generated by the AFS-CRPs and other Platforms will be directly linkable to genebank databases. Where possible, the genebanks will also seek opportunities to expand the genotyping of the collections, either through uplift funding or other means. In this way, less well-known parts of the collection may be genotyped

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[12] www.divseek.org

[13] planttreaty.org/content/gis

and associated with phenotypic traits of interest, contributing to the more complete characterization of the collections.

The genebanks have a suite of both emerging and more mature tools and methods for exploring the collections: mini-cores at ICRISAT; Focused Identification of Germplasm Strategy (FIGS) subsets at ICARDA; a molecular atlas at CIMMYT; whole-genome sequence data for thousands of accessions at IRRI. With improved data, and improved data standardization facilitated by the Genetic Gains Platform, the genebanks will be able to scale up and develop germplasm selections for specific users, traits, taxonomies or geographies. The global web portal, Genesys, will be substantially revamped by enriching data content and building search and visualization tools in collaboration with specialist software developers. Richer data and powerful search tools will provide major incentives for new partners and users to participate in Genesys and stimulate its use further.

Policy Module: Engage in genetic resources policy development and compliance

From a policy perspective, the day-to-day operations of genebanks and their downstream users are subject to an increasingly complex range of international and national laws concerning access and benefit-sharing, intellectual property, and biosafety (Lopez Noriega et al 2013). There is evidence that some of these developments are creating barriers to agricultural research (Heisey and Day Rubenstein, 2015). New scientific and technical capacities, such as gene editing and genomics, are provoking policy-related questions and challenges that are not addressed in existing international agreements. CGIAR genebanks are expected to adhere to the highest standards of compliance and transparency and act as central players in the evolving global system. Their proactive engagement in genetic resources policy development is of utmost importance in pursuit of CGIAR’s mission.

This Module will provide the capacity, authority and expertise to coordinate systemwide consideration of policy developments, engage strategically in international policy fora, and strengthen capacity within the system for full and transparent compliance. Within CGIAR, the genebank community has always been the most immediately affected by the changing policy environment, and has made important contributions to relevant policy fora. The Policy Module will consolidate and build upon the previous achievements of the community and engage other CGIAR constituencies, including the Centers’ Intellectual Property (IP) focal points, Genetic Gains and Big Data Platforms, Science Leaders, breeders, social scientists, and the System Office. Through the establishment of a Multi-stakeholder PGR Policy Group, the Module will ensure engagement with a range of experts from outside the CGIAR.

3. Impact pathway and theory of change

The pathway towards impact of the genebanks and GHUs may be traced by following the route of the germplasm and associated data. The genebanks contribute in multiple ways to IDOs for **Increased resilience of the poor to climate change and other shocks; Improved diets for poor and vulnerable people; Natural capital enhanced and protected, especially from climate change;** and **Enhanced benefits from ecosystem goods and services**. The activities of the Platform, however, are targeted specifically to bring about **Increased Conservation and Use of Genetic Resources** and **Increased productivity.**

The genebanks also distribute germplasm and data to a wide range of users outside the CGIAR, feeding into numerous, diverse outcomes worldwide. In some cases, where breeding or domestication programs are fewer or less developed (e.g. forages, tree species) or where genebanks provide a source of clean planting material (e.g. root, tuber and banana crops), distribution outside the CGIAR may be more prominent than internally (Figure 4).

While the major role of the Platform is to maintain the collections and facilitate GHUs to sustain these distributions, activities will focus on **increasing conservation** of PGRFA through improving efficiency and the representation of diversity in collections, and on **increasing use** of PGR through improving search tools, data and access to diversity. Framing both these efforts is the effort to ensure that the CGIAR operates within a positive policy context. The specific outcomes will be:

1. Disease-free, viable, documented germplasm made available
2. More effective access and use of germplasm enabled
3. Supportive policy environment developed
4. Crop diversity conserved in a rational and effective global system

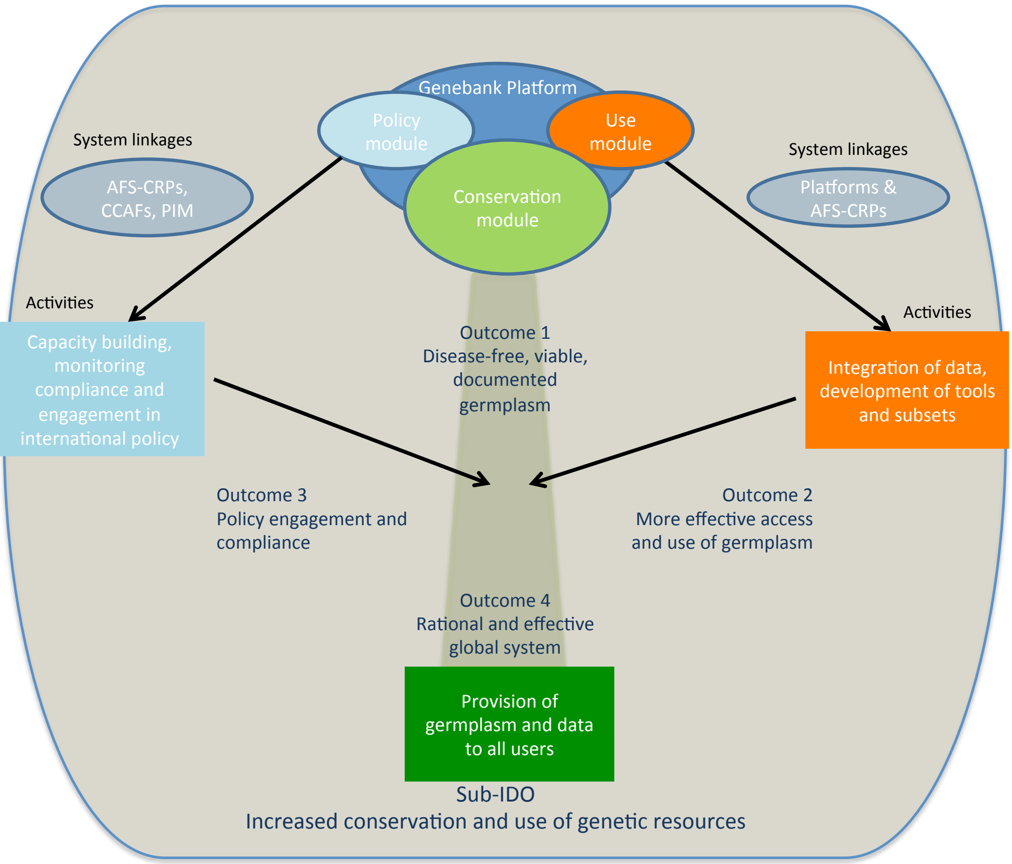

Figure 6. The Platform modules and outcomes are synergistic, leading to increased conservation and use of genetic resources within a rational and effective global system.

These outcomes are illustrated in Figure 6, and within the CGIAR portfolio in Figure 7. The first three outcomes are the result of the work of the three modules: Conservation, Use and Policy. The data, tools and subsets produced by the Use Module provide easier access to the disease-free, viable germplasm of the Conservation Module, and the Policy Module facilitates the delivery of both data and germplasm to the user. All three outcomes are essential to the successful use of germplasm by the AFS-CRPs and contribute to building a stronger global system for conservation and use as a whole.

The role of the Platform is to facilitate and augment these interactions across multiple crops and Centers, and ensure a fulsome collaboration with the Platforms on Genetic Gain and Big Data and the AFS-CRPs, so that the Platform outcomes are attained at scale and result in **Increased Conservation and Use of Genetic Resources** and the achievement of SDG Target 2.5.

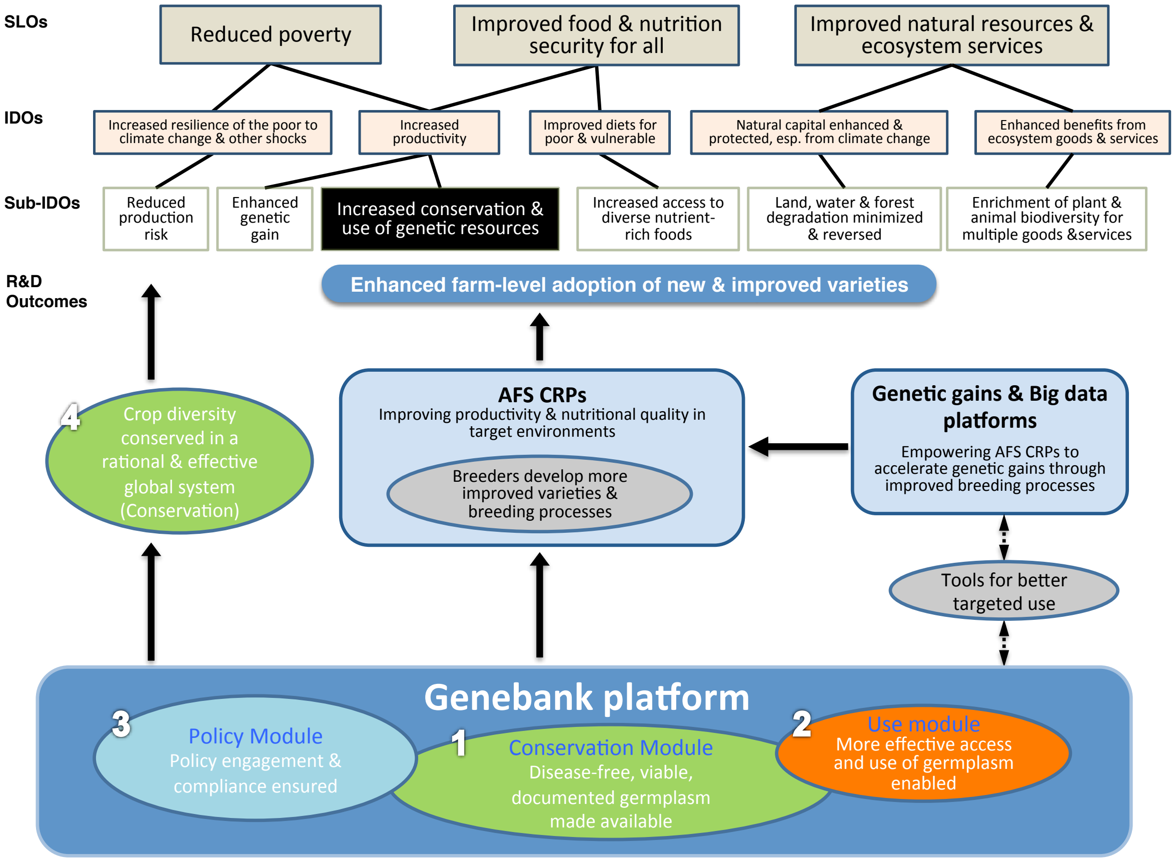

Figure 7. The Genebank Platform provides germplasm, data, knowledge, policy advice and phytosanitary services to the system, and feeds into the generalized theory of change of the AFS CRPs and Platforms.

4. Capacity development

Fundamental to developing a more effective global system of partners contributing on a global level to the conservation and use of genetic resources is the sustaining and augmenting of capacity, both internally and externally to the CGIAR. Capacity development underpins all module activities and is fundamental to the strengthening of genebank operations and efficiency. Given the expertise of genebank staff and the context in which they work, the Platform has the potential to provide large-scale and systematic capacity building worldwide. However, the Platform is conceived primarily as a vehicle to ensure that the core operations and essential activities of the genebanks and GHUs are supported. This is explained further in the section entitled, ‘Expertise and track record’. Therefore, a more systematic approach to capacity development of external partners requires uplift funding. Within the current budget, the Platform will exploit opportunities to strengthen capacity as widely as possible within the framework of project implementation, and by contributing to the wider ranging capacity development efforts of the AFS-CRPs.

The Platform will invest at least 14% of its budget specifically on the capacity strengthening of the genebanks and GHUs. This includes the continued strengthening of QMS for both genebanks and GHUs, upgrading of equipment, storage facilities and data management software, optimization of procedures, development of tools and capacity to associate big data with genebank accessions and activities to develop capacity for policy compliance. QMS provides an important framework by which capacity needs can be assessed and addressed at the level of individual staff as well as at a genebank and institute level. The planned review and validation of standard operating procedures (SOPs) and staff time allocations to specific operations will introduce a means to further monitor capacity and capacity development.

Although these activities generally target internal capacity needs, the regularly organized workshops, open field events and training sessions will be exploited to develop capacity regionally, nationally or locally. The Platform website will also be harnessed as a tool to disseminate protocols, training resources and knowledge related to genebank operations, germplasm health, data management, and policies.

The more experienced and skilled genebank staff will also provide mentoring and backstopping to colleagues and partners alike. Well-documented genebank SOPs have a heightened significance given that staff succession is a key area for strengthening as eight of the 12 current genebank managers and a significant number of national staff, who were recruited 30 or more years ago at the founding of several Center genebanks, will retire in the next six years. Exchanges between such experienced staff and those who are new to the job will be encouraged through GOAL (genebank operations and advance learning) workshops, which bring together national genebank staff to share their expertise and perspectives in implementing and optimizing operations, meeting standards and achieving efficiencies.

5. Platform leadership, management and governance

Platform governance and management is presented in Figure 8. The Executive Board (EB) of the Crop Trust takes the ultimate responsibility for the Platform's governance. The CGIAR representative on the EB will be responsible for ensuring that the opinions of the Systems Board and Office are fully represented. An Independent Advisory Committee (IAC) will be established. The role of this Committee will be to:

- provide external input from key stakeholders, and strategic guidance on major Platform decisions, directions and fund raising;
- facilitate collaboration between genebanks and AFS-CRPs, as well as other key external partners;
- advise on major issues or conflicts between implementing partners or others as needed; and
- advise on specific issues of technical implementation as needed.

The membership of the IAC will comprise: four or more PGRFA conservation and use experts (one of whom should take the role of Chair) drawn from national programs, universities, the private sector or other stakeholders; ex officio delegates, each representing the Centers, AFS-CRPs and Genetic Gain Platform; and the Executive Director of the Crop Trust.

The IAC will have at least one face-to-face meeting per year. Additional expertise or stakeholders may be invited to meetings as required. The Crop Trust will provide the Secretariat. The membership and chair of the IAC will be appointed by the Crop Trust EB, with input from ex officio members.

While Center and genebank management have responsibility for the day-to-day operations of the genebanks, the Platform activities will be implemented under the overall guidance of the Management Team (MT), which has the role to:

- direct funding allocations to collective activities;
- plan and monitor collective activities;
- develop indicators and targets and review progress towards them; and
- provide overall guidance in the management of the Platform and the execution of reviews, meetings and other events.

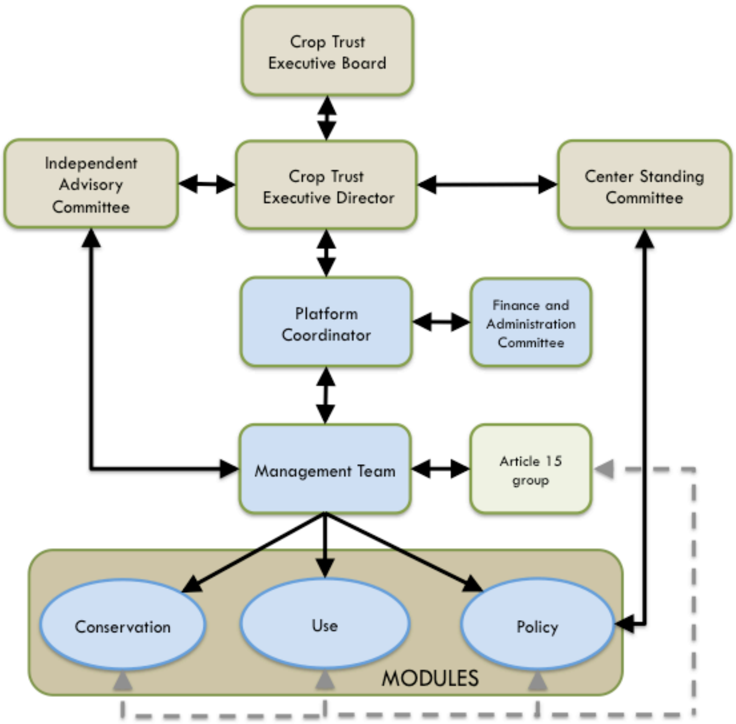

Figure 8. Governance and management structure

The MT comprises the Platform Coordinator, Policy Module coordinator, GHU focal point, Systems Office focal point, Executive Committee of the Article 15 group[14] (A15), and one or two Science Leaders from Platforms or AFS-CRPs. The MT chair will rotate between non-Crop Trust members. It will have monthly virtual meetings, which may extend to include the full group of genebank managers once a quarter. The MT will also meet face-to-face at least twice a year. The agenda and minutes will be shared with all Platform members for comments and input.

The Crop Trust provides an overall coordinating role for the Platform. The Platform Coordinator will oversee the technical and financial management of the Platform as a whole, and coordinate the activities of the Conservation and Use Modules with the guidance of the MT. Annual reporting of genebank and module activities will continue to be submitted in the existing online reporting tool (ORT), monitored by the Platform Coordinator and reported to the Systems Office. A Finance and Administration Committee (FAC) made up of Crop Trust staff will administer contracts and carry out financial monitoring and reporting. They will review the implementation of Financial Guidelines and help develop approaches to a more consistent and fairer allocation of funding across the system.

The Policy Module will be coordinated by Bioversity International with IRRI. While the activities of the PolicyModule will be guided by the MT and come under the same governance as the Platform, official CGIAR positions or decisions will be reviewed and approved by the CGIAR System Standing Committee of Center Directors General.

Each GHU will be subject to individual technical review. The planned reviews for the genebanks will follow a different format from the individual reviews that took place during the CRP, taking a cross-cutting perspective on specific themes such as data quality and management, composition of collections and efficiencies. The independent validation of genebank SOPs will complement these reviews by focusing on individual genebank operations.

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[14] The Article 15 group superseeds the former InterCenter Working Group on Genetic Resources. It comprises the genebank managers of the CGIAR Centers which have designated their collections under Article 15 of the ITPGRFA. Genebank managers from CIMMYT, CIP and IRRI currently make up the Executive Committee.

6.Business case

6.1 Expertise and track record

This proposal builds on the positive outputs and achievements of the SGRP and the Genebank CRP (see Box 3) and has a unique long-term perspective that takes account of the in-perpetuity nature of the work and obligations of the CGIAR genebanks to the global community. As with the current Genebank CRP, the financial underpinning of the Platform proposal is shared between the CGIAR and a growing endowment managed by the Crop Trust (see Annex 2 for projections of the endowment growth). The concepts behind the Platform are based on the "Genebank Options Paper"[15] that was presented to the Fund Council (FC) at their 13th meeting, in April 2015. This proposal corresponds to "Option 2", which was approved for support by the FC. This option covers the core operations of the CGIAR genebanks but has no scope for significant research or capacity building towards development outcomes, which instead should take place within the AFS-CRPs and other Platforms in collaboration with the genebanks. The Genebank Platform expands upon the Genebank CRP by incorporating a new module on policy and activities to strengthen quality management of GHUs. The governance and management will also be strengthened by introducing additional independent oversight, with the aims of managing any potential conflicts of interest, encouraging integration of activities across programs and ensuring that the genebanks are not isolated from the rest of the portfolio. This structure will continue to serve in the longer term, when the endowment is providing the majority of the genebanks' operating funds. The funding of the Platform will be guaranteed, as it has been since 2012, through a special mixed funding mechanism, the details of which are to be determined by the FC in collaboration with the Crop Trust. This *sui generis* approach enables CGIAR Centers to ensure that their formal commitments for the long-term conservation of the collections are not adversely influenced by changing research priorities or financial pressures.

The implementers of the Platform activities are the genebank managers, GHU leaders and their teams, including key specialist staff with expertise in seed longevity, cryopreservation, data management, gap analysis, etc. The Platform will provide a supportive environment for new expertise and fresh faces to lead the genebanks after the retirement of a number of current genebank managers.

The overall coordination of the Platform and specific areas of work (e.g. QMS development, Genesys development) will be managed by the Crop Trust, who have a Science Team with lengthy experience in leading large global PGRFA projects, pulling together international and national institutes from agriculture and conservation domains. The Policy Module will be coordinated by Bioversity International (see Annex 3 for CVs).

The CGIAR and Crop Trust partnership has been highly beneficial to both parties (Box 3). The principles of the Crop Trust's Fund Disbursement strategy are wholly in line with those of CGIAR, striving for science quality, high standards of operation, value for money and a global, rationalized approach to long-term conservation. The Crop Trust has invested heavily in fund raising, improving data management systems such as GRIN-Global and Genesys, partnership with NARS, and collecting and using crop wild relatives (CWR), all of which have contributed synergistically to achieving the objectives of CGIAR genebanks and CRPs. Results of a survey conducted in 2015 of relevant Center staff indicated that 94% of the 36 respondents were satisfied overall with the Crop Trust's implementation of its 'Project Manager' role in the Genebank CRP. The internal audit of the Genebank CRP, which was undertaken on behalf of CGIAR, also highlighted several good financial

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[15] library.cgiar.org/bitstream/handle/10947/3849/CGIAR-Genebanks_OptionsPaper_6April2015_FC13.pdf?sequence=1

and technical practices. The positive reception of the Genebank Options paper at FC13 and the prioritization of genebanks for funding from Window 1 provide welcome signs that the benefits of this productive partnership between the Crop Trust and the CGIAR are widely recognized.

Box 3. Achievements of the Genebank CRP

- Increased availability and security of collections.
- Shared monitoring framework and performance targets.
- Transparent and informative reporting on the status of the collections.
- GRIN-Global (genebank data management software) adopted in three Centers, with a further three in the process.
- Quality Management System tailored to genebanks and implementation of FAO standards.
- Bigger and better Genesys (global portal for accession data).
- Strengthened relationship with key partners (e.g. USDA, EMBRAPA, AVRDC, CGN, MSB, SPC, IPK, etc.) through reviews, meetings and advisory groups.
- Secured annual funding from Window 1.

6.2 Supporting and maintaining access to materials, sites, services and networks

Access to genebank and GHU services, germplasm and data are obligatory as per CGIAR Centers' agreements with the Governing Body of the ITPGRFA. Germplasm and associated data are made available upon signature of the SMTA. The Policy Module will play an important role in ensuring that negotiations to modify the SMTA or conditions surrounding the implementation of the ITPGRFA are positively influenced by the CGIAR and take into account the interests of the genebanks and genebank users. Accessions may be searched for and ordered online through individual genebank websites and through the web portal, Genesys, or by direct requests to genebank staff. Further, the CGIAR genebanks guide on average more than 7000 visitors around their facilities annually.

The genebanks and GHUs provide more than germplasm and data. An overview of the services and expertise that the Genebank Platform provides upon request to users both inside and outside the CGIAR is given in Box 4. The availability of such services will become better known to new users and collaborators through capacity building activities and the Platform website.

The funding available to support some activities (e.g. multiplication of clean seed or clean planting material) on the scale that would ideally be required will be a limiting factor, and strategic approaches will need to be explored (where they do not already exist) to identify partner organizations that are better placed to provide services such as multiplication at a local level. The acquisition policies of the genebanks are also evolving rapidly as the range of genetic stocks expands. In general, the genebanks pursue a rationalized approach to their operations, whereby the most costly genebank activities (e.g. regeneration, cryopreservation) are focused on *in trust*[16] materials that are prioritized for long-term conservation. However, that does not preclude the possibility of the genebanks providing either oversight or the storage conditions for the medium-term conservation of breeders' or researchers' materials, as long as costs are covered where necessary. Each genebank has an acquisition policy that determines the acquisition (or not) and subsequent curation of incoming materials. Where necessary, this policy is being strengthened through QMS and updated in conversation with breeders and researchers.

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[16] The collections that are held *in trust* under Article 15

Box 4. Services and expertise provided by the Genebank Platform

- Provision of germplasm and associated data.
- Health indexing and phytosanitary cleaning of germplasm.
- Advice on selection and use of diversity.
- Taxonomy, identity verification and biogeographic profile of wild and cultivated diversity.
- Provision of germplasm subsets.
- Conservation of breeders' and researchers stocks
- Long-term conservation of safety duplicated materials
- Development of tools to identify germplasm subsets.
- Source of clean planting material for clonal crops.
- Advice on phytosanitary regulations and procedures for the exchange of germplasm.
- Multiplication and processing of clean seed for "orphan" crops and oversight of the distribution of breeders' materials.
- Assessment and development of genebank data management software and tools.
- Evaluation and adoption of GRIN-Global genebank management software.
- Partnership in Genesys for sharing genebank accession data.
- Sharing of QMS standards and practices.
- Training and backstopping in genebank operations (e.g. viability testing, germination, storage conditions).
- Development or optimization of cryopreservation protocols.
- Advice and decision-making tools for operating under applicable legal framework(s).
- Partnership opportunities to influence international policy development processes.

6.3 Interactions between the Platform and users

Primary users within the CGIAR. Researchers and breeders potentially from all CRPs and Platforms within the CGIAR will call upon the Genebank Platform for germplasm, data, associated genebank and GHU services and PGRFA policy advice. More detailed information on the linkages between the Genebank Platform and CRPs, other Platforms and users in general is found in Annex 4. The relationship with primary users has the potential to be highly synergistic in terms of generating data and demand for germplasm. The Platform, especially through the Use Module, will encourage a much stronger engagement with users, and flow of information back to the genebank. Experience has illustrated that this cannot be left to passive or opportunistic collaboration. The genebanks must actively engage with users, on a day-to-day basis, through employing specialist focal points, improving survey tools, and providing incentives, services and in-kind support to leverage improved feedback and data. The new Platform structures of the CGIAR portfolio should facilitate engagement and interoperability among new genotyping, phenotyping, evaluation and research datasets on the one hand and genebank passport data on the other. Formal mechanisms, such as the cross-involvement of scientists in Advisory Groups and a systemwide Community of Practice (CoP) (initiated in 2014 by the Consortium Office) will support stronger planning and integration of research.

Other primary users. Requests for germplasm or support may originate from universities, NARS, advanced research institutes, genebanks, NGOs, farmer groups and the private sector. The genebanks have developed ties with specific communities that have endured for decades. The role of the Platform will be to consolidate and expand these ties to include new users and to encourage a more productive two-way flow of information. As with CGIAR users, the genebanks will leverage feedback and data. Crop User Groups formed through crop conservation strategies may also be deployed to encourage the generation and sharing of evaluation and other data within communities of crop researchers. The Platform is also developing a communication strategy based on a website and newsletter that will provide news updates, tools and information with the aim of encouraging awareness of the collections and building capacity.

Other key institutions: national genebanks and other research partners. CGIAR has strong partnerships with key national institutions, which together form the global system. While numerous institutes are considered to be crucial by individual genebanks, a small subset of these organizations play a particularly significant role across the system because of the size or complementarity of their collections. These include EMBRAPA, USDA, CGN, AVRDC, IPK, FAO, NBPGR, RDA and MSB. Reviewers, expertise and partnership are regularly sourced from such institutions. On a regional level, genebanks regularly engage with national institutes through partnership in projects, participation in meetings, and in training. Communities that have been brought together to develop global conservation strategies for individual crops will continue to be engaged or re-engaged, either informally or through more formal Crop User Groups, depending on the role and existence of other crop-based networks. These communities will aim to drive the implementation of priority conservation actions, rationalization of efforts and strengthening of complementary roles and responsibilities. Efforts to genotype collections or analyze diversity will incorporate major collections held by national partners, where possible, so as to ensure that studies take a global and not just a CGIAR perspective.

6.4 Intellectual asset management

The Platform's management of genetic resources will comply with the CGIAR Principles on the Management of Intellectual Assets (IA) in general, and Article 4.2 in particular. Following the agreements under Article 15 of the ITPGRFA, the CGIAR genebanks will make germplasm available to recipients using the SMTA. CGIAR may also use the SMTA to transfer improved germplasm that incorporates materials received from the Multilateral System of the ITPGRFA (defined as 'PGRFA under Development'). In these cases, conditions may be added, as permitted under the SMTA and Section 6 of the CGIAR Principles on the Management of Intellectual Assets, which establishes the conditions under which CGIAR may enter into 'limited exclusivity' or 'restrictive use' agreements. (See Annex 5a for more details).

All CGIAR genebanks will continue to make their data publicly available and searchable, as part of the strategy to promote more effective use. Research papers, policy briefs, conservation protocols, training materials, and written submissions to international policy fora, will be made public through the Platforms' own website or publication in open access journals. Software and web tools will be made available under open access licenses.
Each Center will enlist its IP Focal Point to make plans for, and monitor, its IA management practices under the Genebank Platform, with general oversight from the Platform IAC. Full compliance with the CGIAR IA principles and its commitments pursuant to the 2006 agreements with the Governing Body will be included in partnership contracts under this Platform.

6.5 Open access management

The platform will ensure that all of its information products are made publicly available in conformity with the CGIAR Open Access and Data Management Policy (OA Policy) and also with the expectations under the ITPGRFA (Articles 13.2.a & 17; SMTA 6.9) that non-confidential information about materials in the Multilateral System will be made available through a global information system.

All CGIAR genebanks make their data publicly available and searchable, as part of the strategy to promote more effective use. Genesys provides a common portal for access to information on all CGIAR accessions and is recognized as an element of the ITPGRFA's GLIS. It collates data from international and national genebanks into a searchable public database under a signed agreement with each data provider, which states that providers should only provide data that can be made publicly available. Genesys is being managed and developed by the Crop Trust under the guidance of an Advisory Committee. The Conservation and Use Modules will contribute to the enhanced functioning of Genesys, and develop new tools and methods for sharing, associating, and harvesting accession level data. Data collected as part of policy-linked research (for example, trends in Centers' and partners' acquisitions, distributions and uses of PGR, data, or traditional knowledge under different policy regimes) will be made available in conformance with the OA Policy. Through IRRI, the CGIAR is also taking a leading role in the further development of GLIS to facilitate data sharing through interoperable systems and thus promote broader open data access. Enhancements to Genesys will focus on interoperability.

IP Focal Points of participating Centers will assist in planning, monitoring, and reporting their Centers' OA practices under the Platform and the IAC will assume ultimate responsibility for ensuring the Platform complies with OA Policy and ITPGRFA-related expectations.
More details may be found in Annex 5b.

