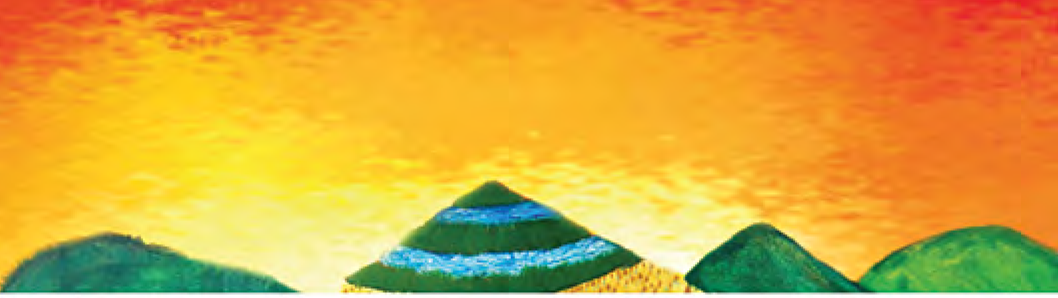


POSITION PAPERS
GCP’S RESEARCH COMPONENT

Paper No 3: Genetic stocks

Generation Challenge Programme

Partnerships in modern crop breeding for food security

www.generationcp.org

GCP in collaboration with external experts has drafted a series of 11 Position Papers (listed below). Two of these 11 papers are 'big-picture' papers on: (a) Programme level overview, and, (b) a synthesis of all the research aspects combined. The other nine component-specific papers drill down into each component, and cover four main areas: (i) research – 5 papers; (ii) services – 1 paper; (iii) capacity building – 1 paper; and, (iv) communications and knowledge sharing – 2 papers.

The goals are to communicate component-level outputs and deliverables during the Programme's lifetime (2004–2014), list products and outcomes, and explore options for enabling and ensuring that the potential benefits of these components will be fully realised in the future. At this stage, the Position Papers are essentially a very preliminary analysis primarily for internal use, but made publicly available in keeping with GCP's culture of transparency and sharing information.

Each of the nine component-specific Position Papers is designed to contribute to GCP's orderly closure in 2014 by considering the following three questions:

1. What assets will be completed by the end of GCP's lifetime in December 2014?
2. What assets can best continue as integral components of the CRPs or elsewhere?
3. What assets may not fit within existing institutions or programmes and may require alternative implementation mechanisms?

The papers were drafted in July–August 2012, externally reviewed in September 2012, and endorsed by the Taskforce, the GCP Executive Board (September–October 2012) and the Consortium Committee (November 2012). Initially conceptualised as 'white papers' to clarify the issues at hand and to help with decision-making by the Taskforce, Consortium Committee and Executive Board, they subsequently advanced to 'Position Papers' in December 2012, once input from these groups as well as external reviewers was incorporated.

List of Position Papers

Context and synthesis

1. Programme overview
2. Research synthesis

Research components

3. Genetic stocks
4. Genomic resources
5. Informative molecular markers
6. Cloned genes
7. Molecular breeding

Services

8. Integrated Breeding Platform

Breeding tools and services spanning:

   a. Breeding information and communities of practice
   b. Data management software
   c. Analysis and decision-support software
   d. Data management service
   e. Breeding and support services

Capacity building

9. Training, learning resources and infrastructure development

Community and knowledge sharing

10. GCP's scientific and social network
11. GCP's institutional memory

Position Papers on GCP's research component

Paper No 3: Genetic stocks

CGIAR Generation Challenge Programme (GCP)

This paper has been authored by the GCP Management Team with
input from the Transition Strategy Taskforce[1] and external reviewers (David Bertioli,
EMBRAPA; Jean Christophe Glaszmann, Agropolis–CIRAD; Luigi Guarino
and Hannes Dempewolf, the Global Crop Diversity Trust; and
Ruaraidh Sackville Hamilton, IRRI)

---

[1] Taskforce members: Vivienne Anthony (Syngenta Foundation), Andrew Bennett (GCP Executive Board [EB] Chair), Stefania Grando (CGIAR Consortium Office), Dave Hoisington (GCP Consortium Committee Chair/ICRISAT), Jurandir Magalhães (EMBRAPA), John O'Toole (Consultant), Markus Palenberg (EB member) and Jean-Marcel Ribaut (GCP Director)

Correct citation: CGIAR Generation Challenge Programme (2012). Paper No 3: Genetic stocks). *Position Papers: GCP's research component*. Texcoco, Mexico. 22 pp.