6.6 Communication strategy

A communication strategy is being developed to help the Platform improve the understanding of the importance of the PGR conservation in genebanks, the efficiency of genebank operations, the use made of genebank material by researchers, and the policies that apply to the acquisition, use and distribution of germplasm. Outreach to the audiences that help fulfil the objectives of the Platform (i.e. plant breeders and evaluation specialists, other research scientists and people in interested organizations) will be the primary thrust of Platform communications.

The main channel for external communications is a Platform website that is currently under development. The website will offer access to: (1) accurate, detailed information on the operations and policies of genebanks and GHUs, including SOPs, annual reports and review results; (2) the conservation of specific crops; (3) Genesys and other relevant databases; (4) publications and capacity building resources; (5) relevant news. A newsletter will also be published and emailed regularly to stakeholders. The newsletter will not contain detailed technical information, but will offer a series of signposts to materials available through the Platform website (and possibly elsewhere).

6.7 Risk management

The operations of a genebank, although relatively routine in that the same activities must be repeated yearly, are actually very susceptible to changes due to a number of major influences. These include:

- unpredictable trends in demand for material;
- serendipitous acquisition of materials (e.g. from projects, institutions or other genebanks);
- fluctuations in costs due to periodic staff cost adjustments and changes in institutional charges and costs;
- ineffective, aging or failing facilities and equipment; or
- unexpected natural and man-made disasters.

During the past five years, every one of these types of events has occurred and affected the functioning of the CGIAR genebanks. Risk management strategies are developed by each genebank and are currently being strengthened through the work on QMS. They are not elaborated here but will be made available through the Platform website.

The fallout from recent budget cuts in other programs included the loss of operating funds and staff for the genebanks, even though there had been no budget cut to the genebanks *per se*. The Crop Trust is working with the Center Finance Directors to build more consistency and fairness in the attribution of costs to the genebanks. However, the genebanks represent a relatively small component of annual expenditures of the Centers, and are expected to conform to the same financial conditions as the other programs. A small group of Finance Directors are tasked to find ways of achieving more consistency in the application of financial guidelines at a system level, but this initiative will need continued high-level support and facilitation.

CGIAR has provided contingency funding (USD 1.6 million) for the relocation of the ICARDA genebank to Lebanon and Morocco during the past three years. The proposed Platform budget would not be able to support such an event, should one occur again. The relocation of the Africa Rice genebank from Benin to Cote D'Ivoire, the development of a new curation strategy for ICRAF's 38 field collections, the building of a new genebank at CIAT and the development of ICRISAT's three African collections: all these may have financial implications that are outside the boundaries of the proposed budget.

The GHUs provide a service not only for the genebanks but also for the AFS-CRPs. A recent informal survey suggested that nine of the GHUs have insufficient budgets to cover costs and that only three receive funds from AFS-CRPs for their services. If costs are not properly covered it is likely that the intended objectives to upgrade GHU facilities and equipment, and to strengthen capacity and quality management, will not be met. This is something that must be addressed at an institutional level for each GHU.

Finally, the time required to build the endowment to its planned target (see Annex 2) remains unpredictable. The Pledging Conference takes place on 15 April 2016, after which the projections for the Genebank Platform budget will be re-assessed in time for the final July 2016 Platform proposal submission.

6.8 Budget and budget breakdown

Conservation Module A very large proportion (83%) of the total budget is made up of the core genebank requirements for operations and upgrading. This represents the part of the budget that will be increasingly supported by the endowment. Costs for each collection are based on the 2010 Costing Study[17], modified according to reported expenditures between 2012 and 2015. Upgrading costs are determined through an analysis of equipment and its serviceable age, and based on needs for known activities (e.g. cryopreservation, seed increase, phytosanitation and health testing), to reach agreed performance targets. Overall costs are projected to decline over the years, as the genebanks reach targets and efficiencies are made.

Funds for conservation research are allocated to leading Centers to retain or hire specialists, who will work with other Centers to research seed longevity in target crops. IRRI will be one of these Centers because of its existing expertise, and the other two will be selected according to defined priorities, which will include a focus on the more expensive seed crops to conserve, such as crop wild relatives and forages. ICARDA and CIAT both have strong expertise in Geographical Information System (GIS)-based diversity analyses and together will lead a global gap analysis for priority setting of targeted collecting in partnership with NARS. Funds for collecting projects will be allocated according to identified priorities. Uplift funds are pegged to the Conservation Module, but are relevant to the entire Platform.

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[17] library.cgiar.org/bitstream/handle/10947/2566/fc4_funding_proposal_CGIAR_Genebanks.pdf?sequence=1

Use Module Funds will be provided to develop the Genesys database software, partner linkages and search tools, and to support each genebank to obtain and manage available evaluation and genotyping datasets so that they are directly linked to genebank databases. A phased approach will be adopted whereby Bioversity, CIMMYT, CIP, CIAT and IRRI will initiate efforts to develop mechanisms and approaches for associating additional data with existing accession passport data over a two-year period, after which all other Centers will be supported to carry out similar work built upon the lessons learned from these initial experiences. Individual Centers, which manage crop collections that are currently not the focus of AFS-CRP activities, will receive limited funding to carry out characterization or data enrichment specifically on these collections.

Policy Module The budget is dedicated to the management of the policy coordinating unit and its activities. Funds will cover the costs of: bringing together the requisite people within CGIAR to build consensus, raise awareness and strengthen capacity; engagement in international meetings; meetings of the Multi-stakeholder PGR Policy Group; supporting participation of CGIAR scientists in policy dialogues; and developing and disseminating research outputs, policy briefs, guides, decision making tools, etc. The budget will cover scientific and administrative staff time and expert consultations.

Management Costs These include the costs of Crop Trust staff to administer the agreements, contracts and disbursements relating to the Platform. These funds also cover the indirect costs of the Crop Trust.

7. Conservation Module: support and improve essential genebank operations

7.1 Rationale and scope

The Conservation Module, first and foremost, supports the core genebank operations, the minimum activities that must be undertaken by the genebanks without which the fundamental security of the collections and their use are at serious risk. However, the aims of the Platform are to increase conservation whilst controlling costs. The Module, therefore, will have a major thrust in improving the long-term sustainability and efficiency of the genebanks and, where possible, the global system as a whole, while strategically increasing the representation of crop gene pools in *ex situ* conservation.

Four key performance targets concerning the availability, security, documentation and quality management of the collections were agreed in 2013 (Table 1). All Centers are now working towards these targets, and through continued support all (except CIP) aim to reach them by the end of 2022.

GHUs are required to adhere to similar high standards of operation as the genebanks. CIP and CIMMYT have pursued ISO 17025 accreditation. However, for several Centers and crops (e.g. IITA, ILRI, ICRAF, CIP), more work is needed to establish routine phytosanitary diagnostics, and to build capacity to accelerate the rate of germplasm indexing and phytosanitary cleaning. The GHUs will work towards externally validated QMS, adopting a similar approach as the genebanks.

Genebank efficiencies will be pursued on several levels, including in data management, routine operations, rationalization across same-crop collections within the global system, and cost-analysis. Activities will focus on improving the quality of data resources and developing or adopting software and tools to support increased efficiency of workflows, implementation of digital labeling and use of more automated processes from field to store. Today, at least six Centers (CIP, CIMMYT, CIAT, ILRI, ICRISAT and IITA) are adopting GRIN-Global as their primary system for genebank data management. This provides an opportunity for increased integration and standardization of data across the system. IRRI and CIMMYT will focus on achieving efficiencies by harmonizing data and systems across the genebank-breeder continuum.

Table 1. Key performance indicators

Indicators		Targets
1	% collection which is clean of pathogens of quarantine risk, viable, and in sufficient quantity to be immediately available for international distribution from medium-term storage (or local distribution for some tree spp.).	Availability 90% accessions
2	For seed crops: % collection held in long-term storage at two locations and also in Svalbard Global Seed Vault (except for tree spp.). For clonal crops: % of the collection held in long-term storage or cryopreservation at two locations; % of the collection held in slow growth conditions *in vitro* at two locations.	Security 90% accessions in seed collections, >50% accessions in cryopreservation OR intermediate target 90% accessions duplicated in *in vitro*
3	% collection with minimum passport and/or characterization data online	Data availability 90% accessions in the collection
4	Quality Management System	QMS Agreed elements of QMS/ISO are in place.

Understanding the specific factors that affect seed longevity, and improving long-term storage, is critical to improving efficiency. Optimized procedures and improved drying and storage conditions have the potential to increase the longevity of germplasm in storage by decades, and to have a substantial impact on management costs. Building large-scale cryobanks of expensive-to-maintain clonal crop collections also presents a tremendous opportunity to improve the security of the collections, rationalize *in vitro* and field collections and eliminate the need for continuous re-culturing of *in vitro* samples for safety duplication. Other efficiencies and cost-savings will be highlighted through the review and validation of individual genebanks' QMS and through ongoing cost analysis.

Genotyping of the whole or large parts of a collection promises a new level of quality and genetic integrity control. Molecular markers and sequence data can be effectively used for accession identification during acquisition, regeneration and multiplication, elimination of duplicates, clarification of taxonomic relationships and ploidy levels, and the stratification of collections according to genetic relationships and gene pools. The genotyping of materials coming into the clonal crop collections is already becoming routine and plays a major role in limiting acquisition to only unique accessions. The funding is not available in this Platform to carry out systematic genotyping of entire collections. However, the genebanks will benefit from such initiatives instigated by the Genetic Gains Platform and the AFS-CRPs, and uplift funds will be sought to strategically expand genotyping efforts to core collections and other important subsets.

Genotyping also feeds into the analysis of diversity within CGIAR genebanks and within the global system as a whole. Where possible, the Module will link genotyping efforts of major collections within the global system to diversity and gap analyses. Collecting activities will be prioritized in collaboration with NARS partners, and multi-crop collecting missions will be implemented through a global GIS-based analysis undertaken with NARS partners. Responsibility for seed longevity research, GRIN-Global development, and research on phytosanitary diagnostics will be devolved to specific Centers or partners with expertise to undertake research on behalf of the Platform.

7.2 Objectives and targets

The activities of the Conservation Module (Table 2) contribute to all four Platform outcomes but most particularly to the first and fourth:

1. **Disease-free, viable, documented germplasm made available**
2. More effective access and use of germplasm enabled
3. Policy engagement and compliance ensured
4. **Crop diversity conserved in a rational and effective global system**

Objective 1.1: To sustain core genebank operations and ensure germplasm is secure and available

Activity 1.1.1 Managing the genebank: germplasm processing, testing, storage, data management, regeneration, safety duplication

Activities cover: accession or sample registration; phytosanitary cleaning and processing; storage in seed, field, in vitro and cryobanks, and safety backup; viability monitoring; regeneration and multiplication; and basic characterization. These activities are driven by the rate of distribution from the collection (1.1.2) and by the degree to which historic and new incoming accessions have been fully tested, processed and safety duplicated. The genebanks are aiming for targets of 90% availability and safety duplication by 2021.

All activities generate a large amount of information that is used for decision-making and improving operations, which requires specialized database systems to manage and query data. Collective development of GRIN-Global will enable the sharing of solutions to bugs and issues, joint backstopping and software improvements across multiple Centers. It will also facilitate the integration of data for analysis or access across Centers.

Activity 1.1.2 Health testing and distributing germplasm

Centers are committed to distribution of disease-free, highly viable and well-documented germplasm in response to requests for use in research, breeding and training in food and agriculture under their agreements with the ITPGRFA. Testing and cleaning accessions that are currently not safe to distribute will be a priority, affecting mainly clonal but also some seed collections. The changing prevalence and spread of pests and diseases influences the need for phytosanitary controls.

Objective 1.2 To improve genebank operations and management

Activity 1.2.1 Quality management and upgrading

Most genebanks will have put in place minimum elements of a QMS by 2017. The next phase of QMS development involves independent validation of SOPs, and the development of new SOPs on phytosanitary processes, information management, and other operations. In addition, genebanks will focus on testing and calibrating equipment and replacing those that have passed their serviceable age and capacity.

Activity 1.2.2 Researching conservation methods

Monitoring the viability of seeds in storage is costly in staff time and the seeds themselves. Most genebanks err on the side of caution, and follow strictly a regime of monitoring every 5 or 10 years. With leadership from IRRI, the genebanks will explore a variety of improved approaches to assess viability, including automation of germination tests and non-destructive methods, and develop better models to predict longevity at the crop, accession, and seed lot level. There will be a particular focus on wild species and crops such as forages, which are highly demanding in terms of regeneration and viability testing. This research will contribute to optimizing and customizing the quantity of seeds to store per accession, and estimating optimal viability monitoring intervals.

Genebanks managing clonal crop collections will continue to systematically cryobank their collections and develop the QMS framework within which they operate.

Activity 1.2.3 Analysing costs and building efficiencies

The individual genebanks' costs to maintain diversity are based on an economic study and costing tool developed in GPG2 (a World Bank-funded project coordinated by Bioversity). The tool will be refined to improve consistency of cost estimates across Centers and used to review and revise current cost estimates. In parallel, a task force of Finance Directors is addressing the need to harmonize the implementation of CGIAR Financial Guidelines. Through building QMS, optimizing processes and comparing the staff needs and costs of individual operations within genebanks holding similar crop types, potential efficiencies will be highlighted and addressed. Bringing all these elements together, the genebanks will be enabled to control costs or redirect resources more efficiently.

Table 2. Activities, outputs and targets of the Conservation Module

Activities	**Strategic Relevance**	**Outputs**	**Indicators and Targets**	**Assumptions**
Objective 1.1: To sustain core genebank operations and ensure germplasm is secure and available				
1.1.1 Managing the genebank: seed processing, testing, storage, data management, regeneration, safety duplication	CGIAR obligations to the ITPGRFA to conserve and make available germplasm from in trust collections are fulfilled	Representative, documented, available and secure germplasm in 35 crop collections	90% of collections conserved, documented and available	Increasing institutional and other costs can be managed so that genebanks receive sufficient operating funds from fixed budgets.
1.1.2 Health testing and distributing germplasm		Disease-free germplasm distributed upon request	80% relevant requests serviced by global system. Customer satisfaction of 80% or higher	The costs of GHUs are fully covered in service charges. Investment is made in developing protocols to test for new diseases.
1.2.1 Quality management and upgrading	High standard of operation and quality management clearly illustrated	SOPs validated and improved for activities including germplasm health in 11 genebanks	50 SOPs and other minimum QMS elements (e.g. risk management, staff succession, barcoding) in place and validated. Equipment is up-to-date and calibrated.	Appropriate level of investment in CGIAR infrastructure. Quality management results in improved management.
1.2.2 Researching conservation methods	Sustainability of operations improved as materials are able to be kept for longer in storage	Step change increase in length of time germplasm may be stored	Storage periods redefined in at least 10 crops	Existing technologies only require optimization to obtain improvements

Table 2. Activities, outputs and targets of the Conservation Module

Activities	Strategic Relevance	Outputs	Indicators and Targets	Assumptions
1.2.3 Analysing costs and building efficiencies	Long-term sustainability of the genebanks is facilitated	Transparent and comparable genebank operations and costs by crop group	Annual increase in cost of core operation less than inflation	Institutional support is provided to build fairer and more consistent application of CGIAR Financial Guidelines across the System.
1.2.4 Improving representation: analysing diversity, identifying gaps, eliminating duplicates and collecting	Increased conservation globally	Representation of genetic, taxonomic, geographical and environmental diversity and traits improved	Representation of crop genepools in *ex situ* conservation quantified Gaps in at least 5 crop genepools addressed	Users provide information on needs and AFS partners provide information on traits. Collecting of threatened and unique germplasm is politically and physically possible
1.2.5 Strengthening capacity in germplasm health management and conservation	Global system for conservation and use of PGRFA is strengthened	Improved capacity in NARS and closer partnership with genebanks	Increase in exchange of germplasm between NARS and CGIAR	NARS have the capacity to comply with international policies on germplasm exchange.

Activity 1.2.4 Improving representation: analyzing diversity, identifying gaps, eliminating duplicates and collecting

Linking with the Use Module, activities will utilize available phenotypic and genomic information generated on an accession level to identify duplicates. This information will also be applied, together with other genebank data, in a global analysis to assess the diversity in collections, and the geographical, taxonomic, trait and genetic gaps in the collection, to be filled through collecting or complementary conservation strategies. CIAT and ICARDA will carry out the analyses using GIS-based tools to identify collecting priorities with a focus on threatened germplasm. Multi-crop collecting missions will be carried out in partnership with national organizations.

Activity 1.2.5 Strengthening capacity in germplasm health management and conservation protocols
Key national genebanks will be identified for partnership by each CGIAR genebank and GHU in collaboration with AFS-CRPs. The planning and scheduling of capacity building events across the year will be shared so that at least 20 key partners will be involved in training and workshops per year. Current systems of internships, exchanges and training courses will be shared and built upon so that resources are pooled and specific expertise is shared across Centers.

7.3 Science quality

Maintaining the genetic integrity of thousands of unique accessions and providing the right accession when requested, demands quality of science and quality of service. After a broad consultative process mediated by FAO, international standards for genebank management were developed and published in 1994, and updated standards published in 2014 (FAO 2014). The CGIAR genebanks have been foremost in implementing these standards. The FAO standards give guidance on the various conditions in which the accessions are managed (e.g. temperature and relative humidity in storage). In the course of the Genebank CRP further targets were agreed by the Centers to ensure that collections are available and secure (Table 1). These high standards are appropriate to the standing of the CGIAR in the global system and their role in safeguarding and making available crop diversity.

A further major advance was achieved, as part of the Genebank CRP, through the establishment of a formal QMS in each genebank. Firstly, the QMS ensures that SOPs are documented in detail. SOPs incorporate numerous essential elements of genebank management, including health and safety measures for staff (exceptionally important in the case of working with liquid nitrogen), risk management, access control, and institutional and genebank policies. In this way, the QMS helps to generate increased transparency and confidence, for the benefit of donors, partners and users. The minimum elements of QMS, which are being put into place in the current CRP, will be validated and reviewed through independent auditing. Additional SOPs will be documented for phytosanitary processes, equipment maintenance and calibration, information management, identity authentication and measuring user satisfaction.

Interactions with centers of excellence and experts in areas such as seed longevity, germplasm health, database management, and communications and knowledge sharing will help ensure that up-to-date science is applied in genebank management and used as the basis for improvements in operations and rationalization of activities. Ultimately, the feedback from genebank users provides the strongest indication of the quality of the genebanks' work. Every genebank will have a process to garner user feedback as part of their QMS, and levels of satisfaction will be monitored annually. The Platform Coordinator, MT and expert leadership in Centers will review each genebank's status with regard to performance targets annually.

7.4 System linkages

Linkages of the Genebanks platform with the Genetic Gains and Big Data Platforms and AFS-CRPs are illustrated in Figure 9. The Conservation Module will support these linkages through the provision of germplasm and information on accessions within the collections upon the request and collaboration of users within the AFS-CRPs, Platforms and other CRPs. This flow of germplasm and data must be better matched with the feedback of research results and information from the CRPs to the genebanks. Through the tools, processes and alliances generated by the Use Module, these new data will be associated with accession data already in genebank databases and Genesys to add value to the collections, and facilitate their further, future use. These data also have a catalytic role to play in enhancing genebank management. A key partner here is the Genetic Gain Platform, given its role to broker genotyping and phenotyping services across CRPs. Making a dramatic improvement in genetic integrity and quality control requires genotyping, which will be generated most effectively through coordination with the Genetic Gains Platform Module 3 (Genotyping Services). Efficiencies also require investment in automation and mechanization of seed processing and accession phenotyping, which should be coordinated with Module 4 (phenotyping / automation / mechanization).

Other forms of linkage occur in the provision of all the services listed above to AFS-CRPs and other users. It is important to note that the GHUs provide phytosanitary testing and cleaning services both to the genebanks and the AFS-CRPS. Also, clonal crop collections, as sometimes the only source of disease-free material, may have a special function of providing clean source material directly to seed systems.

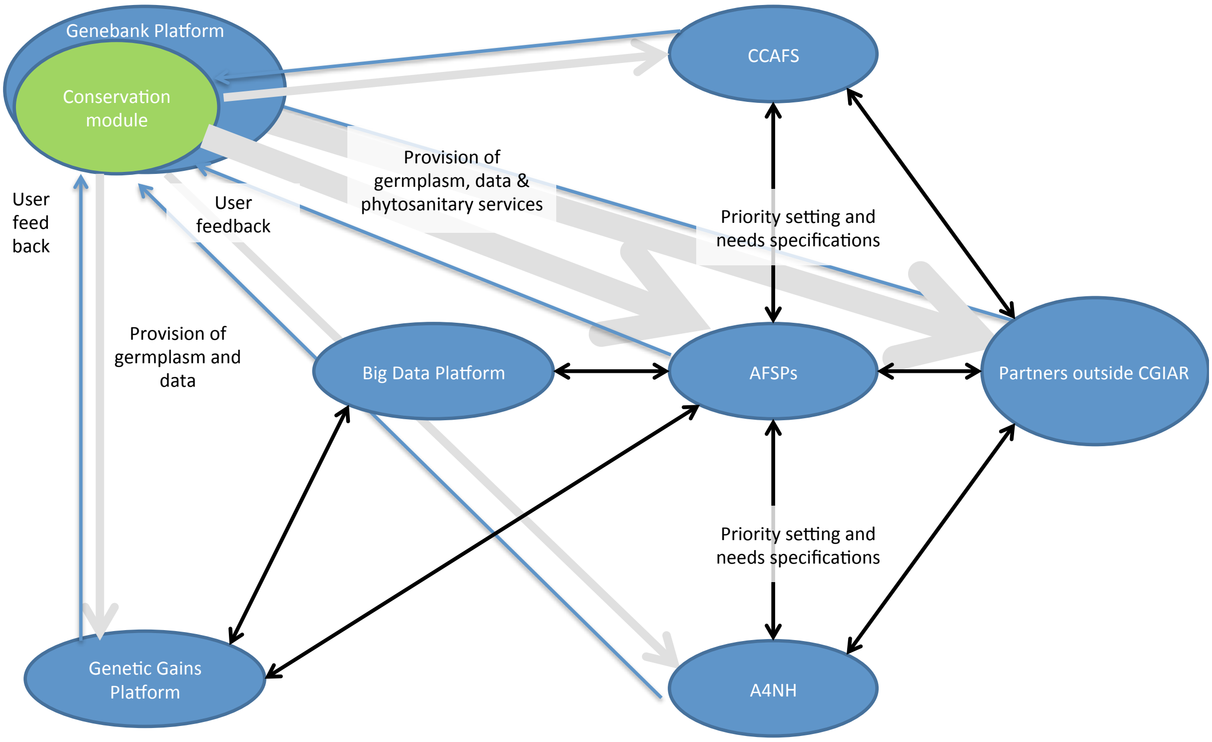

Figure 9. Primary linkages with the Conservation Module within the CGIAR portfolio

To strengthen the global system on conservation and use, the Module will link with key national genebanks and other institutes through training, information exchanges and partnerships in selected activities. The conservation and use practitioners of individual crops will be brought together through formal mechanisms such as crop user groups, or informally as appropriate, to revisit priorities and implement global conservation strategies. The strategies will also be improved to ensure better coordination and sharing of crop-based activities and rationalization among collections at national, regional and global levels.

7.5 Climate change

A key component of successful adaptation to climate change is the development of more resilient varieties able to yield well under future climatic conditions, with resistance to new pests and diseases. More than just a one-off process, the need is for a pipeline enabling broad, continual adaptation to unpredictable changes. The portfolio of varieties and crops deployed on farm must be backed-up by a reservoir of diversity maintained *ex situ,* and be linked to a process for rapidly incorporating *ex situ* diversity into new climate-smart genepools. The genebanks will provide the reservoir of *ex situ* diversity. Improved and efficient conservation and documentation of germplasm will ensure that the materials with traits essential for climate change mitigation and adaptation are available. Investment in upgrading GHUs and research into new diagnostics will also allow CGIAR to respond to a changing prevalence and virulence of pests and diseases related to climate change.

Land use change, urbanization, population growth and development have taken their toll on genetic diversity available in farmers' fields and natural habitats. Many of the accessions held in the CGIAR genebanks are no longer available on farms and in natural habitats *in situ*. By focusing attention, resources and partnership on assessing gaps in collections, the CGIAR will target collecting efforts to ensure that representation of diversity in the collections is increased.

Climate change also affects genebank operations. Rising temperatures and changing rainfall affects drying and storage conditions, the performance of facilities and equipment and the harvest of high quality seed for long-term storage. Genebank procedures ensure an adequate level of safety duplication to avoid accession loss and the SGSV provides a backup of the collections. With uplift funding, the genebanks may improve the sustainability of their facilities and equipment through a specialist assessment of energy efficiency. Solar panels have been installed at CIMMYT and are saving annual costs of around USD 50,000. Customized energy saving technologies may be installed at other genebanks.

7.6 Capacity development

In the course of the current CRP, external reviews and strengthening of QMS, together with a preliminary assessement of staff time allocations to genebank operations, have helped identify priority capacity needs in each Center. The Module will address individual genebanks needs while continuing to nurture cross-Center mentoring and fertilization of ideas to improve operations and efficiencies. These exchanges will extend to partners and, where appropriate, develop into CoPs.

Special attention will be given to strengthening capacity in areas that address recurrent constraints to achieving Platform outcomes. In particular, the Conservation Model will address the following target areas:

- **Compliance and implementation of phytosanitary procedures**: Targeting specific countries and regions, the Module will extend training and capacity building in phytosanitary procedures, QMS and optimization and development of diagnostics to national or regional plant protection organizations.
- **Development and sharing of data management standards and tools:** The adoption and development of GRIN-Global within CGIAR benefits from adoption and development by other major national genebanks in the global system, not least USDA, who originally designed and developed the software. CGIAR will play a role in aiding further adoption by national programs and strengthening the CoP, a major step towards wider harmonization of data and data standards and increased capacity in data management across the global system.
- **Activities to strengthen partnership for collecting:** In developing partnerships for joint collecting missions, the genebanks will build projects that will address individual capacity needs of target partners so that the diversity collected may be conserved both in-country and within the international collections.

7.7 Intellectual assets and open access management

See Sections 6.4 and 6.5.

7.8 Module management

Recognizing that the leadership and implementation of the conservation activities will remain with individual genebanks, the activities of this Module will be coordinated by the Platform Coordinator. The MT will provide oversight and guidance on fund allocation and management to ensure activities reach performance targets and outputs are achieved.

Monitoring and evaluation will be carried out on a continued basis by the Platform Coordinator and through the review of annual reports in the ORT. The audit of QMS will be a core component contributing independent validation of the genebank status and standards of operation. This will be supported by thematic review across or within crop groups, concerning the following areas: data management tools, data quality and availability, representativeness of diversity within the collections and efficiency of operations, rationalization of activities and value for money.

8. Use Module: Empowering effective use of genetic resources

8.1 Rationale and scope

The CGIAR crop improvement programs need to increase the rate of genetic gain to 2% a year, as a vital component of achieving the SLOs to reduce poverty and improve food and nutrition security for human health. Many factors potentially limit the rate of genetic gain: inadequate throughput capacity for phenotyping; evaluation in inappropriate and changing environments; inability to measure precisely the trait(s) required; inadequate knowledge of the genetic control of the trait; inadequate incorporation of genetic knowledge into breeding; inefficient organization of breeding logistics; and insufficient genetic variance.

The challenge addressed by the Use Module is to contribute to increased rates of genetic gain through more effective access and targeted use of genetic materials that better meet the needs of the AFS-CRPs. This does not necessarily mean increasing the total number of accessions delivered, but rather enabling smarter and facilitated use of, and choices in, the germplasm conserved in the genebanks. Activities fall into two key interacting areas: (1) developing, organizing, and facilitating access to, the tools and information resources required to target and deliver the accessions most likely to meet the needs of the AFS-CRPs; and (2) working with the AFS-CRPs and the Genetic Gains and Big Data Platforms to ensure that there are no gaps, no duplication of efforts, and an integrated approach that ensures a seamless connection from genebank to users, be they breeders or other researchers. The interactions between the Use Module and the AFS-CRPs, including those facilitated through the Genetic Gains Platform, are illustrated in Figure 10.

Choosing the accessions that are most likely to contain the variants needed by breeders has always been, and remains, the biggest challenge facing genebanks and their users. Often, it has not been possible to do any better than choosing a random subset. Breeders then have to screen a very large number of accessions to find the right one. If, because their priority traits are difficult, slow or expensive to screen, they simply cannot screen a sufficiently large number of accessions, they are likely to fail in their search. Even where large-scale screening of accessions is possible, it may be ineffective, as the expression of favorable alleles for a trait may be masked by a genetic background, which means that such alleles remain hidden until transferred to a different genetic background.

Overcoming this requires a range of activities. Genebank staff routinely document data on the origins of their accessions and make the data publicly available through databases such as Genesys. Where the latitude and longitude of the original collecting site is known, spatial analysis may be used to make better predictions of which accessions are likely to contain alleles for adaptation to various stresses, including those associated with climate change. This is an approach that has been championed by ICARDA in the past several years under the name FIGS (Focused Identification of Germplasm Strategy), and the Use Module will mainstream this and other methods for forming germplasm subsets, for all genebanks and their users.

Genebank staff also routinely score traits that have high heritability and low genetic by environment (G×E) interaction, and that are easy to measure and record ("characterization data"), and also make these data available through public databases. To address the cases where these data are relevant to the needs of breeders, Genesys will be enhanced to enable user-friendly querying and selection of high-value subsets based on phenotypic data.

However, data that is most relevant to germplasm use are collected by the users of genebank accessions. These include phenotypic data on traits of agronomic importance, expression and "omics" data, genotypic data (increasingly sequence data), estimates of breeding values, and pedigrees. Together, they form a massive resource that could facilitate better-targeted use, although to date they have been underused, because they have not been available to the genebanks and are not always tied to accessions. The Genetic Gains Platform is planning to develop interoperable, distributed data systems to facilitate data sharing among partnerships for faster genetic gain. With relatively small additional investment, and working closely with the Genetic Gains Platform and breeders, the Use Module will develop additional tools that will enable genebanks to piggyback on these data sharing mechanisms in order to mine the data collected by recipients and users of genebank accessions. The additional data will be used to design improved high-value subsets, such as core collections, mini-cores, FIGS and trait-specific subsets, and to make better-tailored selections in response to each individual request and need.