Edited by: Elizabeth McAdam and Antonia Okono

Cover illustrations: Extracts from full artworks *In the house of life* and *Bountiful African Madonna* by Rhoda Okono

Art direction: G Antonio Luna Avila
Available online at: www.generationcp.org/gcp-s-sunset

The online version includes hyperlinks to additional content

CONTENTS

ACRONYMS AND ABBREVIATIONS

AfricaRice	Africa Rice Center
Agropolis	Agropolis International, France
Agropolis–CIRAD	Centre de coopération internationale en recherche agronomique pour le développement, France
Agropolis–IRD	Institut de recherche pour le développement, France
Al	aluminium
Alt_{SB}	major Al tolerance gene in sorghum cross BR007 × SC283
AU	Aarhus University, Denmark
BCNAM	backcross nested association mapping
Bioversity	Bioversity International
CAAS	Chinese Academy of Agricultural Sciences
CERAAS	Centre d’étude régional pour l’amélioration de l’adaptation à la sécheresse, Senegal
CGIAR	No longer an acronym (formerly Consultative Group on International Agricultural Research)
CIAT	Centro Internacional de Agricultura Tropical (International Center for Tropical Agriculture)
CIMMYT	Centro Internacional de Mejoramiento de Maíz y Trigo (International Maize and Wheat Improvement Center)
CIP	Centro Internacional de la Papa (International Potato Center)
CIRAD	see Agropolis–CIRAD
CRP(s)	CGIAR Research Programme(s)
CSSL(s)	chromosome segment substitution line(s)
DSR	Directorate of Sorghum Research, India (of the Indian Council of Agricultural Research)

ACRONYMS AND ABBREVIATIONS

EMBRAPA	Empresa Brasileira de Pesquisa Agropecuária (Brazilian Agricultural Research Corporation)
FEDEARROZ	Federación Nacional de Arroceros, Colombia
GCP	CGIAR Generation Challenge Programme
IBN	*see* IBONE
IBONE	Instituto de Botánica del Nordeste, Argentina
ICARDA	International Center for Agricultural Research in the Dry Areas
ICRISAT	International Crops Research Institute for the Semi-Arid Tropics
IER	Institut d'économie rurale, Mali
IITA	International Institute of Tropical Agriculture
INRAN	Institut National de la Recherche Agronomique du Niger
IP	intellectual property
IRD	*see* Agropolis–IRD
IRRI	International Rice Research Institute
ISPC	Independent Science and Partnership Council (of the CGIAR)
ISRA	Institut sénégalais de recherches agricoles
MAGIC	multiparent advanced generation intercross
NAM	nested association mapping
NIAB	National Institute of Agricultural Botany, United Kington
NIL(s)	near-isogenic line(s)
PGRFA	Plant Genetic Resources for Food and Agriculture (of the Food and Agriculture Organization of the United Nations – FAO)
PI	Principal Investigator
QTLs	quantitative trait loci

ACRONYMS AND ABBREVIATIONS

RI	Research Initiative (of GCP)
RIL	recombinant inbred line
SGRP	System-wide Genetic Resources Programme (of the CGIAR)
SMTA	Standard Material Transfer Agreement (for PGRFA)
SPIA	Standing Panel on Impact Assessment (a subgroup of CGIAR's ISPC)
SSR	simple sequence repeat
UAS	University of Agricultural Sciences (Bangalore), India
USA	United States of America
USD	United States dollar

BACKGROUND AND PROCESS

A series of Position Papers has been drafted by the CGIAR Generation Challenge Programme (GCP) team in collaboration with external experts. The goals are to communicate the outputs and deliverables from each research component during 2004–2014, and to explore options for enabling and ensuring that the potential benefits of these components will be fully realised in the future.

The Position Papers are not static but dynamic in nature: they might evolve over time, shaped by progress made during GCP's remaining time, and our ability to implement our workplan as scheduled, and also shaped by the priorities of our partners. This dynamism is particularly pronounced in the 'moving landscape' of socioeconomic, political and environmental issues in which the CGIAR operates.

Each Position Paper is designed to contribute to GCP's orderly closure in 2014, by considering the following questions:

1. What assets will be completed by the end of GCP's lifetime in December 2014?
2. What assets can best continue as integral components of the new CGIAR Research Programmes (CRPs) or elsewhere?
3. What assets may not fit within existing institutions or programmes, and may require alternative implementation mechanisms?

This paper focuses on the outputs and options for GCP's genetic stocks component. Outputs have been achieved through: (a) collaborative work among three sets of actors – a broad network of partners in regional and country research programmes, in the CGIAR and in academia; and, (b) through capacity enhancement to assist developing-world researchers to tap into new genetic diversity and access modern breeding tools and services.

GCP is supported by several funders.

INTRODUCTION AND RATIONALE

Activities geared towards genetic improvement generally aim at developing products such as new varieties better adapted to the needs of agriculture. GCP's portfolio also includes upstream activities that produce other materials valuable to the whole improvement process. For the purposes of this paper, these are referred to as 'genetic stocks'. GCP's genetic stocks might be best defined by terminology proposed in a February 2012 white paper *Accessions and Genetic Stocks in the Gene Bank* by Ruaraidh Sackville Hamilton, Head of the genebank at the International Rice Research Institute (IRRI):


R Okono

> *"A genetic stock is a line that has been created by modern breeders and researchers, using conventional technologies, specifically to address some specified scientific purpose, typically for gene discovery."*

This definition includes the notion of perpetuation (a 'line'), which is central to genetic stocks: either the materials are genetically stabilised through sexual reproduction, or they can be distributed through vegetative propagation. Genetic stocks are often housed at research universities, and include everything from single-cell life to plants, fish and small mammals such as mice and rats.

GCP's genetic stocks component was born of the recognition that genetic gain in crop germplasm can be significantly increased by: (a) more efficiently exploiting various sources of diversity, and, (b) creating diversity to expand the base for trait discovery and selection. As a result, the development of new genetic stocks has been a cornerstone of the original foundation of GCP research and for its network of partners. Initially, these resources often had a more upstream aspect (eg, genetic studies), but the activity remained at the heart of GCP projects even when GCP shifted to focus more on integrated plant breeding and the use of these resources.

RESOURCES

Successive generations of breeding and selection for lines of specific agronomic types and relatively narrow adaptation have tended to shrink the genetic base and thus the pool for trait diversity in local breeding programmes. Such narrowing of genetic diversity increases germplasm vulnerability to evolving pests and diseases – or to global environmental changes – and reduces opportunities for new trait selection.

The genetic diversity of the most important crops and their wild relatives is held by genebanks, most notably those within the CGIAR system. The collections are extremely large, thus posing a challenge for practical phenotyping and trait discovery by plant breeders across a large number of accessions, even for traits that are easy to select through visual screening. For example, the wheat collection held at the International Maize and Wheat Improvement Center (CIMMYT) contains more than 150,000 accessions, and the maize collection more than 26,000. Accordingly, the initial rationale of the GCP genetic stocks activity was to make the diversity in genebanks more easily accessible and practical for the study – and practical application – of genetic diversity.

Furthermore, different breeding programmes may require a variety of tools to successfully exploit diversity. Consequently, as GCP evolved, the activity was broadened to include the development of a variety of genetic resources that would enrich diversity and increase the use of key traits in breeding, aided by the use of genomic tools and molecular methodologies. Often the sources of useful diversity are unknown or, if known, are in genetic backgrounds such as landraces and wild relatives that are difficult – if not impossible – for breeders to manage.

Two kinds of genetic stocks exist: one that facilitates and enables access to existing diversity (eg, reference sets), and the other that creates new diversity through recombination or mutation. The former is a sub-sample of existing collections, whereas the latter is potentially unlimited in its extent, and is currently under active development in GCP projects. In the sections that follow, we will consider both true genetic stocks and genetic stocks 'under development', which may require 'finishing' steps such as selfing generations before becoming true genetic stocks.

R Okono

Objectives

The objectives of GCP's genetic-stocks activity are as follows:

1. Make genetic diversity and traits of interest available in genebanks more immediately usable and accessible to breeders for crop improvement
2. Create new diversity through recombination
3. Increase the pools of diversity available for research and crop improvement.