Although the focus of Use Module is on the enhanced and facilitated use of *ex situ* crop genetic resources by the AFS-CRPs, the resulting tools and services will also help address the needs of other users outside the framework of the AFS-CRPs. This includes breeders, researchers, farmers and others, and also includes the orphan crops that are conserved in CGIAR genebanks but not addressed in any AFS-CRP. Also included are users whose focus is to enhance the conservation and use of genetic diversity *in situ,* to address the SLO of improving natural resource systems and ecosystem services.

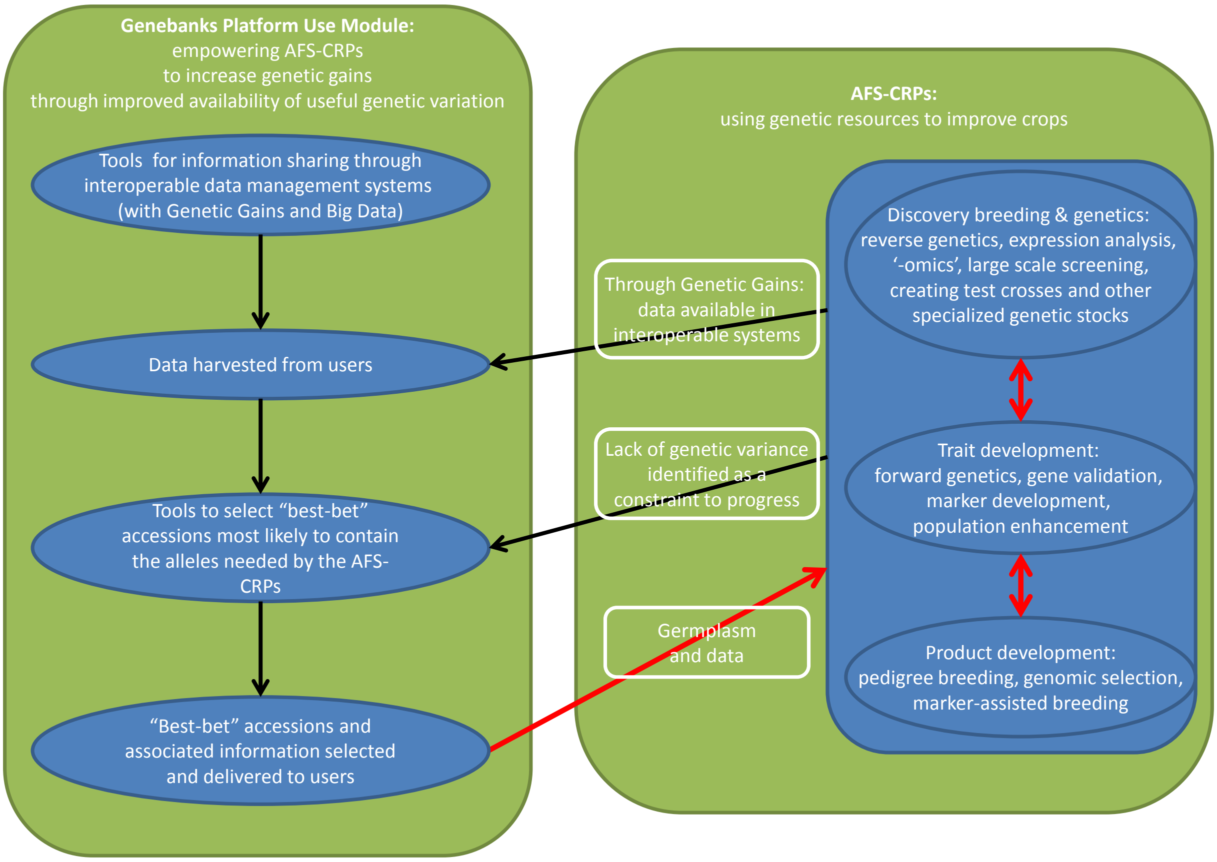

Figure 10. Interactions between the AFS-CRPs and the Use Module of the Genebank Platform required to enable the AFS-CRPs and other users to make more effective use of genetic diversity conserved in the genebanks.

8.2 Objectives and targets

The activities of the Use Module (Table 3) contribute to all four Platform outcomes, but most particularly to the second outcome, focusing on the way genebank collections are accessed and used:

1. Disease-free, viable, documented germplasm made available
2. **More effective access and use of germplasm enabled**
3. Policy engagement and compliance ensured
4. Crop diversity conserved in a rational and effective global system

Activity 2.1.1 Promote information integration between genebanks and breeding programs

In the past, there has been little incentive for real-time integration of data between (pre)breeding efforts and genebanks. With advances in breeding technologies, and an increased reliance on specialist partnerships, AFS-CRPs are better poised to share data among collaborators. The Genetic Gains and Big Data Platforms will work with the AFS-CRPs to develop standards and tools enabling interoperability among genebanks and breeders' databases. This will provide genebanks with unprecedented opportunities to link data collected by users back to genebank accessions and increase the value of the collections.

As part of this activity, Genesys will be enhanced for analytic functionality and enabled to communicate with databases that share standards, such as those to be used as part of the Plant Breeding API[18], and databases that are based on similar tools, like those being developed in the GOBII[19] project. Genesys developers will work within the design specifications provided by the Genetic Gains Platform, particularly the Bioinformatics and Trait Mobilization Modules, to evaluate and adapt tools or mechanisms for storing, managing, and linking phenotypic, genotypic, and environmental data to accessions. A key facilitating element will be a common system for the unique identification and tracking of germplasm samples (accessions and their progeny and other derivatives) through the use of Permanent Unique Identifiers (PUIs), so that data can be traced back to accessions in genebanks.[20].

An expanded Genesys development team or network will make Genesys interoperable with other relevant databases and data warehouses. To guide initial development efforts, a number of 'frontrunner' genebanks will test-drive methodologies and software designed to enable better targeting of genebank materials into breeding programs. Based on the experience gathered during this initial phase, additional genebanks will integrate best methods and practices, starting in 2019.

Activity 2.1.2 Empower genebank clients with intuitive, user-driven query tools

Given the rapid expansion of genomic and phenotypic/phenomic data, visualization tools will increasingly be required to display summarized information at a 'resolution' and format that are appropriate for mainstream breeding work (i.e. 1 or 2 recombination events per chromosome and generation; traits pursued as breeding targets). These visualization tools should be linked to databases holding accession data and integrated so that users can easily move between different tools to visualize trait distributions in relation to genetic similarity, allelic composition, and geographical distribution across adaptation zones.

Based on user feedback, new dynamic query interfaces and search engines will be developed to enable users to rank how likely individual accessions are to meet their needs, based on custom-designed combinations of phenotypic, genetic, passport, and environmental/climatic criteria. To the

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[18] Plant Breeding Application Programming Interface [http://docs.brapi.apiary.io/#]

[19] Genomic & Opensource Breeding Informatics Initiative [http://cbsugobii05.tc.cornell.edu/wordpress]

[20] Such as the Digital Object Identifiers (DOI) to be used for the GLIS of the ITPGRFA [http://www.planttreaty.org/content/gis]

Table 3. Activities, outputs and targets of the Use Module

Activity	Strategic Relevance	Outputs	Indicators and Targets	Assumptions
Objective 2.1 To facilitate more effective access and use through targeted delivery of germplasm that better meets the needs of users				
2.1.1 Promote information integration between genebanks and breeding programs	Users will have access to a new class of information with high value for targeting the selection of genebank accessions to more precisely meet their needs	Genesys (and where applicable in-house databases) contains or has access to all available relevant information from varied user communities on each accession	Genesys is linked to and exchanges information freely with API and GOBII as well as breeders databases in at least 50% of the Centers Unique genetic identifiers available for 50% of accessions in the CGIAR collections.	Genetic Gains and Big Data Platforms jointly succeed in developing the infrastructure, tools and mechanisms for interoperability Collaboration with Genetic Gains and Big Data is effective AFS-CRPs use tools from Genetic Gains to make their data available
2.1.2 Empower genebank clients with intuitive, user-driven query tools	Users are able to target and select germplasm much more effectively, reducing the need for large-scale screening	Genesys (and where applicable in-house genebank databases) available through a user-friendly online interface that facilitates custom designed searches of germplasm based on integration of environmental, phenotypic and genotypic information	User-friendly custom searches and tools	Activity 2.1.1 is successful
2.1.3 Enrich data on collections through use of focal subsets	Users encouraged to explore larger parts of the collections	Availability and use of data-rich subsets of accessions	Individual genebanks have a minimum of 3 subsets of germplasm available and distributed annually	Sufficient information on accessions is available through linkages to AFS-user communities to designate meaningful subsets of the collection

extent feasible, the query interfaces will also tap into methods and algorithms designed to identify associations between collection sites and environmental data (FIGS), genetic and trait data (GWAS), or genetic and environmental data (selection signatures), developed in this or other Platforms, CRPs[21] and elsewhere.

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[21] A Genebanks Platform representative will participate in the Expert Advisory Group of the Genetic Gains Platform's Trait Mobilization Module, which focuses on the selection and pipelining of genetic-analysis tools relevant to this Activity.

Strategic partnerships with advanced bioinformatics groups, particularly those who work at the interface between genomics and breeding informatics and have a track record in designing visualization tools, will be a critical component for success of this activity.

Activity 2.1.3 Enrich data on collections through focal subsets

This activity will encourage individual genebank users to focus in-depth phenotyping efforts on common subsets of accessions to create synergies amongst otherwise disconnected studies. Experience suggests that better-characterized genebank accessions tend to be requested more frequently. Offering pre-formatted and genetically well-characterized 'focal subsets' will act as an incentive for users to focus phenotyping efforts on common groups of accessions. It can also help to manage increased demand for germplasm by providing requesters with ready sets of germplasm.

Over time, these subsets will grow and enable, at little additional cost, meta-analyses of data from multi-site field trials, experiments quantifying physiological component traits, and 'omics-based deep-phenotyping efforts, for example in the context of physiological crop modeling or the identification of causal SNP variants for future CRISPR/Cas9-based genome-editing of elite materials. Focal subsets will include traditional core or mini-core collections, FIGS and other trait-specific subsets, for example focused on climate change mitigation and adaptation.

AFS-CRPs are expected to take a leading role in the molecular characterization of selected genebank accessions, for example through genotyping-by-sequencing or whole-genome re-sequencing. This activity will only invest in sequencing those accessions in 'focal subsets' that are not being characterized by AFS-CRPs. Uplift funding is required for more extensive genotyping. Service providers will be sourced via the Genotyping Module of the Genetic Gains Platform to promote harmonization and optimization of technologies.

8.3 Science Quality

The major challenge of the Use Module over the next six years is to maintain high quality data management and data association when partnering with user communities. Each community has established its own standards, often through independent processes. Traditionally, science quality standards are implemented strictly within a project, starting with formulating hypotheses and designing experiments and finishing with the publication of scientific conclusions. Working in broader partnerships introduces new challenges to harmonize disparate or incompatible standards for identifying and recording data on samples, and differing technical capacities, which will need to be addressed through this Module, in collaboration with the Genetic Gains and Big Data Platforms as well as the AFS-CRPs.

The first key challenge is to overcome the problems of disparate standards for recording and managing data in different communities. Standard crop and trait ontologies are being developed, which will be covered by the Genetic Gains Platform and incorporated into breeders' data management systems. The Use Module will engage with the Genetic Gains Platform to ensure that the long-established genebank standards for recording traits are incorporated and harmonized with these ontologies.

A second key challenge is to overcome the difficulty of tracking germplasm samples across laboratories and breeding programs. Collaborating partners studying the same germplasm must have assurance that they are indeed studying identical accessions. This Module will facilitate the use of globally recognized PUIs for germplasm that are recognized and traceable across laboratories. In some crops, genebank accessions and breeders' materials may be combined in the same database; where this is not done, the minimum requirement will be interoperable databases, using the PUIs to connect data on the same material or derived material from different databases. Since new technologies in informatics, sequencing and phenotyping rely absolutely on collaboration between laboratories, these requirements are becoming almost universally recognized, and are a priority not only for the Genetic Gains Platform, but also for several other initiatives, such as DivSeek and the GLIS. Harmonizing with these initiatives is crucial to ensure quality of science in collaboration with genebank users.

GLIS has selected Digital Object Identifiers (DOIs) as preferred PUIs for germplasm samples. The use of these as unique accession identifiers for conservation in the genebank as well as a mechanism to enhance objective monitoring of the use of accessions and their derivatives, as a complement to seeking feedback from users, will be explored. This approach has the added advantage of enabling users to comply with their obligation, set by the SMTA under which they obtain accessions, to make their results available through GLIS.

8.4 System Linkages

For CGIAR mandate crops, the AFS-CRPs are the primary “doers” that transform genetic resources into impact through the SLOs. For these crops, the primary system linkages required for more effective use of PGR are illustrated in Figure 11. For some crops[22], measures to enhance the effectiveness of use will require more direct linkages with primary users outside the CGIAR system. The Use Module will develop and deliver tools and services for users, such as subsets of germplasm based on priorities and needs set by the primary users.

The AFS-CRPs will interact with CCAFS to set priorities for coordinated mitigation of, and adaptation to, climate change; and similarly with A4NH for coordinated improvement of human nutrition and health. These interactions will be used by the AFS-CRPs to help formulate their priorities and needs from the Use Module. Therefore, although effective use of genetic resources is a vital component of the SLOs and IDOs on climate change and food and nutrition, linkages between this Module and CCAFS or A4NH will be mediated where possible through the AFS-CRPs. Where it is not possible to work through AFS-CRPs, the Module will link directly with the Global Integrating Programs and non-CGIAR organizations.

The AFS-CRPs need tools and services to be developed and delivered by the Big Data Platform and the Genetic Gains Platform; all three platforms need similar interactions with the AFS-CRPs. Development of tools and services must be integrated among the three platforms. The Genebank and Genetic Gains Platforms will use the Big Data Platform’s infrastructure and information services where appropriate. Equally, the Genebank Platform will design tools that build on the tools and technologies and partnerships developed by the Genetic Gains Platform. To achieve their outputs, the Big Data and Genetic Gains Platforms will need to form partnerships with appropriate advanced research institutes and other developers of advanced technologies; the Genebank Platform will only need to tap into these as appropriate, without needing to form independent partnerships. Each genebank manager would be the link between the Module and their corresponding AFS-CRP, responsible for communication to ensure the genebank delivers the tools, germplasm and information needed and the associated accession-specific data from the AFS-CRPs is linked back to accessions.

There will need to be joint planning, regular communication, and cross testing of tools and services with the Genetic Gains and Big Data Platforms. This will require a series of dedicated face-to-face workshops and online meetings, as well as reciprocal representation in each other’s technical meetings and governance structures to ensure full compatibility and interoperability. For example, the Genetic Gains Platform would define and establish protocols for interoperability, and would

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[22] Crops that are conserved in the genebanks but are not part of any AFS-CRP include various forages (ICARDA, CIAT & ILRI), pea & grasspea (ICARDA), finger-, foxtail, barnyard, little, kodo and proso millets (ICRISAT), Andean Root and Tuber Crops (CIP) and some legume species (African yam bean, Bambara groundnut, Winged bean: IITA).

interact with the Big Data Platform to implement them effectively; meanwhile, the Genebanks Platform would facilitate the adaptation of protocols to the genebanks' needs, test the efficacy of connections from genebank data to users' data, and provide feedback to Genetic Gains and Big Data.

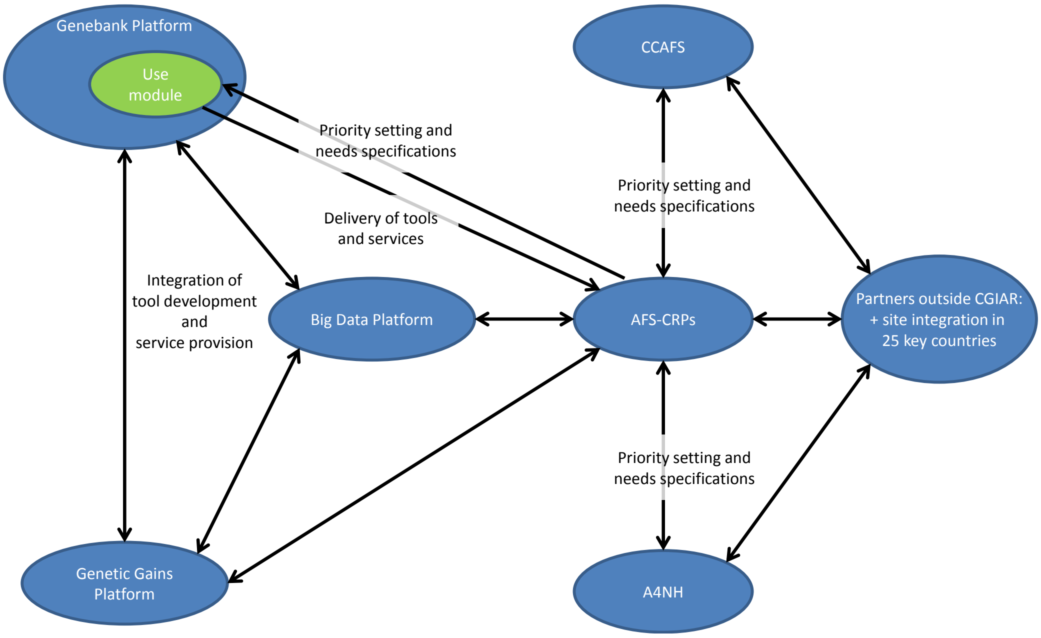

Figure 11. Primary linkages between the Use Module and the rest of the CGIAR portfolio

8.5 Climate change

Working with the Genetic Gains Platform and the AFS-CRPs, the Use Module will add tools and services required to ensure that the genebanks play their expected role in providing the reservoir of *ex situ* diversity needed to enable rapid adaptation to perpetual climate change. Climate change will increasingly require the use of genetic resources that were originally developed in geographies other than the breeders' target markets. This will require more than ever that breeders "think outside the box" in sourcing the most appropriate parents for their breeding. This in turn will be possible only with more effective methodologies to recognize, choose and utilize the right genetic resources.

The Platform's aim of attributing passport, characterization and other relevant data to the accessions in the collections already ensures that users will be able to access diversity through a base set of selection criteria. Core and dynamic subsets developed through the activities of the Use Module will be underpinned by geographical, taxonomic and genotypic data, generated by or in collaboration with users, and will provide an entry point into the collections for traits of relevance to climate change adaptation and mitigation. Once users have identified accessions from subsets with traits of interest, they will be able to explore deeper into the collections and select further accessions with similar geographies, taxonomies or genotypes. As further data are generated through the activities of the AFS-CRPs, the Genetic Gains Platform and other users, the subsets will be refined and tools enriched to support yet more exploration and use of the collections, allowing the genebanks to react ever more smartly to trends and needs driven by climate change and other pressures.

8.6 Capacity Development

The primary goal in capacity development for the Use Module is to help NARS and other national partners benefit from the tools developed. Users outside the CGIAR will need training to enable them to select more appropriate germplasm for their use, and will need enhanced capacity to share their data online.

Bringing the national partners into the project will be done by one-on-one interactions. Workshops for smallholder farmer communities may also take place, as the opportunity arises, to demonstrate the power of linking trait information to accessions, and particularly to solicit their help and advice in targeting germplasm for particular uses or target audiences. Where possible, priorities for such capacity development will be set jointly with the AFS-CRPs and the Genetic Gains Platform.

The concept of sharing data through interoperable databases applies only to databases that are available online. Most genebanks, researchers and breeders in developing countries, do not have such databases; many do not have well-organized databases of any kind and still rely on paper or spreadsheets. This requires multiple levels of capacity building, with the Use Module integrating its efforts with other capacity building initiatives. National genebanks lacking capacity in basic genebank data management will need capacity building through the Conservation Module. Once their basic data management reaches a minimal level, the Use Module can build further capacity to allow them to share their data online. This would normally involve uploading their data to existing online systems such as Genesys, which would automatically enable access to the new tools to search their data.

8.7 Intellectual Property and Open Access Management

See 6.4 and 6.5.

8.8 Module Management

The activities of the Use Module will be implemented and managed by the Centers with coordination from the Platform Coordinator and MT as outlined in Figure 8. Accomplishment of outputs and targets will be responsibility of the Center genebanks, with annual monitoring and evaluation being managed by the Platform Coordinator through the ORT. Annual reports summarizing progress will be compiled and made publicly available. The MT will provide oversight and guidance to ensure that targets are achieved. Progress, challenges and limiting factors for accomplishing targets will be discussed at the Annual Genebank Meeting, with recommendations as needed being forwarded to the MT and Center management.

9. Policy Module: Genetic resources policy development and compliance

9.1 Rationale and scope

The genebanks are being subjected to an evolving and increasingly complex portfolio of international legal agreements. These laws can have, and in some cases already are having, negative impacts on agricultural research and development (Helsey & Day Rubenstein 2015), including the work of CGIAR genebanks, breeders and biotechnologists. (Halewood et al 2013; Lopez Noriega et al 2013). It is essential for CGIAR to harness its scientific expertise and social capital to influence the development and implementation of these agreements, to ensure that they ultimately contribute to an enabling environment, whereby genetic diversity is made available on equitable terms to agricultural researchers, plant breeders, national programs, and ultimately farmers, in pursuance of food security and sustainable agricultural intensification.

At the international level, in the next few years, CGIAR will have significant opportunities to influence policy outcomes at the level of the ITPGRFA's Governing Body, the Conferences of the Parties to the CBD and the Nagoya Protocol on Access and Benefit Sharing, FAO's Commission on Genetic Resources for Food and Agriculture, and the International Plant Protection Convention. As part of these processes, CGIAR will need to engage in smaller inter-sessional intergovernmental 'working groups' created by the larger decision-making bodies to evaluate options. One of the challenges that CGIAR needs to address in this context is the fact that the '–omics' revolution, including cutting edge work of the Genetic Gains Platform and the AFS-CRPs are setting the stage to explore uses of PGR that are not directly addressed by the international agreement listed above. As a result, this research will take place, at least temporarily, in an environment characterized by legal uncertainty and competing visions of how it, and the products of its application, should be regulated. It will be critically important for CGIAR to ensure that the interests of international agricultural research and development are reflected in the decisions that are ultimately taken.

At the national level, CGIAR genebanks and breeders must also contend with the fact that many countries are still developing systems to implement their international obligations. This leads to uncertainty and delays in developing agreements for acquiring new materials and the conditions under which they can be used and distributed. CGIAR can leverage its experience and connections to provide assistance to regional organizations, national programs, and key partners to put systems in place so that countries can fully participate in globally coordinated programs for PGR conservation and use.

At the same time, CGIAR needs to dedicate more resources to ensure that 'its own house is in order,' by complying with its existing PGR legal obligations derived from this increasingly complex mix of international agreements and national implementing laws. The level of awareness concerning scientists' legal obligations related to PGR is generally quite low and unevenly spread across CGIAR. The Centers are still working to get systems in place for long-term compliance with the ITPGRFA. And the practical consequences (and legal uncertainties) associated with compliance with the Nagoya Protocol are only just beginning to emerge.

CGIAR's position in the global system of conservation and sustainable use of genetic resources has changed in the last two decades. Today, a range of actors – including developing country NARS, private sector, universities and development NGOs – are able to play larger roles in agricultural research for development than in the past. To increase its effectiveness in the PGR policy arena, CGIAR must have the capacity to proactively engage with representatives of these groups, along with experts from Secretariats of key international agreements, and farmers' organizations. To this end, a Multi-stakeholder PGR Policy Group will be established, comprising internationally recognized experts, drawn from a range of constituencies outside CGIAR, to provide feedback and advice and identify options for the CGIAR's engagement in PGR policy issues. It will also provide a basis for the development of policy alliances with like-minded groups to influence international policy processes.

Through the Policy Module's activities, the institutional capacity for CGIAR to address the challenges described above will be built in each Center. Representatives will be brought together from the multiple networks and expert groups within the CGIAR that are, or should be, engaged in addressing genetic resources policy issues, including the Article 15 group, CLIPNet (Centers' IP focal points), science leaders, social scientists and germplasm health specialists. The Module will raise awareness and strengthen the capacity of CGIAR genebanks, breeders and other PGR users to understand and comply with their policy obligations. It will coordinate the development of technical inputs to enable evidence-based decision-making at international, national and organizational levels.

9.2 Objectives and targets

The activities of the Policy Module (Table 4) contribute to all four Platform outcomes, but most particularly to the third and fourth:

1. Disease-free, viable, documented germplasm made available
2. More effective access and use of germplasm enabled
3. **Policy engagement and compliance ensured**
4. **Crop diversity conserved in a rational and effective global system**

Objective 3.1 To ensure Centers comply with international policies and laws, increase their influence in policy-making processes and strengthen capacity of national programs

Activity 3.1.1 Monitoring and ensuring compliance with international policies and laws

The Policy Module will conduct a rolling analysis of the Centers' legal and policy obligations (and room to maneuver) that arise from applicable international agreements and the national laws that exist (or do not) to implement them. Information will be collated from across the CGIAR about uncertainties and challenges concerning existing and evolving legal frameworks. The range of options available will be explored and decision-making tools and guidelines developed for CGIAR genebanks and other users (e.g. Centers' Guide to the Use of the SMTA including guidance on the Nagoya Protocol). The Policy Module will carry out targeted awareness-raising sessions at meetings of genebank managers, research managers, other PGR user communities, and Center IP focal points, and provide a 'helpdesk' service for the genebanks, and other PGR users across CGIAR. If and when compliance issues are raised by international bodies (e.g. the ongoing investigations of the CGIAR Centers use of the SMTA at the request of the Governing Body of the ITPGRFA), policy experts will support the staff of genebanks and research programs to ensure they understand the nature of the investigations, assemble their responses, identify options for adopting policies that are in compliance, etc.

Activity 3.1.2 Engaging in the processes of developing international policies and laws

The Policy Module will analyse the actual and potential influences of global, regional and national level policies on CGIAR genebank activities and other scientists' ability to access, use, and distribute genetic resources and related information, and to share related benefits. Strategies for engaging in international policy-making processes will be identified to promote evidence-based decisions for optimizing the potential contributions of genetic resources to agricultural research and development. These contributions will take many forms, including policy briefs, written responses to information requests from Secretariats, discussion papers, side events, and participation as delegates or expert resource persons in international meetings.

The Module will develop a more expansive, flagship publication for submission to the Governing Body of the ITPGRFA. This publication will go beyond the traditional report of the status of the CGIAR collections and distributions of germplasm to include information about developments concerning new tools and methods for targeting useful genetic traits, capacity building events and opportunities, impact stories and spillover benefits at national, regional and global levels. This publication will also present analyses of the influence of international agreements (including ITPGRFA, CBD, Nagoya Protocol, UPOV, IPPC) on Centers' and partners' use of genetic resources and data, and options for policy reforms to overcome challenges identified. The Policy Module will liaise with scientists in the Conservation and Use Modules concerning genebank experiences; it will survey breeders, molecular biologists, natural resources managers, social scientists, IP managers and science leaders through existing CGIAR networks, CRPs and platforms. It will engage representative experts from across CGIAR to develop written contributions, and to participate in intergovernmental meetings as necessary. It will coordinate interactions with regional blocks of delegates and representatives of stakeholder groups attending international meetings.

Table 4. Activities, outputs and targets of the Policy Module

Activity	Strategic Relevance	Outputs	Indicators and Targets	Assumptions
Objective 3.1 To ensure Centers comply with international policies and laws, increase their influence in policy-making processes and strengthen capacity of national programs				
3.1.1: Monitoring and ensuring compliance with international policies and laws	Failure to comply with legal obligations exposes Centers and the CGIAR to legal liability and loss of reputation, and generates disaffection with the global system	Centers' fully compliant with plant genetic resources policy obligations	White paper for internal CG audience. Guidelines, tools published on platform website. Use of the helpdesk	Centers are willing to comply with obligations
3.1.2. Engaging in the processes of developing international policies and laws	CGIAR has opportunities to shape the policies that govern its own and partners' genetic resources work	CGIAR plays recognized role in influencing international policy development Evidence-based policy recommendations to international bodies	White paper for internal CGIAR audience Submissions to negotiating forums: bi-annual report to ITPGRFA, discussion papers, policy briefs, written responses to Secretariats' surveys, forum statements, side-events. Representation of the CGIAR in 6 to 8 international policy meetings.	Delegates at international policy meetings are willing to be engaged on CGIAR perspectives and interests CGIAR and CGIAR Centers contribute timely inputs to the time-limited opportunities to influence international policy outcomes.
3.1.3: Strengthening the capacity of CGIAR and national partners to implement and influence international policies and laws	Positive national policy development that supports CGIAR research and development partnerships.	National partners have tools and mechanisms to support their implementation of plant genetic resources policies.	Online repository of decision-making tools and guides, reports for national-level implementation. PGR policy sessions led by Platform scientists in CGIAR, national and regional workshops. National program representatives invited to training events for CGIAR scientists, IP managers, research leaders.	Partners have commitment from their management and governments to implement and support appropriate national policy.
3.1.4 Convening the Multi-stakeholder PGR Policy group.	The CGIAR will be well positioned to engage in a highly politicized policy field.	Sound inputs guide CGIAR compliance and engagement in international PGR policy-making.	Minutes of the Multi-stakeholder PGR Policy group meetings. Positive references to CGIAR PGR policy engagement in publications of other stakeholders.	All relevant stakeholder groups are willing to engage.

Activity 3.1.3 Strengthening the capacity of national partners to implement and influence international policies and laws

The Policy Module will work to strengthen the capacity of key CGIAR partners and national programs to address PGR policy issues, and provide a means for institutional knowledge retention and re-education. Much of this work will be dedicated to information exchange and engagement of CGIAR scientists in national program policy meetings, and vice versa, with the objective of partners adopting mutually supportive policy approaches. Subject to available bilateral funding, the Module will work directly with national programs and regional organizations to put systems in place to implement international obligations.