To achieve these objectives, GCP commissioned a broad set of partners mostly from CGIAR Centres and scientists from developing countries, with occasional participation of developed-country institutes, to execute about 25 projects. During Phase I (2004–2008), the Programme focused on identifying and characterising reference sets for most of GCP's target crops (Annex 1), and developing mutants (eg, for beans and rice) and synthetics (eg, for groundnuts). Phase II (2009–2014) concentrates on phenotypic characterisation of the reference sets, and the development of chromosome segment substitution lines (CSSLs) and multiparent advanced generation intercross (MAGIC) populations. In addition, a dozen (mainly competitive) projects have been and will be implemented across both phases to develop mapping populations, recombinant Inbred lines (RILS) and near-isogenic lines (NILs).

Overall, GCP will have invested about USD 28 million in developing genetic resources. This sum represents about 18 percent of GCP's total budget of USD 150 million spread over 11 years.

PROJECT ACTIVITIES AND OUTPUTS


D Bernhard

The kind of research that has been undertaken to accomplish these objectives is briefly described below.

EXPLOITING NATURAL DIVERSITY

To help unlock the diversity of crop germplasm, composite collections (a few thousand accessions) of 21 crops (Annex 1) were assembled in collaboration with genebank curators, based on passport and pedigree information to limit similarity among entries. Depending on the crop, between a couple of hundred and several thousand accessions were used mainly from the international collections managed by CGIAR Centres, and the collection of a few large country programmes. These composite collections were then genotyped by validated simple sequence repeat (SSR) markers (30–50) or other available molecular markers to narrow down the number of accessions. Thus, the genetic diversity detected across the accessions was reflected, while at the same time reduction in the global allelic diversity in the selected pool was minimised. The resulting selections – called 'reference sets'[2] – averaged about 300 entries.

Accessions were derived and stabilised by single-seed descent and verified genotypically. Data-kits composed of the SSR markers used to genotype and verify the sets were made available to plant scientists. These kits by themselves allow researchers to assess and compare the diversity of their own collections with that of the reference sets, thus facilitating the introduction of new diversity in their prebreeding programmes. The sets were largely completed by 2009, except the

---

[2] Reference sets follow the same rationale as core collections with a reduced number of genebank accessions to represent the genetic diversity of a large collection, but with genetic information being the driver for identifying reference-set candidates.

one for cassava, which is currently being expanded (an objective within GCP's Cassava Research Initiative) and is due to be completed in 2013. During GCP Phase II (2009–2014), several reference sets, corresponding to GCP's target crops (cassava, chickpeas, common beans, cowpeas, groundnuts, rice, sorghum and wheat) are being phenotyped under different environments, including biotic and abiotic stresses, to facilitate the identification of new alleles with relevant breeding value from these materials.

These sets not only broadly represent the diversity of whole collections but also represent a set of genotypes that are highly suitable for association mapping or direct screening of germplasm for prebreeding. Reference sets have been used successfully to identify and use accessions as new genetic stocks to improve various traits, particularly disease resistance and even more complex traits such as drought tolerance in cassava, chickpeas, cowpeas, maize, sorghum and wheat.

CREATING NEW DIVERSITY

Some crops have narrow genetic diversity for key traits within their domesticated cultivated bases. Bringing in new alleles is therefore a must to make significant progress in breeding. This can be achieved by developing 'wild × domesticated' synthetics, creating new diversity by introgressing favourable alleles through polyploidy, for breeding from wild relatives into cultivars. Even crops that have adequate pools of diversity may benefit from the use of related cultivated species or wild relatives to bring new alleles with relevant agronomic value. Such an approach has been especially successful to find new alleles for simple inherited traits such as disease resistance.

More generally, new genetic diversity is created through recombination, that is, through crossing contrasting materials to create novel haplotypes. Considered collectively as a population of related haplotypes, this type of material bears analytical properties enabling identification of favourable genes or alleles. Moreover, some of the individual haplotypes are unique allele combinations and can — with further crossing — directly contribute higher-performing phenotypes to elite germplasm. Such materials emerge from various segregating populations derived from various kinds of mating schemes, producing diverse types of individual lines (see below).

MULTIPARENT ADVANCED GENERATION INTERCROSS (MAGIC) POPULATIONS

Several parental lines (8–12) from different genetic origins and in some cases, exotic backgrounds, are crossed, following a complex crossing design to maximise the mix of alleles from the parental lines in the offspring. The MAGIC populations serve a dual purpose: (a) they are very useful for better understanding the genetics involved and identifying new alleles for complex traits through association studies; and, (b) when evaluated in an early recombination stage, they allow extraction of highly useful new prebreeding materials. MAGIC populations have been developed for chickpeas, cowpeas, rice and sorghum, and are being developed for common beans. Selected parental lines have been used to combine elite alleles for simple traits like aluminium tolerance and submergence tolerance, as well as for complex traits such as drought or heat tolerance.