Activity 3.1.4 Convening the Multi-stakeholder PGR policy group

In service of all above activities, the Module will convene a Multi-stakeholder PGR Policy Group, which will identify important issues for CGIAR to consider and identify options for addressing them. The Multi-stakeholder Group will not be part of the governance of the Platform or Module, but will provide perspectives and feedback only. It will include eight experts in PGRFA policy drawn from outside the CGIAR, including from the private sector, Northern and Southern governments, civil society and/or farmers organizations, the Secretariats of the ITPGRFA and CBD/Nagoya Protocol, universities and Global Forum on Agricultural Research (GFAR).

It will be essential, based on lessons learned from the operation of the earlier Genetic Resources Policy Committee (GRPC), for a number of representatives of CGIAR Centers, CRPs and CoPs to be included in the committee to ensure relevance, transparency, and systemwide buy-in. Some of the members of the Genebank IAC will also be members of the Multi-stakeholder PGR Policy Group. The Group will meet in person once a year, and a second time virtually, as necessary. Meetings will be held back-to-back with other CGIAR meetings in order to create opportunities for interaction.

9.3 Science Quality

The scientific outputs of the Module will include white papers, policy briefs, decision-making tools, position statements, and peer reviewed research papers. The quality of these outputs will depend upon their being based on a solid appreciation of the day-to-day operations and challenges faced by the genebanks, and other PGR users in the CGIAR system. It will also depend upon systematic peer review by the same users as well as policy experts from both inside and outside the CGIAR. The Module will create space for internationally recognized PGR users and policy experts from outside the CGIAR to contribute to the Module's science quality through a combination of mechanisms, including the Multi-stakeholder PGR Policy Group, the MT, and the IAC.

To tackle policy issues involved in different areas of CGIAR work, scientists and policy experts engaged in the platform activities will be organized into 'pods' of expertise: conventional breeding, biotechnological applications, genebanking, collecting, 'omics' data compilation and sharing, agroforestry and forest trees; and around relevant areas of PGR policy: access and benefit sharing, intellectual property, biosecurity, farmers' and breeders' rights and phytosanitary issues. In each of these areas, the Module will coordinate and support data gathering and pooling and the development of reports and scientific papers in support of the Module's objectives and for wider consumption.

Two of the scientists providing coordination of the Module are from Bioversity International's Genetic Resources Policies, Institutions and Monitoring group. Bioversity has maintained a group of scientists working on PGR policy issues since 1995. Under the auspices of the SGRP, this group coordinated representation of the CGIAR throughout the negotiation of the ITPGRFA, SMTA and Nagoya Protocol. Bioversity's policy experts and the A15 group jointly developed a number of policy briefs, information documents and statements on behalf of the CGIAR for meetings of the Governing

Body of the ITPGRFA, CBD Conferences of the Parties and CGRFA. More recently, some Center IP focal points and the Consortium Office General Legal Counsel have become involved in these efforts.

Under the framework of the Joint FAO/Bioversity/ITPGRFA Secretariat Joint Program, Bioversity has coordinated projects to implement the ITPGRFA in 15 countries. More recently, Bioversity is partnering with the CBD Secretariat, the African Union Commission and the GIZ-hosted ABS Capacity Development Initiative to work on mutually supportive implementation of the Nagoya Protocol. The third member of the coordinating team, Ruaraidh Sackville Hamilton, is the Head of the IRRI genebank and one of the Executive members of the Article 15 Group. For years he has attended meetings of the ITPGRFA on behalf of the CGIAR. He is currently working on GLIS with the ITPGRFA Secretariat.

9.4 System Linkages

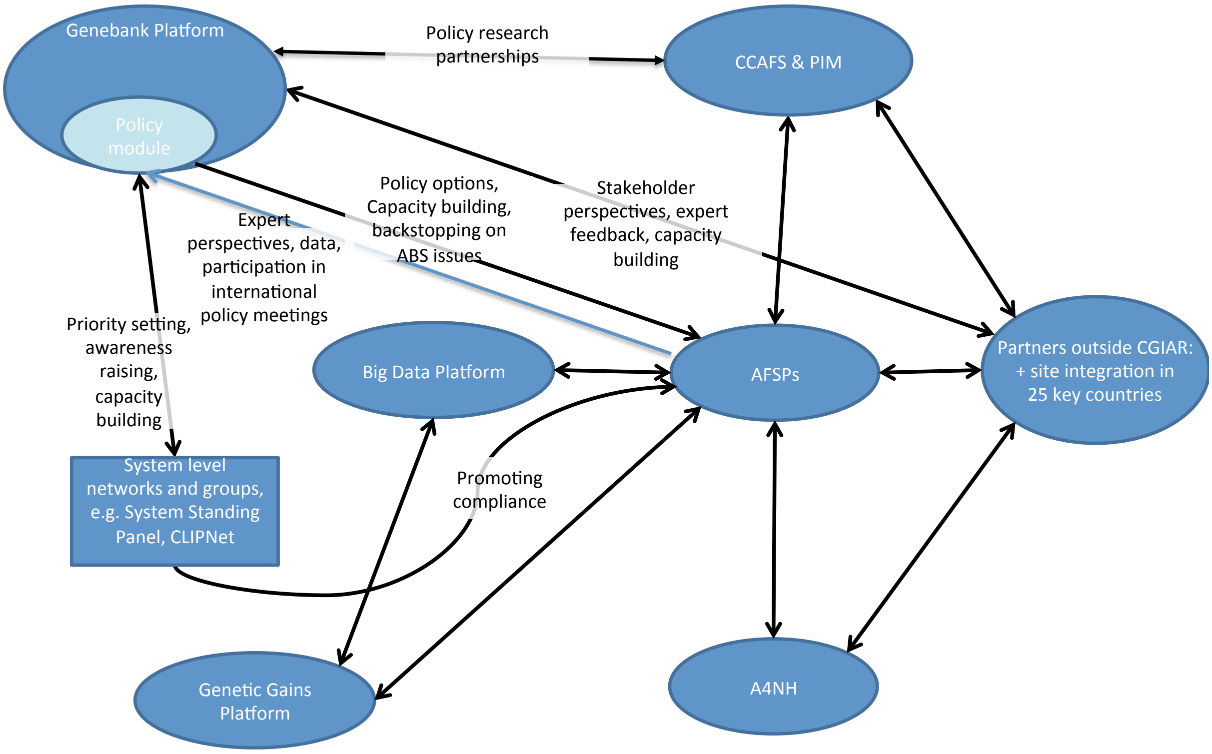

Figure 12. Primary linkages with the Policy Module within the CGIAR portfolio

As stated in the call for proposals, the Policy Module should "provide a means and schedule for independently advising PGR governance, and the CGIAR at large, on high priority matters related to PGR policy." This calls for tailor-made forms of system linkages (Figure 12). The Module will organize PGR policy awareness-raising and consultation sessions during meetings of the Science Leaders and DGs (in addition to other groups listed below). The Module will periodically develop white papers designed for internal CGIAR use, summarizing its analysis concerning priority matters related to PGR policy, with a particular focus on opportunities for the CGIAR to influence international policy developments, and priority actions related to compliance. These papers will be submitted to the MT and IAC, and subsequently circulated to CRP and Platform Leaders, DGs, Systems Office, etc. Submissions setting out CGIAR positions on issues being considered by international bodies (e.g. Governing Body of the ITPGRFA) will be submitted for approval by the CGIAR System Standing Committee. A 'help desk' will provide technical backup for the genebanks and other platforms and

CRPs confronting uncertainties related to the application of policies and laws to their acquisition, use or distribution of genetic resources and related data.

Policy research will be directly linked to, and circumscribed by, the 'service needs' of the genebanks (and other PGR users) in CGIAR. Given a relatively small budget for original research, it will be important for the Module to liaise with CRPs to identify opportunities for linked-up studies of thematically aligned policy research and take advantage of the broader research scope and resources of the CRPs. In this regard, the Module will liaise with CCAFS (under an activity entitled 'Global policy support for biologically diverse, climate resilient agriculture,' in Flagship 1); FTA (under Flagship 1, which tackles tree genetic resources policy issues at local, national and international scales); and PIM (under Flagship 1, Cluster 1.2 on 'Technological innovation and sustainable intensification: Science policy and innovation systems for sustainable intensification').

Similarly, the Module will be reliant on feedback, inputs and participation of breeders, biotechnologists, IP managers and others from across CGIAR in the development of contributions to international policy fora. To this end the Module's *modus operandi* will involve working through networked CoP in CGIAR, including first and foremost, the A15 Group and CLIPNet, building upon the cooperation of members of those networks to address PGR policy-related issues. The Module will also engage the Science Leaders and Genetic Gains and Big Data Platforms. The coordinators or executive committees of these networks will assist in 'pushing and pulling' information through their communication channels, and promoting participation of particular scientists with expertise in issues that require focused attention. This will foster new networks among CGIAR breeders and social scientists, who are able to dedicate time to PGR policy issues.

9.5 Climate Change

Climate change is increasing the already high level of interdependence of countries on genetic resources for food and agriculture. As climates 'migrate' across political borders, breeders, researchers and farmers will need access to adaptive traits in plant populations that evolved under similar climate conditions in other parts of the world, or that reside in materials that have been improved by plant breeders to address climate-related challenges. They will also need access to data related to those materials. The Conservation and Use Modules activities are attempting to address these rapidly changing needs for access to germplasm and data. Equally, the Policy Module will work on PGR policies to increase the availability and use of genetic resources for agricultural research and development, including for use to adapt to, and mitigate, climate-change-related challenges.

Under its activity 'Global policy support for biologically diverse, climate resilient agriculture,' CCAFS addresses these themes in part, supporting national programs to take advantage of (and develop appropriate) policies to access and or share genetic diversity for use in climate change adaptation programs. It has also developed submissions for international policy meetings concerning countries' increasing interdependence as a result of climate change, and the importance of policy support for international systems of sharing genetic diversity. The Policy Module will work closely with CCAFS to ensure complementarity (and no duplication) of efforts. In some cases, they will work together to develop joint submissions to international bodies and develop capacity strengthening activities and materials for national programs.

9.6 Capacity Development

Capacity development is a core component of the Policy Module. Most of the Module's capacity development activities will be concentrated on CGIAR compliance with PGR agreements and laws, and the CGIAR's participation in international policy-making processes.

A relatively small proportion of the Policy Module's resources will be dedicated to complementary forms of capacity development for national programs and partners to be able to address PGR policy challenges. These resources will be used to support: CGIAR scientists to attend workshops and conferences convened by regional organizations wherein genetic resources policy issues are being considered; participation of national program representatives in training workshops organized by the Platform that are primarily targeting CGIAR scientists; and assembling and sharing guides, decision-making tools, and background literature on the platform's website, for use by national program policy actors.

9.7 Intellectual Asset and Open Access Management

See 6.4 and 6.5

9.8 Module Management

Policy Module activities will be coordinated by staff from Bioversity International and IRRI under the guidance of the MT, and come under the same governance as the rest of the Platform. However, official CGIAR positions or decisions will be reviewed and approved by the CGIAR System Standing Committee. The Policy coordinating unit will organize partners' participation and play a substantial role in many of the research, capacity building and awareness raising activities. It will manage the Module's budget, dispense funds and develop contractual arrangements where necessary, ensuring that all activities are well executed and appropriately resourced.

Annex 1. CGIAR Genebanks: status summary

<table>
<tr><th colspan="2">1. Africa Rice</th></tr>
<tr><td>Collections</td><td>Africa Rice is unique in representing an association of 25 African countries, on whose behalf it conserves and makes available a collection of rice originating mostly from African countries, including the world’s largest collection of <i>Oryza glabberima</i>. The genebank will be transferred from Benin and Nigeria to purpose-built facilities in Cote D’Ivoire in 2016. The move will allow Africa Rice to consolidate its collection in one place for the first time in 14 years, with both medium-term and long-term storage facilities.</td></tr>
<tr><td>Expertise</td><td><u>Marie-Noelle Ndjiondjop</u> (Head of Genetic Resources) has more than 20 years experience in rice research as a molecular geneticist.
<u>Dro Daniel Tia</u> (Genebank scientist) has 12 years experience in germplasm characterization and conservation.
<u>Fatimata Bachabi</u> (Genebank scientist) has been working on seed distribution, conservation and safety duplication for 7 years
<u>Alphonse Junior Goungoulou</u> (Genebank scientist) has expertise in database management.</td></tr>
<tr><td>Status</td><td><table>
<tr><td>Accession numbers in 2016</td><td>19,983</td></tr>
<tr><td>Projected accession numbers in 2022</td><td>21,159</td></tr>
<tr><td>Availability in 2015</td><td>78%</td></tr>
<tr><td>Safety Duplication in 2015</td><td>40%</td></tr>
<tr><td>Documentation in 2015</td><td>39%</td></tr>
<tr><td>Quality Management System</td><td>Minimum elements in place by end of 2016</td></tr>
<tr><td>Date to reach Performance Targets (90% availability, safety duplication and documentation)</td><td>2021</td></tr>
<tr><td>Number of staff (FTE[23]s)</td><td>17</td></tr>
</table></td></tr>
<tr><td>Germplasm Health Unit</td><td>Africa Rice has only recently recruited expertise to develop seed testing capacity. Further technical staff will need to be hired and trained in order to ensure sound routine practices are in place.</td></tr>
<tr><td>Plans for improvement</td><td>Aside from consolidating its new genebank in Cote D’Ivoire, Africa Rice plans to:
• Establish a new, improved data management system
• Establish a seed health testing unit and to optimize procedures
• Regenerate and safety duplicate 12,000 accessions to reach targets</td></tr>
<tr><td>Plans for efficiency</td><td>• Reduce the time between harvest and storage in long-term conditions in order to attain better seed longevity.</td></tr>
<tr><td>External review – selected quotes</td><td><i>“Particularly noteworthy was the obviously strong integration of the genebank activities into the overall institutional programme of work, especially with the crop breeding, plant pathology and molecular biology activities”.</i>
<i>“A more assertive role of the GRU in the procedures that facilitate use as well as annual planning meetings between genebank and plant breeders/researchers to plan activities related to the characterization, evaluation and screening of germplasm will further facilitate the use of a broader genetic diversity in Africa’s rice breeding programmes.”</i></td></tr>
<tr><td>Integration with researchers and breeders</td><td>• Collaboration in high throughput and precision phenotyping of accessions for a wide range of stresses.
• Japanese funded project with Africa Rice geneticists to evaluate O. glaberrima for early flowering and tolerance of stagnant flooding</td></tr>
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[23] Full time equivalents

<table>
<tr><td>Distribution between 2012–2014</td><td>46,991 samples were distributed; 47% to users (mostly NARS) outside the CGIAR in 45 countries.</td></tr>
<tr><td colspan="2">**2. Bioversity International**</td></tr>
<tr><td>Collections</td><td>Bioversity International *Musa* Germplasm Transit Centre (ITC) is hosted by the Katholieke Universiteit Leuven (KULeuven) in Belgium. Bioversity does not have its own field stations but instead collaborates closely with national genebanks through its MusaNet network, who carry out fieldwork on its behalf. MusaNet's thematic groups (Conservation, Diversity, Evaluation, Information and Genomics) also provide expert guidance.</td></tr>
<tr><td>Expertise</td><td>Nicolas Roux (*Musa* Genetic Resources Group Leader) coordinates the work on banana genetic resources within Bioversity and within the wider research community as MusaNet coordinator.
Ines van den Houwe (Genebank manager) has 20 years of managing and developing the *in vitro* banana collection in Leuven
Bart Panis (Cryopreservation specialist) a pioneer in developing cryopreservation protocols in numerous crops.
Julie Sardos and Rachel Chase (Characterization specialists) verify the genetic integrity of the material maintained at ITC by molecular characterization and morphological characterization.
Max Ruas (Database manager) has expertise in data management and maintains the *Musa* Germplasm Information System (MGIS) which contains information on the ITC and 17 national collections.
Virus indexing is outsourced to University of Liege and molecular characterisation to the Institute of Experimental Botany, Czech Republic. Field verification is mainly conducted with USDA[24] in Puerto Rico.</td></tr>
<tr><td>Status</td><td><table>
<tr><td>Accession numbers in 2015</td><td>1518 in tissue culture and 945 in cryopreservation</td></tr>
<tr><td>Projected accession numbers in 2022</td><td>1,820</td></tr>
<tr><td>Availability in 2015</td><td>62%</td></tr>
<tr><td>Safety Duplication in 2015</td><td>62% in cryopreservation (meets target)</td></tr>
<tr><td>Documentation in 2015</td><td>31%</td></tr>
<tr><td>Quality Management System</td><td>Minimum elements in place by end of 2016</td></tr>
<tr><td>Date to reach Performance Targets (90% availability, safety duplication and documentation)</td><td>2019</td></tr>
<tr><td>Number of staff (FTEs)</td><td>10.7</td></tr>
</table></td></tr>
<tr><td>Germplasm Heatlh Unit</td><td>The University of Liege provides virus-indexing and sanitation services with backstopping from Queensland Department for Plant Industries. The genebank has a reputation for very high standards of phytosanitary safety.</td></tr>
<tr><td>Plans for improvement</td><td>• The % availability is expected to increase once the quarantine status of the Banana Streak Virus (BSV) complex is resolved. In the meantime, affected accessions are made available for research in the form of lyophilized leaves.
• Research on long-term seed conservation to increase the representation of crop wild relatives in the collection.
• Ensuring availability of good quality characterization and evaluation data on 90% accessions in the collection</td></tr>
<tr><td>Plans for efficiency</td><td>• Elimination of an estimated 5% internal duplication in the collection after molecular and morphological analyses
• Develop molecular tools by 2020 that will detect somaclonal variation, avoiding the need to periodically test trueness-to-type of in vitro accessions in the field
• Develop more effective molecular tools for virus detection to reduce substantially the time required for virus indexing (not yet funded).</td></tr>
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[24] United States Department of Agriculture

<table>
<tr><td>External review – selected quotes</td><td><i>“With solid foundations in the scientific reputation of the university and in close association with the scientific milieu there, the genebank has maintained a high level of conservation management and research … the staff of the genebank has built a highly collegiate and dynamic network of partnerships with research, conservation and crop improvement organizations throughout the tropical world.”</i>
<i>“The review notes that there have been several calls to address gaps in the collection, which have so far met limited response, especially in the case of wild species.”</i></td></tr>
<tr><td>Integration with researchers and breeders</td><td>Evaluation and testing of selected accessions with multiple national partners as part of the International Musa Testing Programme
Genome wide association studies (i.e. GWAS)
Phenotyping for important traits
Development of information system to link genetic resources from genebank, to genome and breeding databases.</td></tr>
<tr><td>Distribution between 2012–2014</td><td>2478 samples distributed; 84% to users (mostly universities but also NARS and private individuals) outside the CGIAR in 29 countries.</td></tr>
<tr><td colspan="2">3. CIAT</td></tr>
<tr><td>Collections</td><td>CIAT manages large and diverse collections of beans and tropical forages as seed and whole plants, and cassava <i>in vitro</i> and as bonsai plants. Facilities are old and ill-suited for a genebank. Part of the funding has been raised to build a state-of-the-art facility. The genebank has use of three “exceptional” field sites to provide specific growing conditions for different forage and bean taxa.</td></tr>
<tr><td>Expertise</td><td>Daniel Debouck (Genetic Resources Program Leader) Leading <i>Phaseolus</i> taxonomist, germplasm collector and genebank manager of 19 years.
Peter Wenzl (Incoming Genetic Resources Program Leader) Specialist in crop genetics and germplasm enhancement with 20 years research and project leadership experience.
Maritza Cuervo Ibáñez: (Germplasm health) Virologist and coordinator of germplasm health laboratory for 12 years.
Luis G. Santos (Agronomist) Coordinator of seed conservation
Ericson Aranzales (Biotechnologist) Coordinator of tissue culture
Angela Hernández (Information engineer) Responsible for software and database improvement
Javier Gereda (Agronomist) Specialist in agronomy and seed germplasm production.</td></tr>
<tr><td>Status</td><td><table>
<tr><th></th><th>Beans</th><th>Forages</th><th>Cassava</th></tr>
<tr><td>Accession numbers in 2016</td><td>37,987</td><td>23,140 (incl. 1,200 trees and whole plants)</td><td>6,643</td></tr>
<tr><td>Projected accession numbers in 2022</td><td>38,500</td><td>23,340</td><td>6,948</td></tr>
<tr><td>Availability in 2015</td><td>63%</td><td>62%</td><td>63%</td></tr>
<tr><td>Safety Duplication in 2015</td><td>73%</td><td>69%</td><td>34%</td></tr>
<tr><td>Documentation in 2015</td><td>68%</td><td>33%</td><td>44%</td></tr>
<tr><td>Quality Management System</td><td colspan="3">Minimum elements in place by end of 2016</td></tr>
<tr><td>Date to reach Performance Targets (90% availability, safety duplication and documentation)</td><td>2019</td><td>2019</td><td>2019</td></tr>
<tr><td>Number of staff (FTEs)</td><td colspan="3">78 (including GHU)</td></tr>
</table></td></tr>
<tr><td>Germplasm Health Unit</td><td>There is a well-established GHU of nine staff at CIAT, together with an onsite branch of the national phytosanitary agency, with whom there is a close collaboration. The GHU has received little investment over the years and is in clear need of upgrading. The building of the new genebank will address this issue.</td></tr>
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<table>
<tr><td>Plans for improvement</td><td>Capture legacy evaluation information from breeders and adopt GRIN-Global data management
Rationalization of the beans and forages collection through morphological and molecular analyses
Regeneration of more than 15,000 accessions to reach targets of 90% availability and safety duplication</td></tr>
<tr><td>Plans for efficiency</td><td>Safety duplication of the cassava collection is frequently hampered by national phytosanitary controls. There are less costly alternatives (bonsai collection or cryopreservation) which need to be established as safety duplicates.
Forage community will agree a conservation strategy, which will lead to rationalization/archiving of parts of the forage collection</td></tr>
<tr><td>External review – selected quotes</td><td><i>“The respected US scientist Paul Gepts called the GRP “... one of the best organised units in the world...” and stated that “... operations of the collection, in terms of seed increase, viability and disease testing, etc., are a model for other PGR Units as to systematic conservation, rigour of operations ...”.</i>
<i>“Given the history of the GRP and the lack of a proper technical review in the past, there is some space to further improve the quality of the operations.”</i></td></tr>
<tr><td>Integration with researchers and breeders</td><td>Partner of the Bean-Adapt genomic project (UC-Davis, USDA, IPK), Harvest Plus for high iron.
Partner of the Cassava TILLING Project, Cassava Brown Streak Virus Project.
Partner of the Livestock-Plus project on Brachiaria germplasm.</td></tr>
<tr><td>Distribution between 2012–2015</td><td><u>Beans</u>: 11,428 samples distributed; 68% to users outside the CGIAR, including wide ranging recipients from universities, NARS, commercial sector and significant numbers of farmers organizations and private individuals.
<u>Forages</u>: 3,138 samples distributed; 83% to users outside the CGIAR, mostly NARS but also significant numbers in universities, commercial sector and farmers organizations.
<u>Cassava</u>: 5,536 samples distributed; 20% to users outside (mostly universities) the CGIAR.
In total, CIAT distributed germplasm to 39 countries.</td></tr>
<tr><td colspan="2">4. CIMMYT</td></tr>
<tr><td>Collections</td><td>The CIMMYT genebank is a well-equipped, purpose-built facility, partly powered by solar panels. The genebank functions at high levels of efficiency, distributing sometimes up to 50,000 samples annually.</td></tr>
<tr><td>Expertise</td><td><u>Tom Payne </u>(Wheat Germplasm Bank manager) with nearly 28 years of involvement as a wheat scientist in various countries with CIMMYT.
<u>Denise Costich</u> (Maize Germplasm Bank manager) with extensive experience in maize crop wild relatives, and the molecular genetic analysis of the crop.
<u>Monica Mezzalama</u> (Seed Health Laboratory manager) responsible for achieving and maintaining ISO 17025 accredidation, and CIMMYT’s Stewardship of Excellence standards.</td></tr>
<tr><td>Status</td><td><table>
<tr><th></th><th>Maize</th><th>Wheat</th></tr>
<tr><td>Accession numbers in 2016</td><td>28,316 (inc. field collection of 161 <i>Tripsacum</i>)</td><td>152,835</td></tr>
<tr><td>Projected accession numbers in 2022</td><td>30,092</td><td>162,838</td></tr>
<tr><td>Availability in 2015</td><td>62%</td><td>86%</td></tr>
<tr><td>Safety Duplication in 2015</td><td>29%</td><td>60%</td></tr>
<tr><td>Documentation in 2015</td><td>100%</td><td>69%</td></tr>
<tr><td>Quality Management System</td><td colspan="2">ISO 9001:2008</td></tr>
<tr><td>Date to reach Performance Targets (90% availability, safety duplication and documentation)</td><td>2021</td><td>2017</td></tr>
<tr><td>Number of staff (FTEs)</td><td colspan="2">17 (not including staff funded by other CRPs)</td></tr>
</table></td></tr>
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Germplasm Health Unit	The CIMMYT GHU is a well-established service unit, which has attained ISO/IEC 17025 accreditation and provides seed health testing services to users at a competitive per-unit cost.
Plans for improvement	• Explore potential for automating viability testing through image analysis • Develop GRIN-Global and better integration of accession data with breeders' data • Regeneration and safety duplication of 50,000 accessions to reach targets
Plans for efficiency	• Increase seed longevity in long-term storage • Increase annual rate of maize regeneration through improving disease and crop management, which will lead to a significant reduction in field costs. • Improve conservation of wheat crop wild relatives in collaboration with ICARDA. • Stratify the collection through diversified management of accessions, including archiving certain parts of the collection.
External review – selected quotes	*"The CIMMYT genebanks have a long history of being relatively well-supported, and an outstanding record of providing germplasm and information, which has supported international crop development and global food security."* *"There is a deficit in understanding the biology behind long and short seed life. Institutions that have held large collections over a long period of time are clearly in a unique position to contribute to this much-needed research."*
Distribution between 2012–2014	Maize: 35,261 samples distributed; 32% distributed to users outside the CGIAR, primarily to NARS and the commercial sector, but also a large number to universities. Wheat: 63,509 samples distributed; 34% distributed to users outside the CGIAR, mainly to NARS, but also a large number to universities. In total, CIMMYT distributed samples to 92 countries.
5. CIP	
Collections	A highly complex collection of difficult-to-conserve crops and the largest *in vitro* collection in the CGIAR. Field and screenhouse collections are managed on three sites in addition to the main Lima campus. The collections include a large number of wild species. A large-scale cryobank for potato and sweet potato is in the process of being developed. Andean Root and Tuber Crops (ARTC) comprise nine families of non-Annex 1 crops, held *in vitro* and in the field.
Expertise	Dave Ellis (Head of Genebank) Joining the CIP genebank from USDA's Fort Collins genebank, Dave has had many years experience in the public and private sector in genetic resources conservation, *in vitro*, cryobiology, molecular biology and physiology. Noelle Berkley (Genetic Resources Conservation Manager) has recently joined CIP. She has expertise in genetic resources conservation, molecular biology and pathology. Rene Gomez (Senior curator) curates the cultivated potato collection. Expert in potato taxonomy with more than 20 years' experience working with native Andean potato. Alberto Salas (Senior advisor) is a retired but very active world expert in wild potato taxonomy and biogeography. He was responsible for collecting much of the CIP potato collection. Genonveva Rossel (Curator) Expert in sweet potato genetic resources with 10 years experience Ivan Manrique (Curator) curates the ARTC collection with more than 10 years experience Ana Panta (*In vitro* specialist) Cryopreservation and *in vitro* specialist who has worked more than 20 years at CIP and heads the *in vitro* labs Rainer Vollmer (Cryopreservation leader) Cryopreservation specialist who leads the large-scale cryopreservation of potato and sweet potato Edwin Rojas (Software developer) leads database development at CIP and advises other CGIAR Centers in data management and barcoding. Oswaldo Chavez (Database manager) data management, software design and statistics Brenda Zea (Phytosanitary/quarantine specialist) manages the quarantine and phytosanitary cleaning of accessions Nataly Franco (*In vitro* specialist) manages seed and *in vitro* safety duplicates in

<table>
<tr><td></td><td colspan="4">Huancayo, SGSV, EMBRAPA and CIAT.
Rosario Franco (Germplasm acquisition and distribution) specializes in germplasm requests and distributions
Fanny Vargas (Curator) manages the herbarium
Jan Kreuse (Head, Virology) specialist in virology, and manages the GHU</td></tr>
<tr><td rowspan="11">Status</td><td></td><td>Potato</td><td>Sweet potato</td><td>ARTC</td></tr>
<tr><td>Seed accession numbers in 2016</td><td>2322</td><td>1144</td><td>868</td></tr>
<tr><td>Clonal accession numbers in 2016</td><td>4725</td><td>6499</td><td>1460</td></tr>
<tr><td>Projected seed accession numbers in 2022</td><td>2650</td><td>1300</td><td>900</td></tr>
<tr><td>Project clonal accession numbers in 2022</td><td>5000</td><td>6600</td><td>1600</td></tr>
<tr><td>Availability in 2015</td><td>38%</td><td>19%</td><td>0%</td></tr>
<tr><td>Safety Duplication in 2015</td><td>91%</td><td>87%</td><td>69%</td></tr>
<tr><td>Documentation in 2015</td><td>62%</td><td>29%</td><td>15%</td></tr>
<tr><td>Quality Management System</td><td colspan="3">ISO 17025</td></tr>
<tr><td>Date to reach Performance Targets (90% availability, safety duplication and documentation)</td><td>2021</td><td>>2021</td><td>>2021</td></tr>
<tr><td>Number of staff (FTEs)</td><td colspan="3">93.9 (incl. cryo team)</td></tr>
<tr><td>Germplasm Health Unit</td><td colspan="4">A well-established unit, which is ISO 17025 accredited. Because of lack of investment over the years, there is need for upgrading facilities, equipment and processes.</td></tr>
<tr><td>Plans for improvement</td><td colspan="4">• Advances in phytosanitary research, if funded, would contribute to substantial improvements in the conservation of the collections, in particular a leap of technology is needed to reduce the time required to test and clean the sweet potato and ARTC collections. (No funding has been available to develop phytosanitary diagnostics for ARTC, rendering them mostly unavailable for international distribution).
• Increased capacity is needed in facilities to accommodate the growing herbarium, DNA bank and cryobank.
• Cryopreservation of 50% of the potato collection and 15% of the sweet potato collection
• Testing and cleaning of 2400 potato and 2100 sweet potato accessions
• Viability testing and regeneration of 1800 wild potato and 600 sweet potato seed accessions</td></tr>
<tr><td>Plans for efficiency</td><td colspan="4">• Completion of ongoing identity verification of field, screenhouse and in vitro collections will allow the field collection to be rationalized by approximately 50%
• More than 50% of the potato collection will be cryopreserved, which will allow a 25% reduction of accessions maintained in vitro and eliminate the need to multiply and ship safety duplicates annually to EMBRAPA.
• Reduction of staff by 10 FTEs as a result of rationalization of the field and in vitro collections</td></tr>
<tr><td>External review – selected quotes</td><td colspan="4">*“The Review Panel recognises that genebank staff are highly skilled and dedicated. They have embraced change … and bought into a push to reduce redundancy in the collections*”
“Closer relations between the genebank and the RTB CRP will generate many benefits, such as the better planning of field trials and accession-specific trait associations. The RP were informed of many areas of research interest, including the impacts of climate change across Peru. Clearly, improved integration of research datasets and genebank accessions information would be beneficial, leading to better decision making on pre-breeding lines for banking; or which clones to clean; etc.”</td></tr>
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<tr><td>Integration with researchers and breeders</td><td>Traits from breeding trials will be linked, where applicable, to accessions
Breeding and genebank databases will be linked to allow key information to be cross referenced
The genebank will be better integrated into the Roots, Tubers and Bananas (RTB) CRP to allow greater synergy and coordination between the groups</td></tr>
<tr><td>Distribution between 2012–2014</td><td>Potato: 9742 samples distributed; 40% to users (mostly universities) outside the CGIAR
Sweet potato: 7276 samples distributed; 9% to users (mostly universities) outside the CGIAR
ARTC: 1563 samples distributed; 46% to users (mostly universities) outside the CGIAR
In total CIP distributed to 41 countries.</td></tr>
<tr><td colspan="2">6. ICARDA</td></tr>
<tr><td>Collections</td><td>ICARDA manage highly diverse collections of eight crop groups, characterized by traditional landraces and wild species from the Fertile Crescent. ICARDA’s FIGS[25] subsets (subsets enriched for specific traits inferred from environmental modelling) are frequently requested. The genebank is located on two sites: Morocco for the conservation of cultivated species of wheat, barley, chickpea and lentil; and Lebanon for crop wild relatives of cereals and legumes.</td></tr>
<tr><td>Expertise</td><td>Ahmed Amri (Head of Genetic Resources Unit) has decades-long expertise in both <i>ex situ</i> and <i>in situ</i> conservation, curation of cereals and their wild relatives, cereal pre-breeding and breeding, establishment of genetic resources programmes.
Athanasios Tsivelikas (Genebank Manager in Morocco) is expert in <i>ex situ</i> conservation and curation of cereals and food legumes, evaluation of genetic resources, gap analysis and collecting novel diversity.
Fawzy Nawar (Senior documentation specialist) is a PGR documentalist who developed Genesys and specializes in linking genebank databases to other databases (e.g. BMS).
Mariana Yazbek (Genebank Manager in Lebanon) is a taxonomist with expertise in <i>in situ</i> conservation and best practices for <i>ex situ.</i> conservation of food legumes and forage legume genetic resources.
Ali Shehadeh (Genebank manager in Syria) has curated the forage and range collection for many years. He has expertise in legume taxonomy, gap analysis and collecting novel diversity.
Abdallah Bari and Kenneth Street (part-time consultants) are responsible for the development of FIGS sub-setting approaches.</td></tr>
<tr><td>Status</td><td><table>
<tr><th></th><th>Barley and wheat</th><th>Grain legumes</th><th>Forages</th></tr>
<tr><td>Accession numbers in 2016</td><td>76,140</td><td>44,175</td><td>35,335</td></tr>
<tr><td>Projected accession numbers in 2022 (seed and clonal)</td><td>80,340</td><td>47,175</td><td>37,135</td></tr>
<tr><td>Availability in 2014</td><td>77%</td><td>49%</td><td>23%</td></tr>
<tr><td>Safety Duplication in 2014</td><td>91%</td><td>71%</td><td>60%</td></tr>
<tr><td>Documentation in 2014</td><td colspan="3">62%</td></tr>
<tr><td>Quality Management System</td><td colspan="3">Minimum elements in place by end of 2016</td></tr>
<tr><td>Date to reach Performance Targets (90% availability, safety duplication and documentation)</td><td>2021</td><td>2021</td><td>2023</td></tr>
<tr><td>Number of staff (FTEs)</td><td colspan="3">20.55</td></tr>
</table></td></tr>
<tr><td>Germplasm Health Unit</td><td>ICARDA is relying on national phytosanitary services while they rebuild their own capacity to carry out routine germplasm health testing. Further funding will be needed to ensure adequate capacity is in place in both Morocco and Lebanon.</td></tr>
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[25] Focussed Identification of Germplasm Strategy

Plans for improvement	• ICARDA is re-establishing its active collection from duplicates received from the Svalbard Global Seed Vault. This demands a 5-year investment in staff and equipment • Increased storage capacity in Morocco to host active and base collections of cereals and food legumes (two cold rooms); • Increase capacity of Seed health laboratories in Morocco and Lebanon to overcome the backlog of health testing and cleaning. • Develop strategic approaches to acquisition, especially breeding materials • Undertake collecting missions to fill the gaps, targeting adaptive traits. • Efficient approaches for mining genetic resources for useful sought-after traits (FIGS development).
Plans for efficiency	• Collaboration with CIMMYT for safe duplication of all genetic resources held at ICARDA • Joint multiplication with CIMMYT of Aegilops and wild Triticum in Lebanon • Multiplication of some range species in New Zealand and other NARS collaborating in the collecting missions
Integration with researchers and breeders	• FIGS subsets development for evaluation by CRPs Wheat, Dryland Cereals and Food Legumes • Joint evaluation of FIGS subsets with ICARDA researchers and students • Joint pre-breeding activities with CRPs Wheat, Dryland Cereals and Food Legumes, focusing on use of wild relative species. • Genotyping and phenotyping of genetic resources (FIGS subsets; others)
Distribution between 2012–2014	Barley and wheat: 18,107 samples distributed; 31% distributed to users (mostly NARs and universities) outside the CGIAR Grain legumes: 5937 samples distributed; 2% distributed to users (private individuals) outside the CGIAR Forages: 187 samples distributed; 6% distributed to users (universities and NARS) outside the CGIAR. In total, ICARDA distributed to 22 countries.
7. ICRAF	
Collections	ICRAF has the task of conserving domesticated, partially domesticated and wild tree species. These include species of value for their fruit, timber, medicinal properties or other products. In total, more than 180 species are held as seed and 43 species are held in the field at 38 sites in 15 countries, mostly in Africa but also in Peru, Bangladesh and Viet Nam. ICRAF manages seed in medium-term storage. Long-term storage is provided by Kunming Institute of Botany, China. Nearly all field sites are managed by national partners and germplasm is made available locally.
Expertise	Alice Muchugi (Genetic Resources Manager) has more than 15 years experience in research on sustainable utilization and conservation of indigenous plant genetic resources. Ramni Jamnadass (Leader in Tree Diversity, Domestication and Delivery) has extensive research experience in utilization, improvement and conservation of tree genetic resources. Zakayo Kinyanjui (Seed scientist) has been managing the ICRAF seed-testing laboratory since 2014 and has wide experience in seed research, developing germination protocols for several species.

<table>
<tr><td>Status</td><td>
<table>
<tr><td></td><td>Multipurpose species held as seed</td><td>Fruit trees held in the field</td></tr>
<tr><td>Accession numbers in 2016</td><td>5219</td><td>3600</td></tr>
<tr><td>Projected accession numbers in 2022</td><td>5319</td><td>3600</td></tr>
<tr><td>Availability in 2015</td><td>40%</td><td>Available locally</td></tr>
<tr><td>Safety Duplication in 2015</td><td>15%</td><td>9%</td></tr>
<tr><td>Documentation in 2015</td><td>70%</td><td>80%</td></tr>
<tr><td>Quality Management System</td><td colspan="2">Minimum elements in place by end of 2017</td></tr>
<tr><td>Date to reach Performance Targets (90% availability, safety duplication and documentation)</td><td>2021</td><td>2021</td></tr>
<tr><td>Number of staff (FTEs)</td><td colspan="2">17.61 (including regional staff)</td></tr>
</table>
</td></tr>
<tr><td>Germplasm Health Unit</td><td>ICRAF depends on the expertise of national partners to provide health monitoring in the field. Genebank staff carry out minimal tests for diseases of quarantine risk. Setting up a qualified GHU should be considered.</td></tr>
<tr><td>Plans for improvement</td><td>Since the collection concerns long-lived species, there is little possibility for multiplying seed within an acceptable time frame. ICRAF will, however, re-collect specific target species to ensure that sufficient seed is available for distribution.</td></tr>
<tr><td>Plans for efficiency</td><td>ICRAF will develop strategic conservation priorities for its seed and field collection by the end of 2016. As a result of this, plans will be made for shifting the responsibility for the maintenance of some field sites and species to other parties and focusing on a defined scope for long-term conservation as part of the ICRAF collection. This will include ensuring that long-lived species have sufficient seed for distribution.</td></tr>
<tr><td>External review – selected quotes</td><td><i>“The GRU’s existing collections are globally significant, and their value will be increased once they are fully characterized, and their passport data is complete. However, in order for ICRAF’s GRU to fulfil its true potential, it needs to develop a collections acquisition and retention policy based on ICRAF’s global mandate, identified user needs and cost-effectiveness.</i>”</td></tr>
<tr><td>Integration with researchers and breeders</td><td>ICRAF Genebank is a source and repository of agroforestry tree germplasm for research under the Forestry, Trees and Agroforestry CRP, especially through Flagship 1 (Tree genetic resources to bridge production gaps and promote resilience) with linkages to other CRPs and Platforms.
The genebank has a unique collection of African dryland forage species that directly support research activities in Flagship 3 (Animal Feed and Forages) in the Livestock CRP.
Field genebanks play a dual role of providing planting propagules and data for biological characterization and growth performance.</td></tr>
<tr><td>Distribution between 2012–2015</td><td>Fruit trees: 8274 samples distributed; 24% to users outside the CGIAR, mostly farmer organizations and NARS.
Multipurpose trees: 2163 samples distributed; 66% to users (mostly farmer organizations) outside the CGIAR
In total, ICRAF distributed to 22 countries.</td></tr>
<tr><td colspan="2">8. ICRISAT</td></tr>
<tr><td>Collections</td><td>ICRISAT manages collections of six crops of dryland cereals and grain legumes: pearl millet, small millets, sorghum, chickpea, groundnut and pigeonpea. As well as managing the international genebank in Hyderabad, ICRISAT carries out conservation activities in three regional stations in Africa, which have limited facilities but represent important portals for collecting and distributing germplasm and interacting with key users regionally.</td></tr>
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<tr><td>Expertise</td><td>Hari Upadhyaya (Director Genebank) Groundnut breeder and genebank manager for many years. Recognized by multiple awards, including the Frank Meyer Medal for Genetic Resources in 2013, for his work on developing mini-core collections to promote use of the collection.
D.V.S.S.R. Sastry (Seed collection manager) has more than 30 years experience working at the ICRISAT genebank and manages the seed collections.
K.N. Reddy (Curator) expert in pearl millet and pigeonpea taxonomy and collection management.</td></tr>
<tr><td>Status</td><td><table>
<tr><th></th><th>Millets and sorghum</th><th>Chickpea, groundnut and pigeonpea</th></tr>
<tr><td>Accession numbers in 2016</td><td>74,102</td><td>49,819</td></tr>
<tr><td>Projected accession numbers in 2022 (seed and clonal)</td><td>94,930</td><td>53,521</td></tr>
<tr><td>Availability in 2015</td><td>89%</td><td>78%</td></tr>
<tr><td>Safety Duplication in 2015</td><td>12%</td><td>18%</td></tr>
<tr><td>Documentation in 2015</td><td>96%</td><td>96%</td></tr>
<tr><td>Quality Management System</td><td colspan="2">Minimum elements in place by end of 2016</td></tr>
<tr><td>Date to reach Performance Targets (90% availability, safety duplication and documentation)</td><td>2020</td><td>2020</td></tr>
<tr><td>Number of staff (FTEs)</td><td colspan="2">44.4 (not including regional staff)</td></tr>
</table></td></tr>
<tr><td>Germplasm Health Unit</td><td>ICRISAT has a well-established GHU and good collaboration with national phytosanitary authorities. Facilitating the movement of germplasm inside and outside India continues to be an important priority.</td></tr>
<tr><td>Plans for improvement</td><td>• Seed increase and safety duplication of more than 90,000 accessions to reach targets
• Establish new data management software and capacity to increase availability of information to users
• Define the role and capacity of operations in Africa and ensure all materials are consolidated in long-term storage in Hyderabad
• Capture legacy data of wild species characterization and evaluation data
• Full implementation of barcoding, including field data collection</td></tr>
<tr><td>Plans for efficiency</td><td>• Reduce number of germplasm lines regenerated and multiplied
• Increase seed longevity in base collections (by transferring seed with higher viability)
• Significantly reduce time taken from introduction to long-term conservation</td></tr>
<tr><td>External review – selected quotes</td><td>*“The Review Panel had an impression of a well-organized and effective operation with dedicated staff. Also the agronomy at the regeneration sites was of high quality.”*
“Much information is generated about the collections (e.g. the tremendous success of the mini-core collections). The RP considers it a missed opportunity that so little of this information is made available for genebank users.”</td></tr>
<tr><td>Integration with researchers and breeders</td><td>• Development of multiple-trait specific germplasm lines in mini-core collections in collaboration with breeders to develop high yielding, climate resilient and nutritionally dense cultivars with a broad genetic base.
• Open field days for researchers and breeders to view genebank accessions during germplasm regeneration and characterization</td></tr>
<tr><td>Distribution</td><td>Chickpea, groundnut and pigeonpea: 25,271 samples distributed; 81% to users outside the CGIAR, mostly universities and some NARS.
Millets and sorghum: 14,538 samples distributed; 60% to users outside the CGIAR, to NARS, universities and the commercial sector.
In total, ICRISAT distributed to 41 countries.</td></tr>
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<table>
<tr><th colspan="2">9. IITA</th></tr>
<tr><td>Collections</td><td>IITA manages a range of crops of importance to Africa (cowpea, maize, soybean, Bambara groundnut, African yam bean and other legume species, banana, cassava and yam) requiring very different conservation methods (seed, field and <i>in vitro</i>), and demanding particular attention to prevalent phytosanitary threats.</td></tr>
<tr><td>Expertise</td><td>Michael Abberton (Genebank manager) has expertise in genetic resources, crop improvement, genomics and climate change.
Badara Gueye (<i>In vitro</i> specialist) specialist <i>in vitro</i> culture, including cryopreservation, plant physiology and cell biology.
Tchamba Marimagne (Database manager) specialist in database design, administration and management specifically for genebanks.
Lava Kumar (Head of GHU) is an expert virologist who oversees the GHU and works in germplasm health and diagnostics.</td></tr>
<tr><td>Status</td><td>
<table>
<tr><th></th><th>Seed collections</th><th>Clonal crop collections</th></tr>
<tr><td>Accession numbers in 2016</td><td>23,317</td><td>9440</td></tr>
<tr><td>Projected accession numbers in 2022 (seed and clonal)</td><td>23,731</td><td>9440</td></tr>
<tr><td>Availability in 2015</td><td>30%</td><td>26%</td></tr>
<tr><td>Safety Duplication in 2015</td><td>50%</td><td>32%</td></tr>
<tr><td>Documentation in 2015</td><td>70%</td><td>69%</td></tr>
<tr><td>Quality Management System</td><td colspan="2">Minimum elements in place by end of 2016</td></tr>
<tr><td>Date to reach Performance Targets (90% availability, safety duplication and documentation)</td><td>2017</td><td>2021</td></tr>
<tr><td>Number of staff (FTEs)</td><td colspan="2">40.64</td></tr>
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</td></tr>
<tr><td>Germplasm Health Unit</td><td>A well-established GHU, but requires significant investment to increase staff capacity and refurbish laboratories and a screenhouse.</td></tr>
<tr><td>Plans for improvement</td><td>• Establish and implement high-throughput germplasm cleaning procedure for yam
• Develop a cryobank for the clonal crop collections
• Promote increased and more effective levels of distribution and use of the clonal collections
• Regenerate and health test more than 14,000 seed accessions to reach targets of availability
• Health test and clean 6952 clonal accessions to reach targets of availability.</td></tr>
<tr><td>Plans for efficiency</td><td>• Reduced regeneration frequency by improvements in seed longevity, particularly in medium-term storage
• Full implementation of CIAT cassava MTS system, using silver nitrate in the conservation culture medium, extending intervals between sub cultures.
• Electricity from solar power.
• Full implementation of electronic data capture and field barcoding.
• Increased efficiency of field management for pest and diseases and field operations.
• Use of LIMS and increased levels of automation.</td></tr>
<tr><td>External review – selected quotes</td><td><i>“The genebank documentation is handled with precision, using inventory software. The data are published on the web in an accessible website, which is being upgraded.”</i>
<i>“Considering IITA’s leadership role, one germplasm accession that has not been characterized is one too many. IITA is therefore encouraged to complete, as a matter of utmost urgency, the characterization of all its germplasm accessions and the provision of the data online.”</i></td></tr>
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<tr><td>Integration with researchers and breeders</td><td>Strong collaborations are in place with breeders under RTB and Grain Legume and Maize CRPs, and these will further develop in the next phase. Research collaborations also include work on important crops outside the CRPs, for example, with Crops for the Future Research Centre on Bambara groundnut, and with NARs on clonal crops in particular.</td></tr>
<tr><td>Distribution between 2012–2014</td><td>Seed collections: 6231 samples distributed; 48% to users (universities and NARS) outside the CGIAR.
Clonal crop collections: 299 samples distributed; 59% to users (universities and NARS) outside the CGIAR
In total, IITA has distributed to 28 countries.</td></tr>
<tr><td colspan="2">10. ILRI</td></tr>
<tr><td>Collections</td><td>ILRI manages a collection of 18,640 accessions of 1,723 tropical forage species in Ethiopia. The extremely wide taxonomic diversity of the collection, and the fact that it is mainly composed of wild species, demands quite a different management approach in comparison with typical crop genebanks. The genebank is currently undergoing major renovation to replace the aged, prefabricated structure in which it was previously housed, and to provide facilities to support a modernized genebank.</td></tr>
<tr><td>Expertise</td><td>Jean Hanson (Genebank manager) has more than 35 years experience in running the ILRI genebank and has co-authored many related manuals and scientific papers.
Chris Jones (Feed & Forages Biosciences Program leader) is developing the ILRI program on feed and forage bioscience and has expertise in phenotyping and genotyping forage diversity.</td></tr>
<tr><td>Status</td><td><table>
<tr><td>Accession numbers in 2016</td><td>17,114 as seed; 1561 in the field</td></tr>
<tr><td>Projected accession numbers in 2022</td><td>18,600</td></tr>
<tr><td>Availability in 2015</td><td>47%</td></tr>
<tr><td>Safety Duplication in 2015</td><td>21%</td></tr>
<tr><td>Documentation in 2015</td><td>0%</td></tr>
<tr><td>Quality Management System</td><td>Minimum elements in place by end of 2016</td></tr>
<tr><td>Date to reach Performance Targets (90% availability, safety duplication and documentation)</td><td>2022</td></tr>
<tr><td>Number of staff (FTEs)</td><td>30</td></tr>
</table></td></tr>
<tr><td>Germplasm Health Unit</td><td>The genebank is responsible for seed health testing.</td></tr>
<tr><td>Plans for improvement</td><td>Develop customized strategies for the conservation of individual species based on improved knowledge of seed longevity, demand and diversity.
Increase the use of the collection by making good quality data more readily available
Increase availability and safety duplication of more than 8,000 accessions with low seed number and viability</td></tr>
<tr><td>Plans for efficiency</td><td>Forage strategy will inform conservation priorities and new research will inform longevity intervals, which will lead to rationalization and stratified management of parts of the forage collection</td></tr>
<tr><td>External review – selected quotes</td><td><i>“A key factor for effectively developing a germplasm collection that serves a dual purpose (i.e. meeting the needs of a broad range of users, and conserving germplasm for the future) yet remains manageable in size, is having a curator that understands the gene pools of the crops in question, who is actively engaged with users and other PGR institutes conserving the same or similar material.”</i>
<i>“… it is essential that the germplasm is made to work and in order for this to happen there needs to be good connection to the potential user community.”</i></td></tr>
<tr><td>Interaction between researchers and breeders</td><td>ILRI germplasm conservation activities are closely linked to forage germplasm use and trait identification, the CIAT and EMBRAPA breeding programmes and forage seed systems for delivery through the Livestock CRP.</td></tr>
</table>

<table>
<tr><td>Distribution between 2012–2014</td><td colspan="2">2948 samples distributed; 98% to users outside the CGIAR, mainly NARS and universities.
ILRI distributed to 28 countries.</td></tr>
<tr><td colspan="3">11. IRRI</td></tr>
<tr><td>Collections</td><td colspan="2">IRRI’s Genetic Resource Centre (GRC) operates at high-levels of efficiency and throughput and has been able to meet increasing demands for germplasm while maintaining high standards of conservation. The facilities have aged significantly and IRRI is raising funds to build new facilities. The collection is also of a significant age and many accessions are now approaching the upper limits of their expected lifetime. If seed longevity drops dramatically, as predicted, this will trigger a major effort in seed rejuvenation.</td></tr>
<tr><td>Expertise</td><td colspan="2">Ruaraidh Sackville Hamilton (Head, Genetic Resources Centre) has expertise in genetic resources conservation, use, data management, policy, genetics and pre-breeding.
Fiona Hay (Deputy Head, Genetic Resources Centre) specializes in seed storage physiology, seed dormancy, process automation and best practices.
Patricia Gonzales (Head, Seed Health Unit) expert in phytosanitary and biosafety testing and compliance with IRRI, national and international regulations.</td></tr>
<tr><td rowspan="8">Status</td><td>Accession numbers in 2016</td><td>127,577</td></tr>
<tr><td>Projected accession numbers in 2022</td><td>130,000</td></tr>
<tr><td>Availability in 2015</td><td>94% (meets targets)</td></tr>
<tr><td>Safety Duplication in 2015</td><td>91% (meets targets)</td></tr>
<tr><td>Documentation in 2015</td><td>86%</td></tr>
<tr><td>Quality Management System</td><td>Minimum elements in place by end of 2016</td></tr>
<tr><td>Date to reach Performance Targets (90% availability, safety duplication and documentation)</td><td>2016</td></tr>
<tr><td>Number of staff (FTEs)</td><td>41.7</td></tr>
<tr><td>Germplasm Health Unit</td><td colspan="2">IRRI has a well-established GHU, which provides services to users at a competitive per-unit cost. It is a recognized component of the Philippines quarantine and phytosanitary certification system with responsibilities to the Philippines Government as well as to IRRI. At times of high throughput the genebank staff may assist GHU staff to process samples. The working space and incubation rooms have reached maximum capacity and there is a need to invest in facilities and equipment.</td></tr>
<tr><td>Plans for improvement</td><td colspan="2">• IRRI has a strong focus on seed conservation research, which is enabling it to make significant inroads into improving operations, automating key processes, streamlining data gathering, increasing the longevity of seeds in storage and improving the precision of predicting seed longevity.
• Conservation of wild species requires improvement to ensure adequate genetic representation in the collection.</td></tr>
<tr><td>Plans for efficiency</td><td colspan="2">• IRRI is currently building an automated seed phenotype sorter, which will allow seed processing to take place overnight and free staff for other routine operations.
• IRRI aims to significantly reduce the time taken by incoming samples to reach long-term storage conditions, and to strategically increase seed harvested.
• Research to increase longevity in storage will in the long term bring efficiency by reducing the frequency of seed rejuvenation. However, any potential gains at this time may be offset by an expected increase in the need for rejuvenation because many accessions in the collection are reaching the upper limits of their expected lifetime.</td></tr>
</table>

External review – selected quotes	*"The review team acknowledged the efforts of IRRI management to forge a strong integration between conservation and use of genetic resources and the product-focused breeding programmes in the context of GRiSP. Such thrust is apparent in the gene discovery research and in the enhanced collaboration between breeders and genebank staff in the use of genebank materials."* *"The GRC applies very high standards in its operations. It would, therefore, create a "Gold Standard" if the GRC completes and consolidates a fully documented Quality Management System for its basic genebank operations. The review team notes that attempts have been made in the past to establish this QMS but that the effort has not been completed."*
Integration with researchers and breeders	GRiSP incorporates a connected suite of activities along the full pathway to impact from the genebank accession to the farmer and consumer. Thanks to additional funding through GRiSP and related bilateral projects, the work of the GRC extends well beyond the scope of the Genebanks CRP and this new Genebank Platform, to include molecular analysis of genetic diversity. In the last five years, the remit of the GRC was extended to include the creation, maintenance and distribution of high-value genetic stocks and the sequencing of accessions. This is reflected in a major increase in requests for seed: at almost 35,000 samples/year averaged over the 5-year period 2011-2015, the number of requests is not far short of double the average (20,000/year) during the previous 5 years. Starting in January 2016, the GRC was integrated into the new Genetics and Biotechnology Division of IRRI, to further tighten links between the genebank and researchers. Regular meetings are held with IRRI breeders to set priorities.
Distribution between 2012-2014	119,330 samples distributed; 35% to a wide range of users outside the CGIAR, in a total of 50 countries.

Annex 2. Projections of the annual income from the endowment fund

The Crop Trust endowment is projected to increase from its current level of approximately USD 175 million to reach USD 500 million in 2020 in order to fund long-term grants for the benefit of the crop collections protected under Article 15 of the ITPGRFA. The current fundraising strategy targets some 50 governments, complemented by private donors such as foundations, corporations, industry associations, wealthy individuals and also private households. An international donors' pledging conference will be held on 15 April 2016 in Washington, DC, in conjunction with the IMF/World Bank Spring Meetings. The conference is expected to generate substantial additional financing commitments from government donors, foundations and selected seed industry partners.

Since the Crop Trust Fundraising Strategy was approved, in October 2013, the Crop Trust has encountered a number of new headwinds that were not anticipated at the time. These include an increasing economic weakness in emerging markets that make outreach with several middle-income economies more challenging. Some of these countries now face fiscal and/or currency crises that reduce near-term prospects for their financial engagement with the Crop Trust. Another challenge is the historically low price of oil, which puts oil-exporting partner countries of the Crop Trust in a more difficult fiscal position. Moreover, the large influx of refugees into Europe since mid-2015 has prompted some European countries to re-allocate parts of their Official Development Assistance budgets towards funding the accommodation of refugees in their own country as well as for funding emergency relief operations abroad.

There are additional assumptions that add uncertainty to the meeting of the endowment target of USD 500 million in 2020. While many of the donor countries targeted for grant contributions will provide firm, legislatively approved financing commitments, some donors may opt to pay their contributions over a number of years, which would delay the build-up of the endowment and reduce the investment income available to support crop collections.

The actual income provided by the target endowment will also be influenced by two financial factors. Firstly, the long-term, average investment return assumption for the endowment is 4.0% per year plus the rate of US dollar inflation. Such a return may, however, not be achievable over the next five years, given historically low capital market interest rates on bonds and high volatility in world equity markets, driven by high levels of liquidity from central banks and an uncertain world economic outlook. Should the Crop Trust experience sustained investment returns below its average long-term target, a restriction in income distributions from the endowment to the CGIAR crop collections may have to be considered so as to protect the capital value of the endowment fund. Secondly, the Crop Trust's withdrawals from the endowment are based on the average endowment value over the preceding 12 quarters. Therefore, as the endowment is growing, the associated investment income available for withdrawal rises with a considerable time lag.

With these substantial caveats in mind, the annual investment income projected to become available for withdrawal from the Crop Trust endowment for support of the collections managed by the CGIAR would be as follows: USD 6.75 million for 2017; USD 9.06 million for 2018; USD 11.53 million for 2019; USD 13.35 million for 2020; and USD 15.03 million for 2021. These projections therefore remain unchanged from prior estimates.

The outcome of the 2016 pledging conference and the subsequent effort to win further governments as new donors, primarily from among the G7 and G20 countries, will be critical for building up the endowment fund. Equally important will be the ability of the Crop Trust to protect the endowment from withdrawals of income to cover the operating cost of the Crop Trust Secretariat while the endowment is being built up, by raising annual funding for this purpose.

Should the speed of growth of the endowment be below current expectations, the Crop Trust would undertake every effort to mobilize short-term grant funding from donor governments to complement investment income to be withdrawn from the endowment, so as to meet the projected overall annual contributions by the Crop Trust to the CGIAR genebanks over the period 2017-2021. This would involve working with individual donor governments to provide time-bound project funding to cover the operating expenditures of selected genebanks over a number of years. Donors may also be asked to support specific projects for the upgrading of individual crop collections in need of such funding. Such near-term resource mobilization efforts would be deployed in parallel to the medium-term objective of building up the endowment further to the target level.

Beyond mobilizing grant funding from donors, the Crop Trust is in discussion with a number of governments about sourcing long-term, low-interest ODA loans, under its new Concessional Borrowing Framework. The Crop Trust is also looking into applying for grants or soft-loans from the Green Climate Fund in order to support selected national crop collections. Work is ongoing with the agri-food industry to further develop an endowing-a-crop concept, targeted at specific crop collections. The new Crop Trust Investment Sharing Facility, which is aims to mobilize private investment funds for the purpose of channeling dividend income towards crop conservation activities, is awaiting its actual placement with investors through partner Deutsche Bank. The Crop Trust will also be studying the feasibility of a bond issue, which would fund upgrading of selected genebanks. Finally, following the April 2016 pledging conference, work will start to prepare for the testing of crowd-funding approaches through web-campaigns, targeting household donors. All of these further fundraising efforts aim to complement new donor grant funding for the endowment over then next years.