NESTED ASSOCIATION MAPPING (NAM)

This approach was created as a means of combining the advantages and eliminating the disadvantages of two traditional methods for identifying QTLs: linkage analysis and association mapping. NAM exploits both historic and recent recombination events to take advantage of low marker density requirements, allele richness, high mapping resolution and high statistical power, without suffering the disadvantages of either linkage analysis or association mapping. Populations were developed for rice and are being developed for sorghum under the Sorghum Research Initiative after a NAM backcross (BCNAM) to locally adapted varieties. They generate genetic stocks in the form of connected sets of RILs sharing common parental lines.

SYNTHETICS

Groundnuts, for example, do not have sufficient diversity that can be effectively exploited for drought tolerance, even with molecular tools. However, some wild relatives of cultivated groundnuts are highly drought-tolerant and these are being exploited by developing amphiploids through cultivated varieties (Annex 2) in the groundnut objective in the Legumes Research Initiative. Groundnut amphiploids developed in Brazil have been crossed with domesticated groundnut varieties in Africa to introduce diversity and – potentially – traits that otherwise would not be available.

RECOMBINANT INBRED LINES (RILS)

A most generic but valuable category of genetic stocks, RILs are stabilised genetic stocks that have been created over many years. Once verified, quantitative trait loci (QTLs) for traits of interest may be efficiently introgressed into breeding lines, thus creating impact in the field. RILs incorporating specific traits of interest – particularly drought – have been developed for cowpeas, maize, rice, sorghum and wheat. For most GCP crops, RILs have been developed to discover and characterise QTLs.

NEAR-ISOGENIC LINES (NILS)

NILs are RILs that possess identical genetic codes, except for differences at a few specific locations, or genetic loci. They thus provide an efficient means of evaluating segments of code from diverse sources (particularly difficult-to-use germplasm such as landraces) in a common parent, which may then be introgressed to incorporate the specific loci into breeding lines. Maize lines introgressed with specific segments from diverse materials – including landrace sources – were donated to CIMMYT by the Syngenta Foundation for Sustainable Agriculture through GCP. These are now being distributed through CIMMYT's maize genebank.

Sorghum NILs incorporating the Alt_{SB} gene for aluminium tolerance are being tested in Africa on problematic acid soils.

CHROMOSOME SEGMENT SUBSTITUTION LINES (CSSLS)

CSSLs are isogenic except for small segments of chromosomes introgressed from a distantly-related donor. For rice, CSSLs provided a means of efficiently accessing QTLs for traits of interest from African rice and wild species for introgression into popular indica and japonica Asian varieties (Annex 2). Rice populations were increased in 2011 and are now available for distribution from IRRI. The groundnut CSSL populations (cultivar introgressed with wild synthetic allotetraploid) are also being advanced and used for QTL mapping at ISRA, Senegal; they have been transferred to the International Crops Research Institute for the Semi Arid Tropics (ICRISAT) for multiplication, conservation and distribution.

MEASURING SUCCESS

The true and incremental value of reference sets and other genetic stocks actually multiplies by distribution, that is, their value is only realised by sharing the germplasm as widely as possible in the public domain. This sharing is mutually beneficial, as the value of the reference sets is enhanced by bringing in new data on additional traits and locations. Therefore, doubtlessly, requests for genetic stocks from users who in fact did not contribute to their development are an excellent parameter for measuring both success and adoption of genetic stocks as sources of new alleles for breeding. Even the mere identification of new alleles or relevant haplotypes for prebreeding within GCP projects indicates a level of success for this approach to creating genetic stocks.

Together with mutants, reference sets may be considered as the ‘oldest’ genetic stocks developed by GCP collaborators. When developing the reference sets, GCP had agreed to share genotyping responsibilities across different institutes for a given crop to enable collaboration and partnership. This inclusive approach however had some undesirable and unexpected outcomes, the main one being poor data documentation and a lack of standardised quality control. GCP commissioned a third party – Agropolis–CIRAD – to salvage the situation by conducting a complementary project to validate the genotyping data. In addition – and despite clear instructions – some sets had to be re-developed because, for example, plants from which genotyping materials were collected had not been self-pollinated, and were therefore unsuitable for generating single-seed descent materials. Seed quality was also poor or – at worst – seeds were simply lost (ie, misplaced).

Although considerable effort was made to standardise protocols for developing the reference sets, the quality of the sets remained variable, as some Centres undertook the task more rigorously than did others. This often simply had to do with internal organisation not being adapted to integrate the activity.

Since 2010, those Centres with higher-quality sets have regularly received ‘external’ requests for use of their sets. By December 2014, such monitoring will have provided enough data to reliably measure the usability of genetic stocks.

POST-GCP SUSTAINABILITY AND PROJECTED IMPACT

Sustainability of genetic stocks has always been an issue, as they are generally not managed in a centralised way but left under the direct responsibility of the scientists who developed them. These resources have therefore been usually handled in a highly *ad hoc* manner, implying unpredictable timing for answering requests for seed, and suboptimal quality control. Because of high staff turnover in CGIAR Centres and breeding programmes in developing countries, and also because their management is neither centralised nor coordinated, these resources are also often lost as staff move from one organisation to another.

Although genetic resources require different management protocols and storage timelines, the idea that genebank curators take on the management of genetic stocks was proposed several years ago. For some Centres like IRRI and ICRISAT, this is already a reality, for at least some of the genetic resources developed. Nevertheless, this is not the general status in the CGIAR system. A major generic question, of course, is who will pay for the maintenance and distribution of these genetic stocks. Resources allocated to genebanks can be used for infrastructure maintenance and fixed costs such as electricity, but specific recurrent as-and-when costs for seed multiplication and distribution must be met by other means.


D Bernhard

Sustainable management of genetic stocks in the CGIAR is a priority today. Ruaraidh Sackville Hamilton, in his white paper cited previously, is playing a key role in promoting best practice and options. His paper proposes to recover costs for managing genetic resources through a chargeback system on a two-tier scale, with non-profit organisations receiving stock at lower costs than commercial organisations. This is possible because “most genetic stocks are Plant Genetic Resources for Food and Agriculture under Development (as defined in the SMTA), and therefore full cost recovery principles could be operated" (cited from the SGRP position paper). GCP contributes actively to these discussions with CGIAR Centres and the Global Crop Diversity Trust. GCP's recommendation is for CGIAR crop Centres to follow the examples shown by IRRI and ICRISAT, and that genetic resources management be centralised at institutional level under the supervision of genebank curators.

Although the funding for genetic stocks maintenance and distribution might be separate from the funding for genebanks, these discussions should take place within the context of the Genebank CRP – an initiative aiming at supporting the management as well as the secure and sustainable funding of the collections of plant genetic resources held by 11 Centres, in partnership with the Global Crop Diversity Trust.

Most genetic-stock development supported by GCP will be accomplished by December 2014. Remaining activities, mainly MAGIC population development for beans and rice, and 'backcross nested' association mapping (BCNAM) in sorghum, are embedded in the respective CRP workplans. Thus, further development of those populations, multilocation testing by partners in developing countries, and extraction of prebreeding material would probably be sustained by the CGIAR institutions responsible, and by country partners. However, it is highly desirable that plans endorsed and agreed upon by all stakeholders be in place well before December 2014, to ensure that these projects will indeed continue and be completed after GCP's lifetime.

Like all GCP projects, these three remaining projects on beans, rice and sorghum have clear delivery plans formulated by the key partners in each project and implemented by respective Product Delivery Coordinators. Each plan defines the project's final deliverables including primary, and – where applicable – secondary users within a specific timeline, indicates responsibilities, and also identifies constraints, capacity needs (and solutions), means of distribution and IP considerations. Germplasm products also have supplementary plans which additionally clarify supply, access, maintenance and storage. These delivery plans, available on request, will be a useful baseline in discussions with partners because they include clear definitions of the added value from further development or distribution (or both) of GCP products.

Although genetic stocks are downstream from a genebank perspective, they are mostly upstream in the delivery chain of crop improvement. Their potential impact can be anticipated by considering the impact of minicore collections worldwide (for reference sets) and the impact of exemplary populations such as the NAM in maize,[3] and the many subsequent publications. GCP's impact in this field is yet to be assessed, given the relatively short timeline between genetic stock creation and GCP's end in 2014. However, science-based mechanisms must be put in place to quantify impacts and thus evaluate GCP's success. The mechanisms adopted so far involve monitoring the genetic stocks that users request from the scientists or institutes that produced them, and providing funding for future *ex ante* studies after GCP's closure.