Annex 3. Curriculum vitae of key personnel

Name: Michael ABBERTON

Current position and affiliation

Head, Genetic Resources Centre, IITA

Profile

Plant breeding, genetic resources, climate change

Employment

2016 to present: Head, Genetic Resources Centre, Deputy Director West Africa, Deputy Director Crop Breeding and Biotechnology, International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria,

2012 to present: Chair in Public Good Plant Breeding, Aberystwyth University, UK

2010- 2012: Head, Genome Diversity and Plant Breeding, Director of International Development, IBERS

2008-2010: Head, Crop Breeding and Genomics, Institute of Biological, Environmental and Rural Sciences (IBERS), Aberystwyth University, UK

2007-2008: Programme Leader, Plant Breeding and Genetics, Institute of Grassland and Environmental Research (IGER)

Education

PhD University of Manchester (1988) Title: Chromosome specific behaviour in an autopolyploid series

BSc Hons Degree in Botany 1st Class, and D.H. Valentine Prize, University of Manchester (1984)

Selected publications:

Istvan Nagy, Susanne Barth, Jeanne Mehenni-Ciz, Michael T Abberton & Dan Milbourne. 2013. A hybrid next-generation transcript sequencing-based approach to identify allelic and homeolog-specific single nucleotide polymorphisms in allotetraploid white clover. *BMC Genomics,* 14(1): 100.

Yates, S., Swain, M., Hegarty, M., Chernukin, I., Lowe, M., Allison, G., Ruttink, T., Abberton, M., Jenkins, G. & Skot, L. 2014. *De novo* assembly of red clover transcriptome based on RNA-Seq data provides insight into drought response, gene discovery and marker identification. *BMC Genomics*, 15(453): 1–33.

Shitta, N.S., Abberton, M., Adesoye, A.I., Adewale, D.B. & Oyatomi, O. 2015. Analysis of genetic diversity of African yam bean using SSR markers derived from cowpea. *Plant Genetic Resources – Characterization and Utilization*, 14(1): 50–56.

Abberton *et al*. 2015. Global agricultural intensification during climate change: a role for genomics. *Plant Biotechnology Journal.* 2015: 1–4.

Kole, C. and 39 others. 2015. Application of genomics-assisted breeding for generation of climate resilient crops: progress and prospects. *Frontiers in Plant Science*. 6: 563. 16p. [doi: 10.3389/fpls.2015.00563]

Other evidence of leadership, large-program management and delivery

Delivery of plant breeding programs, large multinational projects and large UK-funded projects, including public-private partnerships.

Role in the Genebank Platform

Genebank Manager. Implementation of activities under the Platform.

Name: Ahmed AMRI

Current position and affiliation

Head of Genetic Resources Unit, and Deputy Director for Biodiversity and Integrated Gene Management Program at ICARDA

Profile:

Cereal breeding: 21 years of experience, with release of 26 cereal varieties. In situ/on-farm conservation of agrobiodiversity: 15 years. Conducted 5 projects in West Asia and North Africa. Conservation of genetic resources: participated in 12 collecting missions. 40 years of experience in aspects related to genetic resources conservation and use.

Employment

2008 to date: Head of Genetic Resources Unit at ICARDA.

2005–2008: Regional Coordinator of ICARDA for West Asia.

1999–2005: Regional Coordinator for GEF *in situ* conservation project in West Asia at ICARDA.

1980–1999: Cereal breeder, INRA-Morocco.

Education

PhD Genetics and breeding, Kansas State University, Manahattan, KS, USA

MSc Course work at University of Minnesota, USA, and degree from IAV-Hassan II in Morocco.

Selected publications

Amri, A., Hatchett, J.H., Cox, T.S., El Bouhssini, M. & Sears, R.G. 1990. Resistance to Hessian fly from North African Durum Wheat Germplasm. *Crop Science*, 30: 378–381.

Amri, A., Cox, T.S., Hatchett, J.H. & Gill, B.S. 1990. Complementary action of genes for Hessian fly resistance in the wheat cultivar "Seneca". *Journal of Heredity*, 83(2): 378–381.

Rawashdseh, I. & Amri, A. 2006. Genetic characterization of date palm varieties using RAPD markers. *Jordan Journal of Agricultural Sciences*, 2(3): 234–242.

Mohammadi, R. & Amri, A. 2012. Analysis of genotype×environment interaction in rain-fed durum wheat of Iran using GGE-biplot and non-parametric methods. *Canadian Journal of Plant Science*, 92: 757–770.

Mazid, A., Shideed, K. & Amri, A. 2014. Assessment of on-farm conservation of dryland agrobiodiversity and its impact on rural livelihoods in the Fertile Crescent. *Renewable Agriculture and Food Systems,* 29(4): 366–377.

Shehadeh, A., Amri, A. & Maxted, N. 2013. Ecogeographic survey and gap analysis of Lathyrus L. species. *Genetic Resources and Crop Evolution*, 60(7): 2101–2113.

Mohammadi, R. & Amri, A. 2013. Phenotypic diversity and relationships among a worldwide durum wheat (*Triticum turgidum* L. var. *durum*) germplasm collection under rainfed conditions of Iran. *Crop & Pasture Science*, 64: 87–99.

Other evidence of leadership, large-program management and delivery

National Coordinator of Cereal Research in Morocco (15 years; strong breeding programs with release of 60 varieties, including the first hessian fly resistant ones); Regional Coordinator West Asia Program at ICARDA (6 years. Management of GEF project in four countries); Head of Genetic Resources Unit and Deputy Director BIGM program at ICARDA (8 years; coordination of 9 projects).

Role in the Genebank Platform

Applying best practices for conservation of genetic resources; building linkages between Genebanks CRP/Platform and AFS-CRPs; contribute to the building of the Global System for conservation and sustainable use of PGRFA; contribute to gap analysis, FIGS development, policy aspects.

Name: Paula BRAMEL

Current position and affiliation

Scientific Advisor, Global Crop Diversity Trust, Bonn, Germany

Profile

Plant breeding, genetic resources, climate change, research management

Employment

2015 to date: Scientific Advisor, Global Crop Diversity Trust

2012-2015: Global Crop Diversity Trust, Deputy Executive Director

2006-2012: IITA, Deputy Director General, Research for Development

2004-2006: IITA, Director for East and Southern Africa, Research for Development

2002-2004: CRS, CARE, and others as consultant for biodiversity and seed systems

1996-2002: ICRISAT, Principal Scientist, Genetic Resources and Head of Genebank

1985-1996: Kansas State University, Assistant Professor

Education

Ph.D. Iowa State University, 1985, Plant Breeding and Cytogenetics

M.S. Iowa State University, 1980, Plant Breeding

B.S. Iowa State University, 1978, Agronomy

Selected publications:

Kamala, Venkateswaran, Hari C, Sharma, Daggu Monohar Rao, Kodeboyina S. Varaprasad, Paula J. Bramel, and Subhash Chandra. 2012. Interactions of spotted stem borer Chilo partellus with wild relatives of sorghum. Plant Breeding 131: 511-521

Ferguson, Morag E., Richard B. Jones, Paula J Bramel, Carlos Dominguez, Carla Torre do Vale, and Jie Han. 2011. Post-flooding disaster crop diversity recovery: A case study of cowpeas in Mozambique. Disasters

Rupakula Aruna, D. Manohar Rao, S. Sivaramakrishnan, L. Janardhan Reddy, Paula Bramel and Hari Upadhyaya. 2009. Efficiency of three DNA markers in revealing genetic variation among wild Cajanus species. Plant Genetic Resources, Volume 7, Issue 02, pp 113-121

Bhattacharjee, Ranjana, I. S. Khairwal, Paula J. Bramel and K. N. Reddy. 2007. Establishment of a pearl millet [Pennisetum glaucum (L.) R. Br.] core collection based on geographical distribution and quantitative traits. Euphytica 155:35-45.

Other evidence of leadership, large-program management and delivery

More than 30 years of experience as a researcher, which includes 11 years as a Tenured Associate Professor of Agronomy at Kansas State University as a sorghum breeder, and 12 years of experience in research management at ICRISAT and IITA. In additions, more than 10 years of experience at Executive Management, at IITA and Crop Trust She has extensive experience with managing large scale research for development projects in Southeast \asia and Africa at ICRISAT and IITA. Was Chair of the Genebank CRP management team and member of Crop Trust implementation team;

Role in the Genebank Platform

Member of technical and management team at the Crop Trust. Provide technical advice as needed, especially to the Use Module.

Name: Janny van Beem

Current position and affiliation

Genebank Quality Management Systems (QMS) specialist, Global Crop Diversity Trust

Profile:

Conservation standards of plant genetic resources under the Multilateral System of the ITPGRFA

Employment

2014 to date: Genebank QMS specialist, consultant for the Global Crop Diversity Trust

2010–2014: Head of Acquisition and Distribution Unit, International Potato Center (CIP)

1996-2003: Wheat breeder, Centro Internacional de Mejoramiento de Maíz y Trigo (CIMMYT)

Education

Ph.D. 1995 Cornell University, Plant Breeding and Genetics Department

B.Sc. 1986 Colorado State University, Department of Biology

Selected publications

Vargas, F., A. Salas, G. Rossel, R. Gomez, I. Manrique and J. van Beem. 2012. Preservation of Biodiversity in CIP' Ochoa Herbarium at the International Potato Center. XIV Botanical Congress, Trujillo Peru, 9-12 October 2012.

van Beem, J., V. Mohler, R. Lukman, M. van Ginkel, M. William, J. Crossa and A.J. Worland. **2005.** Analysis of Genetic Factors Influencing the Developmental Rate of Globally Important CIMMYT Wheat Cultivars. Crop Science 45:2113-2119.

van Beem, J., A.J. Worland, and M. van Ginkel. 2001. The influence of earliness per se genes on flowering time in CIMMYT wheats. In: the Kronstad Symposium, Ciudad Obregon 15-16 March 2001.

van Beem, J., M. van Ginkel, and S. Rajaram. 2000. Differences in development rate of CIMMYT wheats adapted to irrigated, rain-fed, and semi-arid environments. In: Wheat in a Global Environment. International Wheat Conference, 6; Budapest, Hungary; 5-9 Jun 2000. p. 281.

van Beem, J., T. Farquhar, H. Meyer, M.P. Reynolds., R. Singh, and M. van Ginkel. 1998. Influence of Rht dwarfing genes on stem morphology, biochemistry and biomechanics, and associated lodging effects in wheat. In: Proceeding of the 9th International Wheat Genetics Symposium, Vol 2, Aug 2-7, Saskatoon, Saskatchewan, Canada. p.366-368.

Other evidence of leadership, large-program management and delivery

Implementation at CIP of ISO-accredited quality standards (ISO 17025) in relevant genebank activities that guaranteed safe conservation, maintenance and distribution of plant genetic resources

Focal point at CIP in establishing networks with Peruvian policy makers (National Institute in Defense and Protection of Intellectual Property Rights (INDECOPI), INIA, SENASA, and the National Committee against Biopiracy)

Oversight and coordination of the deployment and data collection of the Global Wheat Yield Trial (GAWYT) in 92 countries with the aim to identify desirable genetic traits for specific eco-regional programs

Role in the Genebank Platform

Coordinate the development of individualized Quality and Risk Management Systems in nine Centre Genebanks and the QMS framework as a whole.

Name: Denise Costich

Current position and affiliation

October 2012 to present. Head, Wellhausen-Anderson Maize Genetic Resources Collection. CIMMYT-Mexico.

Profile

Maize (and grasses) genetics and genomics; population biology; ecological genetics; plant evolution and systematics.

Employment

2011–2012: Plant Biologist USDA-ARS, Cornell University, USA.

2006–2011: Research Biologist and Lab Manager, USDA-ARS, Cornell University, USA.

2007–2011: Project Manager, USDA-DOE Plant Feedstock Genomics for Bioenergy, USDA-ARS, Cornell University, USA.

2004–2006: Research Associate Department of Plant Biology, Cornell University, USA.

Education

PhD in Biology, The University of Iowa, Iowa City, USA. 12/1989

BSc in Biology (Concentration in Ecology and Systematics), Cornell University, Ithaca, NY, USA.

Selected publications

Yongsheng Wu, Felix San Vicente, Kaijian Huang, Thanda Dhliwayo, Denise E. Costich, Kassa Semagn, Nair Sudha, Michael Olsen, Boddupalli M. Prasanna, Xuecai Zhang & Raman Babu. 2016. Molecular characterization of CIMMYT maize inbred lines with genotyping-by-sequencing SNPs. *Theoretical and Applied Genetics* Online 5 Feb 2016. DOI: 10.1007/s00122-016-2664-8

Paul L. Sanchez, Denise E. Costich, Bernd Friebe, Terry A. Coffelt, Matthew A. Jenks & Michael A. Gore. 2014. Genome size variation in guayule and mariola: Fundamental descriptors for polyploid plant taxa. *Industrial Crops and Products,* 54: 1–5.

Lu, F., A. Lipka, R. Elshire, J. Glaubitz, J.H. Cherney, M.D. Casler, E. Buckler & D.E. Costich. 2013. Switchgrass genomic diversity, ploidy and evolution: novel insights from a network-based SNP discovery protocol. *PLoS Genetics* 9(1): e1003215. doi:10.1371/journal.pgen.1003215.

Chia, J.-M., Costich, D., Buckler, E. and 36 others .2012. Maize HapMap2 identifies extant variation from a genome in flux. *Nature Genetics* 44: 803–807.

Costich, D.E., Friebe, B., Sheehan, M.J., Casler, M.D. & Buckler, E.S.. 2010. Genome-size variation in Switchgrass (*Panicum virgatum*): Flow cytometry and cytology reveal rampant aneuploidy. *The Plant Genome,* 3: 130–141.

Blakey, C.A., Costich, D.E., Sokolov, V. & Islam-Faridi, M.N. 2007. *Tripsacum* genetics: from observations along a river to molecular genomics. *Maydica,* 52: 81–99. [Walton Galinat Commemorative Issue].

Role in the Genebank Platform

Genebank manager. Manage activities on conservation and use.

Name: Daniel G. Debouck

Current position and affiliation

Leader, Genetic Resources Program, International Center for Tropical Agriculture (CIAT), Cali, Colombia.

Profile

Genebank manager (78 Staff) for 3 major collections (over 68 000 accessions of Phaseolus beans, Manihot cassava and tropical forages). Plant conservation geneticist, and plant explorer. Awardee of the Frank N. Meyer Medal of plant genetic resources in 2010. Reviewer of articles for 16 international journals.

Employment

2009–2016: Leader, Genetic Resources Program, CIAT, Colombia.

1996–2009: Head, Genetic Resources Unit, CIAT, Colombia.

1992–1996: Senior Scientist, IPGRI-Americas, Colombia.

1990–1992: Research Officer, IBPGR, Italy.

Education

1983: Doctorat en Sciences Agronomiques, cum maxima suma laude, major in Plant Physiology and minor in Ethnobotany and Plant Ecology. Faculté des Sciences Agronomiques de l'Etat, Gembloux, Belgium.

1976: Certificat en Phytotechnie Tropicale, cum maxima suma laude. Faculté des Sciences Agronomiques de l'Etat, Gembloux, Belgium.

Selected publications

Gujaria-Verma, N., Ramsay, L., Sharpe, A.G., Sanderson, L.-A., Debouck, D.G., Tar'an, B. & Bett, K.E. 2016. Gene-based SNP discovery in tepary bean (*Phaseolus acutifolius*) and common bean (*P. vulgaris*) for diversity analysis and comparative mapping. *BMC Genomics*, 17(239): 1–16.

Andueza-Noh, R.H., Serrano-Serrano, M.L., Chacón-Sánchez, M.I., Sanchéz del Pino, I., Camacho-Pérez, L., Coello-Coello, J., Mijangos-Cortés, J., Debouck, D.G. & Martínez-Castillo, J. 2013. Multiple domestications of the Mesoamerican gene pool of Lima bean (*Phaseolus lunatus* L.): evidence from chloroplast DNA sequences. *Genetic Resources & Crop Evolution,* 60(3): 1069–1086.

Porch, T.G., Beaver, J.S., Debouck, D.G., Jackson, S., Kelly, J.D. & Dempewolf, H. 2013. Use of wild relatives and closely related species to adapt common bean to climate change. *Agronomy,* 3: 433–461.

Chacón-Sánchez., M.I., Motta-Aldana, J.R., Serrano-Serrano, M.L. & Debouck, D.G. 2012. Domestication of Lima beans: a new look at an old problem. pp. 330–343, *in*: P. Gepts, T.R. Famula, R.L. Bettinger, S.B. Brush, A.B. Damania, P.E. McGuire and C.O. Qualset (eds.). Biodiversity in Agriculture: domestication, evolution and sustainability. Cambridge University Press, Cambridge, United Kingdom.

Salcedo-Castaño, J., Arraya-Villalobos, R., Castañeda-Alvarez, N., Toro-Chica, O. & Debouck, D.G. 2011. *Phaseolus hygrophilus* (Leguminosae, Papilionoideae), a new wild bean species from the wet forests of Costa Rica, with notes about section *Brevilegumeni*. *Journal of the Botanical Research Institute of Texas,* 5(1): 53–65.

Ramírez-Villegas, J., Khoury, C., Jarvis, A., Debouck, D.G. & Guarino, L. 2010. A gap analysis methodology for collecting crop genepools: a case study with *Phaseolus* beans. *PLoS ONE Biology*, 5(10): 1–18.

Other evidence of leadership, large-program management and delivery

While as Head of GRU, co-PI for a US$ 1.2 million project on Gene flow analysis for environmental safety, involving Colombia and Costa Rica, and two institutions in Germany (with support of BMZ, Germany); While at IPGRI Americas, led a native fruit germplasm program on Passifloraceae for 3 Andean countries, and on Sapotaceae for 4 Central American countries, approved by the InterAmerican Development Bank for US$ 500 000 (renewed).

Role in the Genebank Platform

Collaborator in conservation science and genetic diversity studies.

Name: David Ellis

Current position and affiliation

International Potato Center, Lima, Peru, Head of Genebank.

Leader, Program for Conserving Biodiversity for the Future

Profile

Over 30 years of genetic resources management in academia, industry and the private sector.

Expertise in plant development, medicinal compounds in plants (taxol), plant molecular biology (modification of plant cell walls and control of plant reproduction), plant and insect ecology, cryobiology and conservation of plant genetic resources and diversity.

Employment

2012 to present: Head of Genebank & Leader, Program for Conserving Biodiversity for the Future, CIP

2004–2012: Plant Physiologist/Curator, NCGRP, USDA-ARS, Fort Collins, CO, USA.

2002–2004: Director of Operations, CellFor Inc., Victoria, B.C., Canada.

2000–2002: Founding Scientist and Director of Molecular Biology, CellFor Inc., Vancouver, B.C., Canada.

Education

PhD in Botany, University of Montana, Missoula, Montana, USA.

BA in Botany with Honors, University of Montana, Missoula, Montana. USA.

Selected publications

Cruz, J.L., Alves, A.A., LeCain, D.R., Ellis, D.D. & Morgan. J.A. 2016. Interactive effects between nitrogen fertilization and elevated CO$_2$ on growth and gas exchange of papaya seedlings. *Scientia Horticulturae*, 202: 32–40.

Panta, A., Panis, B., Ynouye, C., Swennen, R., Roca, W., Tay, D. & Ellis, D. 2015. Improved cryopreservation method for the long-term conservation of the world potato germplasm collection. *Plant Cell Tissue and Organ Culture,* 120(1): 117–125.

Vollmer, R., Panta, A., Tay, D., Roca, W. & Ellis. D. 2014. Effect of sucrose pre-culture and PVS2 exposure on the cryopreservation of sweet potato shoot tips [*Ipomoea batatas* (L.) Lam.] using the PVS2 droplet vitrification. *Acta Horticulturae,* 1039: 265–271.

Jenderek, M.M., Ambruzs, B., Tanner, J., Holman, G., Ledbetter, C., Postman, J., Ellis, D. & Leslie, C. 2014. Extending the dormant bud cryopreservation method to new tree species. *ISHS Acta Horticulturae,* No. 1039: II International Symposium on Plant Cryopreservation. [DOI: 10.17660/ActaHortic.2014.1039.16]

Perez, W., Nahui, M., Ellis, D. & Forbes, G.A. 2014. Wide phenotypic diversity for resistance to *Phytophthora infestans* found in potato landraces from Peru. *Plant Disease,* 98(11): 1530–1533.

Alves, A.A.C., Manthey, L., Isabelle, T., Ellis, D. & Jenderek, M.M. 2014. Diversity in oil content and fatty acid profile in seeds of wild cassava germplasm. *Industrial Crops and Products,* 60: 310–315.

Kaya, E., Alves, A., Rodrigues, L., Jenderek, M., Hernandez-Ellis, M., Ozudogru, A. & Ellis, D. 2013. Cryopreservation of *Eucalyptus* genetic resources. *CryoLetters* 34(6): 608–618.

Hay, F.R., de Guzman, F., Ellis, D., Makahiya, H., Borromeo, T. & Sackville Hamilton, N.R. 2013. Viability of *Oryza sativa* (L.) seeds stored under genebank conditions for up to 30 years. *Genetic Resources and Crop Evolution*, 60: 275–296.

Other evidence of leadership, large-program management and delivery

Member of Scientific Advisory Board for SeedSavers and ANDES

2009–2011, Chair, Plant Germplasm Organizing Committee, National Plant Germplasm System.

Role in the Genebank Platform

Member of the current Management Team; member of the Executive Committee for the Article 15 Genebank Managers. Genebank manager at CIP responsible for budget and deliverables from the platform.

Name: Luigi GUARINO

Current position and affiliation

Director of Science & Programs, Global Crop Diversity Trust

Profile

Plant genetic resources conservation

Employment

2016: Director of Science & Programs, Global Crop Diversity Trust, Germany

2007–2015: Senior Scientist, Global Crop Diversity Trust, Italy

2002–2007: Plant Genetic Resources Adviser, Fiji

1987–2002: Scientist, Bioversity International, Cyprus, Kenya & Colombia

Education

BA Applied Biology, University of Cambridge, UK

Selected publications

Guarino, L., Ramanatha Rao, V. & Reid, R. (eds). 1995. Collecting Plant Genetic Diversity. Technical Guidelines. CAB International, Wellesbourne.

Burke, M.B. Lobell D.B. &Guarino L. 2009. Shifts in African crop climates by 2050, and the implications for crop improvement and genetic resources conservation. *Global Environmental Change*, 19(3): 317-325.

Dawson, I.K. Hedley, P.E. Guarino L. & Jaenicke H. 2009. Does biotechnology have a role in the promotion of underutilised crops? *Food Policy,* 34(4): 319–328.

Jaenicke, H. Dawson, I.K. Guarino L. & Hermann, M. 2009. Impacts of underutilized plant species promotion on biodiversity. *ISHS Acta Horticulturae*, no. 806. International Symposium on Underutilized Plants for Food Security, Nutrition, Income and Sustainable Development. 621–628. DOI: 10.17660/ActaHortic.2009.806.77

Guarino, L. & Lobel, D.B. l. 2011. A walk on the wild side. *Nature Climate Change,* 1: 374–375.

Westengen, O.T., Jeppson, S. & Guarino, L. 2013. Global *ex situ* crop diversity conservation and the Svalbard Global Seed Vault: assessing the current status. *PLOS one,* 8(5).

Khoury, C.K., Bjorkman, A.D., Dempewolf, H., Ramirez-Villegas, J., Guarino, L., Jarvis, A., Rieseberg, L.H. & Struik, PC. 2014. Increasing homogeneity in global food supplies and the implications for food security. *Proceedings of the National Academy of Sciences of the United States of America,* 111(11): 4001–4006.

Castañeda-Álvarez, N., Khoury, C., Achicanoy, H., Bernau, V., Dempewolf, H., Eastwood, R., Guarino, L., Harker, R., Jarvis, A., Maxted, N., Müller, J., Ramirez-Villegas, J., Sosa, C., Struik, P., Vincent, H. & Toll, J. 2016. Global conservation priorities for crop wild relatives. *Nature Plants*, 16022.

Other evidence of leadership, large-program management and delivery:

Pacific Agricultural Plant Genetic Resources Network (PAPGREN). Organized from scratch and ran for 4 years a regional PGRFA network covering two dozen countries and territories.

Securing the Biological Basis of Agriculture and Promoting New and Fuller Use of Crop Genetic Resources. On management team of global project implemented by Crop Trust, funded by Bill and Melinda Gates Foundation.

Adapting Agriculture to Climate Change: Collecting, Protecting and Preparing Crop Wild Relatives. Developed and helped implement global project supported by Government of Norway.

Role in the Genebank Platform

Member of Management Team.

Name: Michael HALEWOOD

Current position and affiliation

Leader, Genetic Resources Policies, Institutions and Monitoring group, Bioversity International.

Profile

Designing, overseeing and conducting policy-relevant research and capacity building projects concerning the management and conservation of agricultural biological diversity from local to global levels. Main research areas: factors affecting availability and use of crop diversity on-farm, and in globally developed systems of conservation and sustainable use; access and benefit sharing.

Employment

2001 to present: Leader, Genetic Resources Policies, Institutions and Monitoring Group, Bioversity International, Italy

1997–2001: Coordinator, Crucible Group, International Development Research Centre, Canada

Education

Doctor of Jurisprudence, Osgoode Hall Law School, York University

Bachelor of Law, University of Toronto

Bachelor of Arts and Science (Political Science), University of Toronto

Selected publications

Galuzzi, G., Halewood, M., Lopez, I. & Vernooy, R. (forthcoming). Twenty five years of international exchanges of plant genetic resources facilitated by the CGIAR genebanks: a case study on international interdependence. *Biodiversity and Conservation* .

Halewood, M. (ed.) 2016. *Farmers' Crop Varieties and Farmers' Rights: Challenges in Taxonomy, Agriculture and Law.* Routledge, Oxon.

Bedmar Villanueva, A., Halewood, M. & López Noriega, I. 2015. Agricultural Biodiversity in climate change adaptation planning: an analysis of the National Adaptation Programs of Action. CCAFS Working Paper no. 95.

Halewood, M. 2014. International efforts to pool and conserve crop genetic resources in times of radical legal change. *In:* M. Cimoli, G. Dosi, K.E, Maskus, R.L., R.L. Okediji, J.L. Reichman, and J.E. Stiglitz (eds). *Intellectual Property Rights: Legal and Economic Challenges for Development*. Oxford University Press, Oxford, UK.

Halewood, M., Lopez Noriega I. & Louafi, S. (eds.). 2013. *Crop Genetic Resources as a Global Commons: Challenges in international governance and law*, Routledge, Oxon.

Halewood, M. 2013. What kind of goods are plant genetic resources for food and agriculture? Towards the identification and development of a new global commons. *International Journal of the Commons*. 7(2): 278–312.

Halewood, M., Andrieux, E., Crisson, L., Gapusi, J.R., Wasswa Mulumba, J., Koffi, E.K., Yangzome Dorji, T., Bhatta, M.R. & Balma, D. 2013. Implementing 'Mutually Supportive' Access and Benefit Sharing Mechanisms under the Plant Treaty, Convention on Biological Diversity, and Nagoya Protocol. Law. *Environment and Development Journal* 9/1

Other evidence of leadership, large-program management and delivery

Managed Genetic Resources Policy Initiative I, 2005–2009 (US$ 5 million). Managed Genetic Resources Policy Initiative II, 2011–2015 (US$ 5 million); Managed numerous smaller projects with partners in Asia, Africa and South America; Nominated as a facilitator of a "Friends of Co-Chairs" group with mandate to develop text for ongoing renegotiations of the ITPGRFA multilateral system of access and benefit-sharing; Coordinated international 50-member 'think tank' called the Crucible Group, focusing on genetic resources and intellectual property-related issues.

Role in the Genebank Platform

Coordinator of the Policy Module, coordinating on behalf of the Platform Management Team.

Name: Ruaraidh Sackville Hamilton

Current position and affiliation

Principal Scientist, Evolutionary Biology, and Head, T.T. Chang Genetic Resources Center, International Rice Research Institute (IRRI).

Profile

Over 40 years of experience in the conservation and use of crop genetic resources, including best practices and workflow management systems for genebank management; database design and data management; statistics, genetics and genomics; crop wild relatives; pre-breeding; plant breeding; plant ecology; GM biosafety; and international policy on access and benefit-sharing.

Employment

2002 to present: Head, T.T. Chang Genetic Resources Center, IRRI, Los Baños, Laguna, Philippines.

1991–2002: Head, Biodiversity Group and Genetic Resources Unit, IGER, Aberystwyth, UK

1986–1991: Senior Research Fellow, University of Wales at Bangor, Bangor, UK

1984–1986: Senior Research Fellow, CIAT, Cali, Colombia

Education

PhD Plant Genetic Resources, University of Cambridge, UK

MA Applied Biology, University of Cambridge, UK.

Selected publications

Zhao, X., Daygon, V.D., McNally, K.L., Sackville Hamilton, N.R., Xie, F., Reinke, R.F. & Fitzgerald, M.A. 2016. Identification of stable QTLs causing chalk in rice grains in nine environments. *Theoretical and Applied Genetics*, 129: 141–153.

Hay, F.R., de Guzman, F. & Sackville Hamilton, N.R. 2015. Viability monitoring intervals for genebank samples of *Oryza sativa*. *Seed Science and Technology*, 43: 218–237.

Leung, H., Raghavan, C., Zhou, B., Oliva, R., Choi, I.R., Lacorte, V., Jubay, M.L., Cruz, C.V., Gregorio, G., Singh, R.K.& Sackville Hamilton, N.R. 2015. Allele mining and enhanced genetic recombination for rice breeding. *Rice*, 8: 1–11.

Alexandrov, N., Tai, S., Wang, W., Mansueto, L., Palis, K., Fuentes, R.R., Ulat, V.J., Chebotarov, D., Zhang, G., Li, Z. & Sackville Hamilton, N.R. 2015. SNP-Seek database of SNPs derived from 3000 rice genomes. *Nucleic Acids Research,* 43: D1023–D1027.

Banaticla-Hilario, M.C.N., McNally, K.L., van den Berg, R.G., & Sackville Hamilton, N.R. 2013. Crossability patterns within and among *Oryza* series *sativae* species from Asia and Australia. *Genetic Resources and Crop Evolution,* 60: 1899–1914.

Halewood, M., Sood, R., Sackville Hamilton, N.R., Amri, A., Van den Houwe, I., Roux, N., Dumet, D., Hanson, J. Upadhyaya, H.D., Jorge, A. & Tay, D. 2013. Changing rates of acquisition of plant genetic resources by international gene banks. pp. 99–132, *in:* M. Halewood, I.L. Noriega and S. Nouafi (eds). Crop Genetic Resources as a Global Commons. Publ. for Bioversity International by Routledge, Oxon, UK.

McCouch, S.R., McNally, K.L., Wang, W., & Sackville Hamilton, N.R. 2012. Genomics of gene banks: A case study in rice. *American Journal of Botany,* 99: 407–423.

Other evidence of leadership, large-program management and delivery

Currently managing a budget of US$ 5.98 million under Genebanks CRP and GRiSP and associated special projects. Major past successes include the GPG1 and GPG2 genebank upgrading projects, establishing a new conservation research program at IRRI, and the 3000 rice genomes project. Expert on loan to help develop ITPGRFA’s “Global Information System”. Member of steering, advisory or executive committees of Svalbard Global Seed Vault, Divseek and Genesys.

Role in the Genebank Platform

Head of IRRI genebank; member of executive committee of A15G and the Management Team. Also contributing to the coordination of the Policy Module.

Name: Jean Hanson

Current position and affiliation

Leader, Forage Diversity, ILRI

Profile

Genetic resources specialist with 40 years of experience in seed conservation and genebank management, mostly in developing countries. Current research interests include management of forage genetic resources, seed longevity in genebanks, morphological and nutritional characterization, seed production, forage adoption, and knowledge sharing.

Employment

2014 to date: Leader, Forage Diversity, International Livestock Research Institute, Ethiopia

1986–2010: Leader, Forage Diversity/genebank manager, ILRI, Ethiopia

1978–1983: Technical co-operation officer in DFID, National Biological Institute, Indonesia

1976–1978: Post-doctoral fellow, Maize Programme, CIMMYT, Mexico

Education

PhD seed storage, University of Birmingham, UK.

MSc Conservation and Utilization of Plant Genetic Resources, University of Birmingham, UK.

Selected publications

Maass, B.L., Jamnadass, R.H., Hanson, J. & Pengelly, B.C. 2005. Determining sources of diversity in cultivated and wild *Lablab purpureus* related to provenance of germplasm by using amplified fragment length polymorphism. *Genetic Resources and Crop Evolution*, 52: 683–695.

Pengelly, B.C., Cook, B.G., Partridge, I.J., Eagles, D.A., Peters, M., Hanson, J., Brown, S.D., Donnelly, J.L., Mullen, B.F., Schultze-Kraft, R., Franco, A. & O'Brien, R. 2005. Selection of Forages for the Tropics (SoFT) – a database and selection tool for identifying forages adapted to local conditions in the tropics and subtropics. *In:* F.P. O'Mara, R.J. Wilkins, L. t'Mannetje, D.K. Lovett, P.A.M. Rogers and T.M. Boland (eds). XX International Grassland Congress. Academic Publishers, Wageningen, The Netherlands.

Ponsens, J., Hanson, J., Schellberg, J. & Moeseler, B.M. 2010. Characterization of phenotypic diversity, yield and response to drought stress in a collection of Rhodes grass (*Chloris gayana* Kunth) accessions. *Field Crops Research*, 118: 57–72.

Reid, R.S., Serneels, S., Nyabenge, M. & Hanson, J. 2005. The changing face of pastoral systems in grass dominated ecosystems of Eastern Africa. pp. 19–76, *in:* J.M. Suttie, S.G. Reynolds and C. Batello (eds.). *Grasslands of the World*. FAO Plant Protection and Production Series, No. 34. FAO, Rome.

Rao, N.K., Hanson, J., Dulloo, M.E., Ghosh, K., Nowel, D. & Larinde, M. 2006. Manual of seed handling in genebanks. Handbooks for Genebanks, No. 8. Bioversity International, Rome, Italy.

Van de Wouw, M., Hanson, J. & Luethi, S. 1999. Morphological and agonomic characterization of a collection of Napier grass (*Pennisetum purpureum*) and *P. purpureum* × *P. glaucum*. *Tropical Grasslands*, 33(3): 150–158.

Wanjala, B.W., Obonyo, M., Wchira, F.N., Muchugi, A., Mulaa, M., Harvey, J., Skilton, R.A., Proud, J. & Hanson, J. 2013. Genetic diversity in Napier grass (*Pennisetum purpureum*) cultivars: Implications for breeding and conservation. AoB PLANTS, 5: Article plt022. doi:10.1093/aobpla/plt022.

Other evidence of leadership, large-program management and delivery

Managing a project of US$ 1.5 to 2 million in recent years, and has developed funding proposals for up to US$ 10 million on use of forage diversity.

Role in the Genebank Platform

Genebank platform. Implementation of Conservation and Use Module activities in ILRI.

Name: Fiona HAY

Current position and affiliation

Senior Scientist I, Genetic Resources Expert, T.T. Chang Genetic Resources Center, IRRI HQ.

Profile

More than 20 years research on seed collection, germination/dormancy, storage behaviour and longevity in relation to genebank management and use of collections. Chief Editor, Seed Science and Technology.

Employment

2012 to date: Senior Scientist I, Genetic Resources Expert, T.T. Chang Genetic Resources Center, IRRI

2009–2012: Scientist II, Genetic Resources Expert, T.T. Chang Genetic Resources Center, IRRI

1997–2009: Seed Physiologist, Millennium Seed Bank Partnership, Royal Botanic Gardens Kew, UK

Education

PhD The development of seed longevity in wild plant species. King's College, University of London, UK

MSc Applied statistics and operational research. Birkbeck College, University of London, UK.

Selected publications

Hansen, M.A.E., Hay, F.R. & Carstensen, J.M. 2015. A virtual seed file: the use of multispectral image analysis in the management of genebank seed accessions. *Plant Genetic Resources*. http://dx.doi.org/10.1017/S1479262115000362

Whitehouse, K.J., Hay, F.R. & Ellis, R.H. 2015. Increases in the longevity of desiccation-phase developing rice seeds: response to high temperature drying depends on harvest moisture content. *Annals of Botany*, 116: 247–259.

Hay, F.R., de Guzman, F. & Sackville Hamilton, N.R. 2015. Viability monitoring intervals for genebank samples of *Oryza sativa. Seed Science and Technology*, 43: 218–237.

Hay, F.R., Timple, S. & van Duijn, B. 2015. Can chlorophyll fluorescence be used to determine the optimal time to harvest rice seeds for long-term genebank storage? *Seed Science Research*, 25: 321–334.

Hay, F.R., Mead, A. & Bloomberg, M. 2014. Modelling seed germination in response to continuous variables: use and limitations of probit analysis and alternative approaches. *Seed Science Research*, 24: 165–186.

Hay, F.R. & Probert, R.J. 2013. Advances in seed conservation of wild plant species: a review of recent research. *Conservation Physiology*, 1: Issue 110.1093/conphys/cot030

Other evidence of leadership, large-program management and delivery

PI for two collecting projects (East Africa and Bangladesh)

IRRI Recommendation Action Plan (Genebank CRP project)

Seed Longevity Initiative of CGIAR Genebanks (Genebank CRP project).

Role in the Genebank Platform

Deputy Head, T.T. Chang Genetic Resources Center at IRRI, Head of conservation research and leading research activities on seed longevity.

Name: Lava KUMAR

Current position and affiliation

Head, Germplasm Health Unit/Virologist; International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria

Profile

Virology; molecular biology; epidemiology; diagnostics; phytosanitation; germplasm health management; host plant resistance; IPM & IDM; germplasm indexing; production of disease-free planting material; international exchange of germplasm; knowledge and technology dissemination; R&D coordination and program management.

Employment

2010 to present: Head, Germplasm Health Unit / Virologist, IITA, Nigeria

2007 to 2010: Virologist (West & Central Africa): IITA, Nigeria

2005 to 2007: Scientist – Virology: ICRISAT, India

2004 to 1999: Special Project Scientist (Virology): ICRISAT, India

Education

PhD Virology. Sri Venkateswara University, Tirupati, India

MSc Virology Sri Venkateswara University, Tirupati, India

Selected publications

Kumar, P.L., Selvarajan, R., Iskra-Caruana, M.-L., Chabannes, M. & Hanna, R. 2015. Biology, etiology and control of virus diseases of banana and plantain. *Advances in Virus Research,* 91: 229–269. [http://dx.doi.org/10.1016/bs.aivir.2014.10.006]

Kamowa-Mbewe, W., Kumar, P.L., Changadeya, W., Ntawuruhunga, P. & Legg, J.P. 2015. Diversity, distribution and effects on cassava cultivars of cassava brown streak viruses in Malawi. *Journal of Phytopathology,* 163(6): 433–443. [doi: 10.1111/jph.12339]

Silva, G., Bömer, M., Nkere, C., Kumar, P.L. & Seal, S.E. 2015. Rapid and specific detection of Yam mosaic virus by reverse-transcription recombinase polymerase amplification. *Journal of Virological Methods,* 222: 138–144. [Doi: http://dx.doi.org/10.1016/j.jviromet.2015.06.011]

Patil, B.L. & Kumar, P.L. 2015. Pigeonpea sterility mosaic virus: a legume-infecting *Emaravirus* from South Asia. *Molecular Plant Pathology,* 16(8): 775–786. [Doi. No. 10.1111/mpp.12238]

Kumar, P.L., Hanna, R., Alabi, O.J., Soko, M.M., Oben, T.T., Vangu, G.H.P. & Naidu, R.A. 2011. *Banana bunchy top virus* in sub-Saharan Africa: investigations on virus distribution and diversity. *Virus Research,* 159: 171–182.

Gerald Otti, G., Bouvaine, S., Kimata, B., Mkamillo, G., Kumar, P.L., Tomlins, K., Maruthi, M.N. 2016. High throughput multiplex real time PCR assay method for the simultaneous quantification of DNA and RNA viruses infecting cassava plants. *Applied Microbiology* (forthcoming).

Seal, S., Turaki, A., Muller, E., Kumar, P.L., Kenyon, L., Filloux, D., Galzi, S., Lopez-Montes, A. & Iskra-Caruana, M.-L. 2014. The prevalence of badnaviruses in West African yams (*Dioscorea cayenensis-rotundata*) and evidence of endogenous para retrovirus sequences in their genomes. *Virus Research,* 186: 144–154.

Other evidence of leadership, large-program management and delivery

Initiated BBTV Alliance in 2009, for BBTD control in Africa; Led disease component of GLCI, funded by BMGF, which led to the mapping of cassava brown streak in East Africa and also development of diagnostic capacity; Led, plant health component of seed yam of YIIFSWA project funded by BMGF;

Advisory member and observer of the Inter-African Phytosanitary Council.

Role in the Genebank Platform

Liaison with CGIAR GHUs on needs assessment and priorities; link to AFS CRPs on RTB, MAIZE and DCLASS.

Name: Isabel LÓPEZ NORIEGA

Current position and affiliation

Policy specialist, Bioversity International

Profile

Policy research, analysis and advocacy in the area of plant genetic resources for food and agriculture; design and coordination of multi-country projects on the conservation and use of crop diversity, involving research and development partners at local, national and international levels; capacity building for the implementation of international conventions on genetic resources; representation in the CGIAR Centres (up to 2012) and Bioversity International in the governing bodies and negotiating working groups of the Convention on Biological Diversity, the Treaty on Plant Genetic Resources for Food and Agriculture, and the WIPO Intergovernmental Committee on Intellectual Property and Genetic Resources, Traditional Knowledge and Folklore.

Employment

2006 to Present: Scientist and Policy specialist, Bioversity International

2000–2006: Junior researcher at the Unesco Chair for the Environment, Universidad Rey Juan Carlos, Madrid

Education

MA International Biodiversity Law, Universidad Rey Juan Carlos, Madrid, Spain

Law, five year degree, Universidad Complutense de Madrid, Spain

Selected publications

López Noriega, I. 2016. Defensive protection of farmers’ varieties. *In:* M. Halewood (ed.). *Farmers' Crop Varieties and Farmers' Rights: Challenges in Taxonomy and Law*. Routledge, London & New York.

Jarvis, D.I., Hodgkin, T., Brown, A., Tuxill, J., López Noriega, I., Smale, M. & Sthapit, B. 2016. *Crop Genetic Diversity in the Field and on the Farm. Principles and Applications in Research Practices*. Yale University Press, New Haven & London.

Maggioni, L., López Noriega, I., Lapeña García, I. & Engels, J. 2015. Collecting plant genetic resources in Europe: a survey of legal requirements and practical experiences. *In:* B. Coolsaet, F., Batur, A. Broggiato, J. Pitseys and Dedeurwaerdere (eds.). *Implementing the Nagoya Protocol: Comparing Access and Benefit-sharing Regimes in Europe.* Brill/Nijhof, Enschede, Netherlands.

Halewood, M., López Noriega, I. & Louafi, S. (eds.). 2013. *Crop Genetic Resources as a Global Commons. Challenges in international law and governance*. Routledge, London & New York.

López Noriega, I., Halewood, M., Galluzzi, G., Vernooy, R., Bertacchini, E., Gauchan, D. & Welch, E. 2013. How Policies Affect the Use of Plant Genetic Resources: The Experience of the CGIAR. *Resources*, 2(3): 231–269.

Other evidence of leadership, large-program management and delivery

2012–2016 Grant manager and coordinator of the project “Improving seed systems for smallholder farmers’ food security”, US$ 2 million, funded by SDC and implemented in five countries.

2006–2016 Member of the Bioversity team in charge of the Genetic Resource Policy Initiative, ca. US$ 10 million , funded by DGIS and implemented in 13 countries and two regions.

2006–2012 Policy-related assistance to CGIAR Centres under the System-wide Genetic Resource Programme.

Role in the Genebank Platform

Policy specialist.

Name: Charlotte Lusty

Current position and affiliation

Genebank Program Coordinator, Global Crop Diversity Trust

Profile

Project management, genetic resources conservation, animal-plant interactions, botany

Employment

2008 to present Senior Scientist, Global Crop Diversity Trust, Italy & Germany

2000–2007 Scientist, Bioversity International, France

1994–2000 Research Officer, UNEP-World Conservation Monitoring Center, UK

1991–1993 Field Researcher, Jane Goodall Insitute, Tanzania

Education

BSc (Hons) Degree in Zoology (2.1) University of Edinburgh

Selected publications:

Lusty, C., Guarino, L, Toll, J. & Lainoff, B. 2014. Genebanks: past, present and optimistic future. *In:* N Van Alfen (ed.). Encyclopedia of Agriculture and Food Systems. Academic Press.

McCouch, S. *et al*. 2013. Agriculture feeding the future. *Nature,* 499: 23–24. doi:10.1038/499023a

Ngoh Newilah, G., Lusty, C., Van den Bergh, I., Akyeampong, E., Davey, M.W., & Tomekpe, K. 2008. Evaluating bananas and plantains grown in Cameroon as a potential source of carotenoids. *Food-Global Science Books,* 2 (2): , 135 –138.

Davey, M.W., E. Stals, E., G. Ngoh Newilah, G., K. Tomekpe, K., C. Lusty, C., R. Markham, R., R. Swennen, R., & J. Keulemans, J. 2007. Sampling strategies and variability in fruit pulp micronutrient contents in West and Central African bananas and plantains (*Musa* species). *Journal of Agricultural and Food Chemistry,* 55(7): . 2633–2644.

Lusty, C. & J. Yuen, J. 2005. Documenting the ‘3M’ Approach in Genetic Resources Policy Initiative. GRPI working paper.

Oldfield, S., Lusty, C. & MacKinven, A. 1998. The world list of threatened trees. World Conservation Press.

Other evidence of leadership, large-program management and deliver

Coordinates the current Genebank CRP. Coordinated and played a key role in the genebank costing study which lead to the publication of Shands, H., Hawtin, G. & MacNeil, G. 2010. The Cost to the CGIAR Centres of maintaining and distributing germplasm.

Also managed or managed components of the following large projects: “Securing the Biological Basis of Agriculture and Promoting New and Fuller Use of Crop Genetic Resources”funded by Bill and Melinda Gates Foundation; HarvestPlus Challenge Programme initiative to address micronutrient-deficiencies with high-provitamin A plantain cultivars; Global Conservation Strategy for Musa; “Conservation and Sustainable Management of Trees”, funded by the Government of the Netherlands.

Role in the Genebank Platform

Platform Coordinator

Name: Alice MUCHUGI

Current position and affiliations

January 2014 to date Genetic Resource Unit Manager, World Agroforestry Centre (ICRAF) Nairobi.

Profile

More than 15 years' experience in research on sustainable utilization and conservation of indigenous plant genetic resources. Research mainly on morphological, biochemical and genetic characterization of plant germplasm

Employment History

2007–2013: Consultant, Genetic Resource Unit Manager, World Agroforestry Centre (ICRAF) Nairobi.

2002 –2013: Senior Lecturer: Dept of Biochemistry and Biotechnology, Kenyatta University, Kenya.

2001 –2002: Lecturer: Nairobi Technical Training Institute, Kenya

Education

PhD in Population Genetics, Kenyatta University, Kenya

MSc in Biotechnology, Kenyatta University, Kenya

BSc in Agriculture, Egerton University, Kenya

Selected publications:

Makueti, J.T., Otieno, G., Tchoundjeu, Z., Muchugi, A., Tsobeng, A., Asaah, E. & Kariba, R. 2015. Genetic diversity of *Dacryodes edulis* provenances used in controlled breeding trials, *Journal of Plant Breeding and Crop Science,* 7(12): 327–339. DOI: 10.5897/JPBCS2015.0511

Gwali, S., Vaillant, A., Nakabonge, G., Lamoris Okullo, J.B., Eilu, G., Muchugi, A. & Bouvet, J.M. 2014. Genetic diversity in shea tree (*Vitellaria paradoxa* subspecies *nilotica*) ethno-varieties in Uganda assessed with microsatellite markers. *Forests, Trees and Livelihoods*, 24(3): 163-175.

Macharia, M.W., Run, S., Muchugi, A. & Palapala, V. 2014. Genetic structure and diversity of East African taro (*Colocasia esculenta* L Schott) *African Journal of Biotechnology*, 13(29): 2950–2955.

Russell, J.R., Hedley, P.E., Cardle, L., Dancey, S., Morris, J., Booth, A., Odee, D., Mwaura, L., Omondi, W., Angaine, P., Machua, J., Muchugi, A., Milne, I., Kindt, R., Jamnadass, R. & Dawson, I.K. 2014. tropiTree: An NGS-Based EST-SSR Resource for 24 Tropical Tree Species. *PLoS ONE*, 9(7): e102502. [doi:10.1371/journal.pone.0102502]

Wanjala, B.W., Obonyo, M., Wachira, F.N., Muchugi, A., Mulaa, M., Harvey, J., Skilton, R.A., Proud, J. & Hanson, J. 2013. Genetic diversity in Napier grass (*Pennisetum purpureum*) cultivars: implications for breeding and conservation. *AoB PLANTS,* 5: plt022; doi:10.1093/aobpla/plt022

Muchugi, A., Muluvi, G.M., Kindt, R., Kadu, C.A.C., Simons, A.J. & Jamnadass, R.H. 2008. Genetic structuring of important medicinal species of genus *Warburgia* as revealed by AFLP analysis. *Trees Genetics and Genome,* 4: 787–795.

Muchugi, A.M., Lengkeek, A.G., Agufa, C.A.C, Muluvi, G.M., Njagi, E.N.M. & Dawson, I.K. 2006. Genetic variation in the threatened medicinal tree *Prunus africana* in Kenya and Cameroon: implications for current management and evolutionary history. *South African Journal of Botany,* 72: 498–506.

Other evidence of leadership, large-program management and deliver

ICRAF Focal person CRP Genebanks (2012–2016), managing Genebank in Nairobi and field genebanks in six regions.

Project PI Lake Victoria Research (VicRes) Grant (2008–2011) implemented in Kenya, Uganda and Tanzania.

Role in the Genebank Platform

ICRAF Genebank Manager-Focal point person in the platform. Oversee activities in the Conservation and Use Modules.

Name: Marie-Noëlle Ndjiondjop

Current position and affiliation

Head of Genetic Resources, Africa Rice Center (AfricaRice), Cotonou, Benin

Profile

Scientist and manager in agricultural research for development, with progressive career as Post-Doctoral fellow, Associate Principal Scientist and Principal Scientist at international levels. Attained Doctorate Degree in Plant Biology with emphasis on biochemistry and molecular biology, and with strong background in research for development in rice genetic resources and biotechnology for rice improvement; research management and coordination; and leadership and team management. Received the 2005 Director General's Service award for an impressive contribution to resource mobilization and strengthening scientific capacity at The Africa Rice Center (AfricaRice). Received Dr. Robert J. Carsky Memorial Award in recognition of outstanding service and contribution to the Africa Rice Center (AfricaRice) for the period 2011–2012.

Employment

2013 to date: Head of Genetic Resources (AfricaRice)

2012 to 2013: Senior Molecular Biologist and GRiSP Theme 1 Leader for Africa (AfricaRice)

Education

PhD in Plant Biology, University of Montpellier

MSc in Nutrition in Developing Countries, University of Montpellier

MSc in Molecular and Cellular Biology, University of Montpellier

BSc in Biochemistry and Molecular Biology, University of Montpellier

Selected publications:

Number of publications in international journals: 23. Hirsch index (Web of Science): 9

Wang, M., Yu, Y., Haberer, G., Marri, P.R., Fan, C., Goicoechea, J.L., Ndjiondjop, M.N. & Wing, R.A. 2014. The genome sequence of African rice (*Oryza glaberrima*) and evidence for independent domestication. *Nature Genetics*, 46: 982–988.

Ndjiondjop, M.N., Futakuchi, K., Cisse, F., Baimey, H., & Bocco, R. 2012. Field evaluation of rice genotypes from the two cultivated species (*Oryza sativa* L. and *Oryza glaberrima* Steud.) and their interspecifics for tolerance to drought. *Crop Science,* 52(2): 524–538. [DOI: 10.2135/cropsci2011.05.0]

Bocco, R., Lorieux, M., Seck, P.A., Futakuchi, K., Manneh, B., Baimey, H. & Ndjiondjop, M.N. 2012. Agro-morphological characterization of a population of introgression lines derived from crosses between IR 64 (*Oryza sativa indica*) and TOG 5681 (*Oryza glaberrima*) for drought tolerance. *Plant Science*, 183: 65–76.

Ndjiondjop, M.N., Manneh, B., Cissoko, M., Drame, N.K., Glele Kakai, R., Bocco, R., Baimey, H. & Wopereis, M. 2010. Drought resistance in an interspecific backcross population of rice (*Oryza* spp.) derived from the cross WAB56-104 (*O. sativa*) × CG14 (*O. glaberrima*). *Plant Science,* 179: 364–373.

Albar, L., Bangratz, M., Hébrard, E., Ndjiondjop, M.N., Jones, M.P. & Ghesquière, A. 2006. Mutations in the eIF(iso)4G translation initiation factor confer high resistance of rice to *Rice yellow mottle virus*. *Plant Journal,* 47: 417–426.

Other evidence of leadership, large-program management and delivery

I worked with several projects for more than US$ 1.7 million funded by The Generation Challenge Programme. 3-year USAID-funded project to support the training of scientists and young students from NARS countries, and to invest in facilities with the view to establish molecular biology laboratories in the NARS countries.

Role in the Genebank Platform

Genebank manager. Implement activities of Conservation and Use Modules.

Name: Matija, Obreza

Current position and affiliation

Information Systems Manager, Global Crop Diversity Trust

Profile

20 years of experience in design and development of software applications. He moved from the private sector to IITA in 2007, where he implemented a series of IT solutions, including barcoding the genebank collections. Matija joined the Crop Trust in 2013 to manage development of Genesys, the global database on PGRFA maintained in genebanks around the world. Since then Matija’s role extended to include responsibility for internal IT systems of the Crop Trust as well as overseeing information needs of all projects implemented by the organization.

Employment

2014–2016: Information Systems Manager, Global Crop Diversity Trust

2013–2014: Genesys II Project Manager, Global Crop Diversity Trust

2011–2013: Software Developer, CELSTEC, Open Universiteit Nederland

2007–2011: Software Development Service Manager, International Institute of Tropical Agriculture.

Education

BSc in Computer and Information Science (level ISCED 5A) at University of Maribor, Slovenia.

Selected publications

N/A

Other evidence of leadership, large-program management and delivery

N/A

Role in the Genebank Platform

Software developer and manager of Genesys, Backstopping of information management activities in the genebanks

Name: Thomas PAYNE

Current position and affiliation

Head, Wellhausen-Anderson Wheat Genetic Resources Collection;

Head, International Wheat Improvement Network. CIMMYT-Mexico;

Profile

Wheat breeder, pathologist

Employment

2005 to present: Head, Wellhausen-Anderson Wheat Genetic Resources Collection. CIMMYT-Mexico.

2000 to present: Head, International Wheat Improvement Network. CIMMYT-Mexico.

2003 –2005; 2009 – present: Secretary, CIMMYT Board of Trustees.

2001 –2003: Assistant/Interim Director, Wheat Program. CIMMYT-Mexico..

1997 –2000: Regional Wheat Breeder/Pathologist. CIMMYT-Ethiopia.

1994 –1997: Team Leader and Wheat Breeder. CIMMYT-Zimbabwe.

1991 –1994: Facultative and Winter Wheat Breeder. CIMMYT-Turkey and CIMMYT/ICARDA-Syria.

Education

PhD. Winter Wheat Breeding. University of Nebraska. Major: Agronomy – Plant Breeding.

MSc. Oats Breeding. University of Minnesota. Major: Plant Breeding.

Selected publications

Prashant Vikram, Jorge Franco, Juan Burgueno-Ferrera, Huihui Li, and 18 others. 2016. Unlocking the genetic diversity of Creole wheats. 2016. *Nature Scientific Reports,* 6: Article number: 23092 [doi:10.1038/srep23092].

Huihui Li, et al., 2015. A high density GBS map of bread wheat and its application for dissecting complex disease resistance traits. *BMC Genomics*, 16: 216 [DOI 10.1186/s12864-015-1424-5]

Sehgal, D., Vikram, P., Sansaloni, C.P., Ortiz, C., Pierre, C.S., Payne, T., Ellis, M., Amri, A., Petroli, C.D., Wenzl, P. & Sukhwinder-Singh. 2015. Exploring and mobilizing the gene bank biodiversity for wheat improvement. *PLoS ONE*, 10(7): e0132112. [doi:10.1371/journal.pone.0132112]

Vivi, N., Arief, I.H., DeLacy, J.C.,, Payne, T. Singh, R., Braun, H.-J., Tian, T., Basford, K.E. & Dieters, M.J. 2015. Evaluating testing strategies for plant breeding field trials: redesigning a CIMMYT International Wheat Nursery. *Crop Science*, 55: 164–177 [doi: 10.2135/cropsci2014.06.0415]

Hazekamp, Th. Payne, T. S. & Sackville Hamilton, N.R. 2014. Assessing rice and wheat germplasm collections using similarity groups. Genetic Resources and Crop Evolution, 61: 841–851 [DOI 10.1007/s10722-014-0079-4]

Ortiz, R., et al., 2008. Wheat genetic resources enhancement by the International Maize and Wheat Improvement Center (CIMMYT). *Genetic Resources and Crop Evolution* 55(7): 1095–1140.

Mathews, K.L., Chapman, S.C., Trethowan, R., Pfeiffer, W., van Ginkel, M., Crossa, J., Payne, T., DeLacy, I., Fox, P.N. & Cooper, M. 2007. Global adaptation patterns of Australian and CIMMYT spring bread wheat. Theoretical and Applied Genetics, 115(6): 819–835 [DOI 10.1007/s00122-007-0611-4]

Trethowan, R.M., van Ginkel, M., Ammar, K., Crossa, J., Payne, T.S., Cukadar, B., Rajaram, S. & Hernandez, E. 2003. Associations among twenty years of international bread wheat yield evaluation environments. *Crop Science,* 43: 1698–1711.

Pretorius, Z.A., Singh, R.P., Wagoire, W.W. & Payne. T.S. 2000. Detection of virulence to wheat stem rust resistance gene Sr31 in *Puccinia graminis* f. sp. *tritici* in Uganda. *Plant Disease,* 84: 203.

Role in the Genebank Platform

Genebank manager, Member of Executive Committee of A15 Group and Management Team, Oversee “Frontrunner” position for GRIN-Global development and adoption. Activities in Conservation and Use Modules.

Name: Nicolas ROUX

Current position and affiliation

Senior scientist, Genetic Resources Group Leader, Bioversity International, Montpellier, France.

Profile

Main interest in genetic resources and more specifically in the conservation and use of vegetatively propagated crops. 28 years experience in research on bananas and plantains (Musa spp.) from plant to tissue culture, cell culture, cytogenetics and DNA sequences.

Employment

2003 to present: Senior scientist, Genetic Resources Group Leader, Bioversity International, Montpellier, France.

2002–2003: Consultant, Musa Genome Resource Centre at the Institute of Experimental Botany (IEB), Olomouc, Czech Republic.

1993–2002: Research Scientist, FAO/IAEA Laboratories in Seibersdorf, Austria.

1990–1993: Laboratory director for Agricar c.a., Hacienda Carabobo, Caracas, Venezuela.

Education

PhD Plant Botany, Palacky University, Olomouc, Czech Republic.

MSc Biotechnology, Horticulture, Superior Industrial Institute of State, Gembloux, Belgium

Selected publications

Kagy, V., Wong, M., Van den Broucke, H., Jenny, C., Dubois, C., Ollivier, B., Cardi, C., Mournet, P., Tuia, V., Roux, N., Dolezel, J. & Perrier, X. 2016. Traditional banana diversity in Oceania: an endangered heritage. PLoS ONE, 11(3): e0151208 [doi:10.1371/journal.pone.0151208]

Čížková, J., Hřibová, E., Christelová, P., Van den Houwe, I., Häkkinen, M., Roux, N., Swennen, R. & Doezel, J. 2015. Molecular and cytogenetic characterization of wild *Musa* species. *PLoS ONE,* 10(8): e0134096. doi:10.1371/journal.pone.0134096

Cenci, A., Guignon, V., Roux, N. & Rouard, M. 2014. Genomic analysis of NAC transcription factors in banana (*Musa acuminata*) and definition of NAC orthologous groups for monocots and dicots. *Plant Molecular Biology,* 85(1-2): 63–80.

Hribova, E., Christelova, P., Roux, N. & Dolezel, J. 2013. A simple and robust approach for genotyping in Musaceae. *Acta Horticulturae,* no. 986: 241–246.

D'Hont, A., Denoeud, F., Aury, J.M., Baurens, F.C., Carreel, F., Garsmeur, O., Noel, B., Bocs, S., Droc, G., Rouard, M. & Roux, N. 2012. The banana (*Musa acuminata*) genome and the evolution of monocotyledonous plants. *Nature,* 488(7410): 213–217. http://dx.doi.org/10.1038/nature11241

Other evidence of leadership, large-program management and delivery

Leading the Musa Genetic Resources Group at Bioversity International, MusaNet Coordinator, GMGC Coordinator, Genetic Resources Theme Leader (Theme 1) of Roots, Tubers and Bananas (RTB) CRP during Phase 1.

Role in the Genebank Platform

Focal point for Bioversity International. Role in Conservation and Use Modules. Cryopreservation, genomics to genebanks, new methods for virus indexing and sanitation.

Name: Hari Deo UPADHYAYA

Current position and affiliation

Head, Genebank, and Principal Scientist, ICRISAT, Patancheru, India

Profile

Experience: 18 years (1997 to present) as genetic resources specialist and 24 years as groundnut breeder at ICRISAT Patancheru, India.

Employment:

2009 to present: Principal Scientist and Head/Director (Genebank), ICRISAT, Patancheru, India

2010–2013: Assistant Director, Grain Legumes Research Program, ICRISAT, Patancheru, India

1991 to present: Senior Groundnut Breeder, ICRISAT, Patancheru, India

1987–1991: Oilseed Breeder, and Head of Oilseed Project, Univ. Agric. Sci., Dharwad, India

Education

PhD, Plant Breeding, GB Pant Univ. Agric. Technology, Pantnagar, India

MSc, Plant Breeding, GB Pant Univ. Agric. Technology, Pantnagar, India

Selected publications

Upadhyaya, H.D., Bajaj, D. Naroliya, L. Das, S. Vinod Kumar, C.L.L. Gowda, S. Sharma, A. Tyagi, and S.K. Parida. 2016. Genome-wide scans for delineation of candidate genes regulating seed-protein content in chickpea. *Frontiers in Plant Science,* 7: 302.

Upadhyaya, H.D., S.L. Dwivedi, S. Singh, K.L. Sahrawat, and S.K. Singh. 2016. Genetic variation and post-flowering drought effects on seed iron and zinc in ICRISAT sorghum mini core collection. Crop Science. 56, 374-384.

Lasky, J.R., Upadhyaya, H.D., Ramu, P., Deshpande, S., Hash, C.T., Bonnette, J., Juenger, T.E., Hyma, K., Acharya, C., Mitchell, S.E., Buckler, E.S., Brenton, Z., Kresovich, S. & Morris. G.P. 2015. Genome-environment associations in sorghum landraces predict adaptive traits. *Science Advances*

Kujur, A., Bajaj, D., Upadhyaya, H.D., Das, S., Ranjan, R., Shree, T., Saxena, M., Badoni, S., Kumar, V., Tripathy, S. Gowda, C.L.L. Sharma, S. Singh, S. Tyagi, A. &Parida S. 2015. A genome-wide SNP scan accelerates trait-regulatory genomic loci identification in chickpea. *Nature Scientific Reports,* 5: 11166

Westengen, O.T., Okongo, M.A. Onek, L.Berg, T. Upadhyaya, H.D. Birkeland, SKhalsa, .S.D.K. Kristoffer, H. K.H. Ring, N.C. Stenseth, and A.K. Brysting. 2014. Ethnolinguistic structuring of sorghum genetic diversity in Africa and the role of local seed systems. *PNAS* 111: 14100–14105.

Morris, G.P., Ramu, P., Deshpande, S.P., Hash, C.T., Shah, T., Upadhyaya, H.D., Riera-Lizarazu, O., Brown, P.J., Acharya, C.B., Mitchell, S.E., Harriman, J., Glaubitz, J.C., Buckler, E.S. & Kresovich. S. 2013. Population genomics and genome-wide association studies of agroclimatic traits in sorghum. *PNAS* 110: 453–458.

Upadhyaya, H.D., Dronavalli, N., Dwivedi, S.L., Kashiwagi, J., Krishnamurthy, L., Pande, S., Sharma, H.C., Vadez, V., Singh, S., Varshney, R.K. & Gowda, C.L.L. 2013. Mini-core collection as a resource for identifying new sources of variation. *Crop Science,* 53: 2506–2517.

Other evidence of leadership, large-program management and delivery

As Assistant Research Program Director, Grain Legumes, provided critical support in managing global research program on Grain Legumes at ICRISAT: Implemented GPG projects and upgraded genebank facility at Patancheru and regional genebanks in Africa; BMZ/GTZ project promoting on-farm conservation and utilization Asia (india) and Africa (Kenya, Tanzania, Uganda).

Role in the Genebank Platform

Head of ICRISAT genebank, implement the activities at the main genebank at Patancheru, India and three regional genebanks in Africa and implement activities of Conservation and Use Modules, assist in management of the Genebank Platform.

Name: Peter WENZL

Current position and affiliation

Incoming Genetic Resources Program Leader, CIAT, Colombia

Profile

Characterization of genetic resources to identify and mobilize novel variation that accelerates genetic gains in breeding programs.

Genotyping service provision; configuration of genotyping assays for a variety of purposes.

Information management at the interface between genebanks and breeding programs.

Employment

2015–2016: DivSeek Liaison, Global Crop Diversity Trust, Germany

2010–2014: Leader, Seeds of Discovery (SeeD) Project, CIMMYT, Mexico

2009–2010: Manager, Crop Informatics Team, CIMMYT, Mexico

2002–2009: Principal Scientist, Diversity Arrays Technology (DArT) Pty. Ltd., Australia

Education

PhD, Plant Physiology & Genetics, University of Vienna, Austria

MSc, Biochemistry and Biophysics, University of Vienna, Austria

Selected publications

Sehgal, D., Vikram, P., Sansaloni, C.P., Ortiz, C., Pierre, C.S., Payne, T., Ellis, M., Amri, A., Petroli, C.D., Wenzl, P. & Singh, S. 2015. Exploring and mobilizing the gene bank biodiversity for wheat improvement. *PLoS ONE,* 10: e0132112

McCouch, S. *et al.* 2013. *Feeding the future*. *Nature,* 499: 23–24.

Bedo, J., Wenzl, P., Kowalczyk, A. & Kilian, A. 2008. Precision-mapping and statistical validation of quantitative trait loci by machine learning. *BMC Genetics,* 9: 35.

Wenzl, P., Raman, H., Wang, J., Zhou, M., Huttner, E. & Kilian, A. 2007. A DArT platform for quantitative bulked segregant analysis. *BMC Genomics,* 8: 196.

Wenzl, P., Carling, J., Kudrna, D., Jaccoud, D., Huttner, E., Kleinhofs, A. & Kilian, A 2004. Diversity arrays technology (DArT) for whole-genome profiling of barley. *Proceedings of the National Academy of Sciences of the United States of America,* 101: 9915–9920.

Other evidence of leadership, large-program management and delivery

Led CIMMYT's SeeD project team of 15 IRS and ca. 70 staff overall; SeeD systematically identifies and mobilizes useful genetic variation in genebanks into maize and wheat breeding programs.

Substantially contributed to the start-up and success of a biotech company that provides high-throughput genotyping and informatics services to plant breeders and researchers.

Completed the Emerging Leaders Training Program, Thunderbird School of Global Management, Arizona State University, Phoenix, USA.

Role in the Genebank Platform

(a) contribute to devising strategies to incorporate genotyping for quality-control purposes in the Conservation Module;

(b) contribute to shaping the Use Module, particularly by forming interfaces to 'genomics-of-genebanks' projects;

(c) act as liaison to the Genetic Gains Platform

Annex 4. Interactions between the Genebank Platform, CRPs and other users

The table below summarizes the interactions between the Genebank Platform and the Agri-Food System CRPs, Global Integrating CRPs, other Platforms and outside users. The table lists activities by the Genebank Platform that **contribute** benefits to the CRPs/Platforms/user and benefits **received** by the Genebank Platform from the activities of the same CRPs/Platforms/users. The table combines information from the shared CRP draft proposals and the Genebank Platform proposal. Discussions concerning integration between CRPs and Platforms have been *ad hoc* until now. Further iterations and fine-tuning will be required, based on one-to-one interactions with each CRP and Platform, once all proposals have been finalized.

CRP	**Conservation Module:** Support and improve essential genebank operations	**Use Module:** Empower effective use of genetic resources	**Policy Module:** Engage in genetic resources policy development and compliance	**Comments**
Agrifood Systems CRPs				
DCL	***Contributes:*** Source and repository of germplasm and data. Capacity strengthening. ***Receives:*** Novel trait and allele creation (FP2). Develop and test farmer preferred varieties (FP3). SOPs for nursery research and seed health maintenance (FP4).	***Contributes:*** Develop and deliver tools and services for users, such as subsets of germplasm based on priorities and needs set by the primary users. Improved data to promote use of diversity ***Receives:*** Variety deployment management systems and phenotyping platform (FP3). Innovations to manage abiotic and biotic stresses to facilitate access and use (FP4).	***Contributes:*** Assistance dealing with genetic resources access and benefit-sharing issues (under ITPGRFA, Nagoya Protocol, etc) Opportunities for coordinated engagement in international genetic resources policy making processes ***Contributes & Receives:*** Specific link with DCL FP3 (Variety & hybrid development) regarding access to genetic material and PGR-related knowledge and FP 4, regarding the development of guidelines on restoration methods based on genetic diversity and locally adapted varieties.	Links with FP2 (Pre-breeding and trait discovery), FP3 (Variety & hybrid development) and FP4 (Integrated land water and crop management).

CRP	**Conservation Module:** Support and improve essential genebank operations	**Use Module:** Empower effective use of genetic resources	**Policy Module:** Engage in genetic resources policy development and compliance	**Comments**
			Receives: Information on CRP's experiences under different policy frameworks.	
FTA	***Contributes:*** Source and repository of germplasm and data. Feedback on germplasm evaluation. Collaboration on collecting where there are threats to *in situ* conserved tree genetic resources. Capacity strengthening. ***Receives:*** Tree genetic resources.	***Contributes:*** Develop and deliver tools and services for users, such as subsets of germplasm based on priorities and needs set by the primary users. Improved data to promote use of diversity ***Receives:*** Flowback of information on use of accessions	***Contributes:*** Assistance dealing with genetic resources access and benefit-sharing issues (under ITPGRFA, Nagoya Protocol, etc.). Opportunities for coordinated engagement in international genetic resources policy making processes. ***Contributes & Receives:*** Specific linkage with FP1 which tackles PGR policy issues at local, national and international scales. ***Receives:*** Information on CRP's experiences under different policy frameworks.	Mainly working with FP1: Tree genetic resources to bridge production gaps and promote resilience.
Livestock	***Contributes:*** Source and repository of forage germplasm and data. Capacity strengthening. ***Receives:***	***Contributes:*** Develop and deliver tools and services for users, such as subsets of germplasm based on priorities and needs set by the primary users. Improved data to promote use of diversity	***Contributes:*** Assistance dealing with genetic resources access and benefit-sharing issues (under ITPGRFA, Nagoya Protocol, etc.). Opportunities for coordinated	Key collaborator will be FP3: Animal Feeds and Forages

CRP	**Conservation Module:** Support and improve essential genebank operations	**Use Module:** Empower effective use of genetic resources	**Policy Module:** Engage in genetic resources policy development and compliance	**Comments**
	Knowledge about utilization of genetic resources.	Framework for enhanced use of forage seed material. Database & information management. ***Receives:*** Flowback of information on use of accessions	engagement in international genetic resources policy making processes ***Receives:*** Information on CRP's experiences under different policy frameworks.	
Maize	***Contributes:*** Source and repository of germplasm and data. Capacity strengthening. ***Receives:*** Characterization and exploration of the genomic diversity of maize to identify and develop genetic diversity for use by breeding programs (FP2).	***Contributes:*** Develop and deliver tools and services for users, such as subsets of germplasm based on priorities and needs set by the primary users. Improved data to promote use of diversity ***Receives:*** Tools for phenotyping and genotyping maize germplasm for unlocking useful traits, and utilizing genetic resources in breeding for target traits (FP3). Database management/decision support systems (FP2).	***Contributes:*** Resources and support to deal with genetic resources access and benefit-sharing issues (under ITPGRFA, Nagoya Protocol, etc.). Opportunities for coordinated engagement in international genetic resources policy making processes. ***Receives:*** Information on CRP's experiences under different policy frameworks. Stronger maize seed systems (FP3).	Key collaborators are FP 2: Novel diversity and tools to increase genetic gains and FP 3: Stress tolerant and nutritious maize.
Rice	***Contributes:*** Source and repository of germplasm and data to increase the diversity used in breeding activities.	***Contributes:*** Develop and deliver tools and services for users, such as subsets of germplasm based on priorities and needs set by the primary users.	***Contributes:*** Assistance dealing with genetic resources access and benefit sharing issues (under ITPGRFA, Nagoya Protocol, etc.).	Key partners are FP4: Global Rice Array and FP5: New rice varieties.

CRP	**Conservation Module:** Support and improve essential genebank operations	**Use Module:** Empower effective use of genetic resources	**Policy Module:** Engage in genetic resources policy development and compliance	**Comments**
	Capacity strengthening. ***Receives:*** Link to the International Rice Informatics Consortium (IRIC) (FP5). Use of stored rice seeds (FP5). Knowledge and advice about health and longevity of stored seeds (FP5).	Improved data to promote use of diversity ***Receives:*** Data integration platform to store and analyse large dataset generated from phenotyping and genotyping. Knowledge of traits and genes for different climate conditions (FP4) Physical phenotyping platform (FP5).	Opportunities for coordinated engagement in international genetic resources policy making processes. ***Receives:*** Information on CRP's experiences under different policy frameworks.	
RTB	***Contributes:*** Source and repository of healthy clonal genetic resources and data. Database & information management. Capacity strengthening. ***Receives:*** Enhanced and characterized genetic diversity (FP1). Methods for more efficient, cost – effective and secure methods for ex situ	***Contributes:*** Develop and deliver tools and services for users, such as subsets of germplasm based on priorities and needs set by the primary users. Improved data to promote use of diversity Framework for enhanced use of clonal material. Database & information management. ***Receives:*** Molecular and phenotypic characterization of material, including CWR	***Contributes:*** Assistance dealing with genetic resources access and benefit-sharing issues (under ITPGRFA, Nagoya Protocol, etc.). ***Contributes & Receives:*** Collaboration to influence changes in policy and regulatory frameworks for enhancing conservation and safe exchange of RTB genetic diversity.	Collaboration mainly through RTB FP1: Discovery research for enhanced utilization of RTB genetic resources; to a lesser extent FP2: Adapted productive varieties and quality seed of RTB crops are key collaborators (for pre-breeding activities).

CRP	**Conservation Module:** Support and improve essential genebank operations	**Use Module:** Empower effective use of genetic resources	**Policy Module:** Engage in genetic resources policy development and compliance	**Comments**
	conservation (FP1). Marker systems to monitor genetic integrity (FP1). Strengthened seed production technologies, seed quality control and improved disease diagnostics (FP2).	(FP1).		
Wheat	***Contributes:*** Source and repository of germplasm and data. Capacity strengthening. ***Receives:*** New knowledge, data per accession (FP2&3). Efficient seed delivery systems (FP3). ***Contributes & Receives:*** Jointly ensure international germplasm exchange and use of PGRFA by researchers (FP2&3).	***Contributes:*** Develop and deliver tools and services for users, such as subsets of germplasm based on priorities and needs set by the primary users. Improved data to promote use of diversity Framework for enhanced use of genetic material. Database & information management. ***Receives:*** Developing of phenotyping network (FP2&3).	***Contributes:*** Assistance dealing with genetic resources access and benefit-sharing issues (under ITPGRFA, Nagoya Protocol, etc.). Opportunities for coordinated engagement in international genetic resources policy making processes. ***Receives:*** Information on CRP's experiences under different policy frameworks.	Key interaction with FP2: Novel diversity and tools for improving genetic gains and breeding and FP3: Better varieties reach farmers faster.
Global Integrating CRPs				
A4NH	***Contributes:*** Source and repository of	No direct links; will link through appropriate AFS CRPs.	No direct links.	Module 1 will link with A4NH FP1: Biofortification in

CRP	**Conservation Module:** Support and improve essential genebank operations	**Use Module:** Empower effective use of genetic resources	**Policy Module:** Engage in genetic resources policy development and compliance	**Comments**
	germplasm and data. Capacity strengthening. ***Receives:*** Contribution to the genetic characterization of staple crops and under-utilized plant genetic resources.			the genetic characterization of PGR.
CCAFS	No direct links; will link through appropriate AFS CRPs.	No direct links; will link through appropriate AFS CRPs.	***Contributes & Receives:*** Joint case studies, foresight activities, analyses of global movements and uses of genetic resources for climate change adaptation and mitigation and related policy frameworks, and economic analysis in CCAFS CoA 1.3.	Link specifically between Policy Module and CCAFS FP1: 'Priorities and policies for climate-smart agriculture'.
PIM	No direct links.	No direct links.	***Provides and Receives:*** Research partnership assessing the impacts of changes in the global policy landscape governing the conservation, exchange, and use of genetic resources for food and agriculture, particularly for national research systems.	Interaction mainly through the Policy Module with PIM FP1: Flagship 1, Cluster 1.2 on 'Technological innovation and sustainable intensification: Science policy and innovation systems for sustainable intensification' and FP5: Governance of Natural Resources
WLE	No direct links.	No direct links.	No direct links.	
Platforms				

CRP	**Conservation Module:** Support and improve essential genebank operations	**Use Module:** Empower effective use of genetic resources	**Policy Module:** Engage in genetic resources policy development and compliance	**Comments**
Genetic Gains	***Contributes:*** Source and repository of germplasm and data. Information on workflows (GGP M2). ***Contributes & Receives:*** Interaction with GGP M3 (Genotyping / sequencing tools & services) and M4 ("Phenotyping tools & services") in support of seed characterization and automation.	***Contributes:*** Integration of tool development and service provision. Joint workshops and online meetings to avoid duplication of efforts and to enhance cross-compatibility of tools. Specifically, coordination with GGP modules 1 ("Breeding program excellence") and 5 ("Bioinformatics and data management tools & services"). ***Receives:*** Tools that facilitate germplasm use (from GGP M5).	***Contributes:*** Assistance dealing with genetic resources access and benefit-sharing issues (under ITPGRFA, Nagoya Protocol, etc.). Opportunities for coordinated engagement in international genetic resources policy making processes ***Receives:*** Information on platform's experiences under different policy frameworks.	Links provided through representation in the module expert advisory groups.
Big Data	***Contributes:*** TBD ***Receives:*** TBD	***Contributes:*** Integration of tool development and service provision. Joint workshops and online meetings to avoid duplication of efforts and to enhance cross-compatibility of tools. ***Receives:*** TBD	No direct links.	
Users outside CGIAR				
NARS, universities	***Contributes:*** Source and repository of germplasm and data.	***Contributes:*** Develop and deliver tools and services for users, such as subsets of germplasm based on	***Contributes:*** Capacity building for compliance and implementation of the ITPGRFA and other	There will be representatives of NARS in Multistakeholder PGR Policy Group.

CRP	**Conservation Module:** Support and improve essential genebank operations	**Use Module:** Empower effective use of genetic resources	**Policy Module:** Engage in genetic resources policy development and compliance	**Comments**
	Safekeeping of safety duplicates. Backstopping & support for national phytosanitary agencies. Capacity strengthening (phytosanitary procedures, genebank operations, seed longevity, QMS, data management, collecting). ***Receives:*** Source and repository of germplasm and data. Partnership in diversity studies, collecting, capacity development, certain services (e.g. regeneration, disease-indexing) for some crops.	priorities and needs set by the primary users. Improved data to promote use of diversity Capacity building (data management to promote the use of diversity, Genesys). ***Receives:*** Links will generally be through AFS CRPs, although for several Centers and crops, especially those not covered by AFS-CRPs, there are direct links with users in generating characterization/ evaluation data.	genetic resources policies and laws. ***Contributes &*** ***Receives:*** Knowledge exchange. Capacity building for implementing the ITPGRFA.	
Farmer groups	***Contributes:*** Source and repository of germplasm and data. ***Receives:*** Partnerships in collecting.	***Contributes:*** Develop and deliver tools and services for users, such as subsets of germplasm based on priorities and needs set by the primary users. Improved data to promote use of diversity	***Contributes &*** ***Receives:*** Knowledge exchange.	Direct links with farmers/farmer groups will likely be rare and usually through the CRPs; they are often the result of historical links and projects. There will be farmer representatives in

CRP	**Conservation Module:** Support and improve essential genebank operations	**Use Module:** Empower effective use of genetic resources	**Policy Module:** Engage in genetic resources policy development and compliance	**Comments**
	Source of germplasm and data. Some special relationships linking to *in situ* conservation.	***Receives:*** Links will generally be through AFS CRPs, although for several Centers and crops, especially those not covered by AFS-CRPs, there may be direct links with users in generating characterization/ evaluation data.		Multistakeholder PGR Policy Group.
Private Sector	***Contributes:*** Source and repository of germplasm. ***Receives:*** Exchange of PGRFA.	Links will generally be through AFS CRPs, although for several Centers and crops, especially those not covered by AFS-CRPs, there may be direct links with users in generating characterization/ evaluation data.	***Contributes & Receives:*** Knowledge exchange	There will be representatives of PS in Multistakeholder PGR Policy Group.

Annex 5a. Intellectual Asset management

The Platform's management of genetic resources will comply with the CGIAR Principles on the Management of Intellectual Assets (CGIAR IA Principles) in general, and article 4.2 in particular, which states:

> "Facilitated access to Plant Genetic Resources for Food and Agriculture within the purview of the Treaty shall be provided in accordance with the Treaty and these CGIAR IA Principles. In addition, the acquisition or transfer of any other genetic resources by the Centers shall be conducted in accordance with all applicable laws including those implementing the CBD, as well as these CGIAR IA Principles."

In this quotation, 'Treaty' refers to the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA). The eleven CGIAR Centers hosting international collections of 'in trust' PGRFA (pursuant to their 1994 In Trust Agreements with FAO) signed agreements in 2006 with the Governing Body of the ITPGRFA (pursuant to its Article 15) placing those collections under the ITPGRFA's framework. (Full texts of those agreements are available on the ITPGRFA's website.) Following these agreements, which came into force in January 2007, each Center 'recognizes the authority of the Governing Body to provide policy guidance relating to *ex situ* collections held by it and subject to the provisions of the Treaty.' Furthermore, the CGIAR Centers undertake to make 'in trust' germplasm available to recipients using the standard material transfer agreement (SMTA) adopted by the Governing Body in 2006. They will also use the SMTA to redistribute materials that they receive after January 2007, under the SMTA or any form of transfer agreement that allows the Center to do so.

On occasion, the CGIAR genebanks may transfer germplasm that has been improved by the Centers and which incorporates materials received from the multilateral system (defined as 'PGRFA under Development' in Article 2 of SMTA). In such cases, the genebanks will use the SMTA for transferring such materials, though they may add conditions, as permitted under the SMTA paragraph 6.6. Any such additional conditions will also be in conformity with section 6 of the CGIAR IA Principles, which establishes the conditions under which CGIAR Centers may enter into 'limited exclusivity', and 'restrictive use' agreements for the transfer of Centers' intellectual assets. The genebanks will report to the Governing Body information on all their SMTA transfers, following instructions provided by the Governing Body.

New collecting of genetic resources by the CGIAR Centers will be in compliance with applicable laws, including domestic laws implementing the ITPGRFA, the Convention on Biological Diversity, and the Nagoya Protocol on access and benefit sharing.

Each participating Center will enlist the participation of its Intellectual Property Focal Point (IP Focal Point) to make plans for, and monitor, its intellectual asset management practices under the Genebank Platform. The IP Focal Points will report upon those practices in their annual Center Intellectual Assets Report to the Consortium Office, as required under paragraph 10.1.2 of the CGIAR IA Principles. Compliance with the IA Principles will be monitored through the Platform Management Team and linked to the tracking of outputs/deliverables. Where the Platform Management Team has concerns, it will address the Platform scientists and relevant Center IP focal points directly. Where concerns persist, the Platform Coordinator will alert the CGIAR General Legal Counsel and request advice and assistance. Full compliance with the CGIAR IA Principles and the genebanks' commitments pursuant to their 2006 agreements with the Governing Body will be included in partnership contracts under this Platform.

Annex 5b. Open Access management

The platform will ensure that all of its information products are made publicly available in conformity with the CGIAR Open Access and Data Management Policy (OA Policy) and also with the expectations under the ITPGRFA (Articles 13.2.a, 17; SMTA 6.9) that non-confidential information about materials in the multilateral system will be made available through a global information system. Research papers, policy briefs, conservation protocols, training materials, written submissions to international policy fora, will be made publicly available through the Platforms' own website or publication in open access journals. Software and web tools will be made available under open access licenses.

All CGIAR genebanks make their data publicly available and searchable, as part of the strategy to promote more effective use. Genesys provides a common portal for access to information on all CGIAR accessions and is recognized as an element of the ITPGRFA's Global Information System (GLIS). It collates data from international and national genebanks into a single, public, searchable database under a signed agreement with each data provider, which states that providers should only provide data that can be made publicly available globally through Genesys or other databases. Genesys is being managed and developed by the Global Crop Diversity Trust under the guidance of a dedicated Advisory Committee. The 'Conservation' and 'Use' Modules will contribute to the enhanced functioning of Genesys, and develop new tools and methods for sharing, associating, harvesting and visualizing accession-level data.

Data collected as part of policy-linked research (for example, trends in Centers' and partners' acquisitions, distributions, and uses of genetic resources, data, and traditional knowledge, under different policy regimes) will be made available in conformity with the OA Policy.

The Platform will institutionalize the same processes for ensuring compliance with open access standards as for intellectual assets standards. The Platform Management Team will assume ultimate responsibility for ensuring that the Platform complies with OA Policy and ITPGRFA-related expectations. Intellectual Property Focal Points of participating Centers will assist in planning, monitoring, and reporting their Centers' open access practices under the Platform; they will also meet together (virtually) to discuss best practices and identify challenges for the Platform as a whole. The Modules will submit annual reports to the Platform Coordinator concerning their information products and their management of them consistent with their open access obligations.

Annex 6. References

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Annex 7. Abbreviations

A15	Article 15 Group of genebank managers
A4NH	Agriculture for Nutrition and Health CRP
ABS	access and benefit sharing
AFS-CRP	Agri-food System CRP
API	application programming interface
AVRDC	The World Vegetable Center, Taiwan
Bioversity	Bioversity International, Rome
CBD	Convention on Biological Diversity
CCAFS	Climate Change, Agriculture and Food Security CRP
CGN	Centre for Genetic Resources, the Netherlands
CGRFA	Commission on Genetic Resources for Food and Agriculture, FAO
CIAT	International Center for Tropical Agriculture, Colombia
CIMMYT	International Maize and Wheat Improvement Center, Mexico
CIP	International Potato Center, Peru
CLIPNet	Centers' IP Focal Points Network
CoP	community of practice
CRISPR	clustered regularly-interspaced short palindromic repeats
CRISPR/cas9	CRISPR-associated endonuclease
Crop Trust	Global Crop Diversity Trust
CRP	CGIAR research program
CWR	crop wild relative(s)
DOI	digital object identifiers
EB	Executive Board
EMBRAPA	Empresa Brasiliera de Pesquisa Agropecuária, Brazil
FAC	Finance and Administration Committee, Crop Trust
FAO	Food and Agriculture Organization of the United Nations
FC	Fund Council, CGIAR
FIGS	Focused Identification of Germplasm Strategy
FTA	Forests, Trees and Agroforestry CRP
G×E	genetic by environment [interaction]
GFAR	Global Forum on Agricultural Research, Rome
GHU	germplasm health unit
GIS	geographical information system
GIZ	Deutsche Gesellschaft für Internationale Zusammenarbeit Gmbh.,

	Germany
GLIS	Global Information System of the ITPGRFA
GOAL	genebank operations and advance learning
GOBII	Genomic and Opensource Breeding Informatics Initiative
GPG2	Global Public Goods project 2nd phase (Bioversity International coordinated)
GRIN	Genetic Resources Information Network
GRPC	Genetic Resources Policy Committee
GWAS	genome-wide association study
IA	intellectual asset(s)
IAC	Independent Advisory Committee, Genebank Platform
ICARDA	International Center for Agricultural Research in the Dry Areas, Lebanon
ICRAF	World Agroforestry Center, Kenya
ICRISAT	International Crops Research Institute for the Semi-Arid Tropics, India
IDO	intermediate development outcome
IITA	International Institute of Tropical Agriculture, Nigeria
ILRI	International Livestock Research Institute, Kenya
IP	intellectual property
IPPC	International Plant Protection Convention, FAO
IPK	Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung, Germany
IPR	intellectual property right
IRRI	International Rice Research Institute, the Philippines
ITPGRFA	International Treaty on Plant Genetic Resources for Food and Agriculture, FAO
MSB	Millennium Seed Bank, UK
MT	Management Team, Genebank Platform
NARS	national agricultural research system(s)
NBPGR	National Bureau of Plant Genetic Resources, India
NGO	non-governmental organization
OA	open access
ORT	online reporting tool
PGR	plant genetic resources
PGRFA	plant genetic resources for food and agriculture
PUI	persistent unique identifier
RDA	Rural Development Administration, Republic of Korea
QMS	quality management system

SGRP	Systemwide Genetic Resources Program
SGSV	Svalbard Global Seed Vault, Norway
SINGER	Systemwide Information Network on Genetic Resources
SLO	system level outcome
SMTA	standard material transfer agreement
SNP	Single-nucleotide polymorphism
SOP	standard operating procedure
SPC	Secretariat of the Pacific Community, New Caledonia
SRF	Strategy and Results Framework, CGIAR
UPOV	International Union for the Protection of New Varieties of Plants, Switzerland
USDA	United States Department of Agriculture