Indeed, GCP plans to allocate resources and work in close collaboration with the CGIAR Standing Panel on Impact Assessment (SPIA) to define post-GCP impact assessment for a series of key products. SPIA is a subgroup of the CGIAR Independent Science and Partnership Council (ISPC).

Considering the upstream nature of GCP's research activities, impact shall be measured based on concrete indicators three to five years after the Programme ends (see *Transition Strategy* for these indicators). On a relative scale of 1 to 5, where 5 represents the largest impact across all GCP products regardless of activity or crop, and 0 no impact, GCP's efforts to develop and deploy genetic stocks are estimated to have an impact factor of 3. Such a score indicates that the genetic stock development has a significant impact on genetic study and plant-breeding efficiency in developing countries.

---

[3] McMullen et al (2009). Genetic properties of the maize nested association mapping population. *Science* 325:737–740.

ANALYSING THE POST-GCP PLACEMENT OF THE GENETIC STOCKS COMPONENT

As best as is known, GCP is unique, in that it supports the development of genetic stocks for such a broad array of crops. Considerable funds have been invested to support this effort. Tapping into new diversity is really at the heart of GCP, and a major, if not the, rationale for its establishment eight years ago. These resources are now at various stages of use. Many have already been used to introduce locally adapted germplasm, and to enhance its diversity and performance.

Developing genetic stocks, tapping into existing genetic resource collections and creating new diversity will always be required, and must always continue at some level for most crops. But this can be done within the respective CRPs and other initiatives (depending on research objectives), thus building on GCP's achievements.

WHAT WILL BE FINISHED BY DECEMBER 2014

In light of the original objectives, a claim can be made that the job has been 80 percent accomplished. The reference sets are ready, even if the quality of genotyping data is not optimal for all sets, and even as their development could have been done more efficiently, as outlined above. Also, a large number of mapping populations have been used to identify genes and QTLs for breeding (see companion Position Papers), and the effort to develop MAGIC populations is ongoing.

Of course, continued phenotypic and genotypic characterisation of these genetic stocks will clearly add value to these products as new alleles and traits continue to emerge in evaluations under different environmental conditions or stresses, thus significantly benefiting further breeding efforts. Such information should be stored in respective Centre databases and might require some global analysis under the leadership of the Centres that developed the genetic stocks. Almost none of the research projects aimed at developing genetic stocks will require extension beyond December 2014 to achieve their specific research objectives. The exceptions are MAGIC population development and BCNAM for sorghum.

EXTENDING ACTIVITIES TO CGIAR CRPS, CENTRES OR OTHER INSTITUTIONS

By their nature and timeline, some research activities will not have ended by GCP's closure, including the projects on MAGIC and BCNAM population development, deployment and use. Such research activities are now embedded in the respective crop CRPs, and post-GCP work on these product lines would be carried out by the commodity CRPs. The specifics are currently under discussion to arrive at mutual agreement.

For both the bean and rice projects, the initiative to develop MAGIC populations came from Centres looking at the progress and potential of other crops. For example, IRRI, using its own funds, is already developing more populations, combining different genetic backgrounds of interest, thus demonstrating strong ownership. Likewise for sorghum, ICRISAT has developed one of three BCNAM populations, using their own germplasm. The Centre will evaluate the other two populations developed by Mali's country programme (IER), with support from Agropolis–CIRAD.

Most genetic stocks are destined for storage, maintenance and distribution from CGIAR Centre genebanks. CRPs may be viewed as the ideal vehicle for these activities for several reasons: they have specific breeding targets, a need and capacity to exploit the use of genetic resources found in entities such as genebanks, and can readily access available funding. In their proposals, all crop CRPs aim to characterise and use the genetic resources in their associated genebanks, and conduct prebreeding to enhance their use. Although products are yet to be specifically defined, these objectives would largely address the continuing and evolving needs for genetic resources.

Most partner non-CGIAR institutions have at least some capability for storing – and even distributing – genetic stocks generated within their own countries. Indeed, selected breeding lines of some crops (eg, chickpeas) will be distributed regionally by appropriate country programmes. Such 'finished' materials can be maintained relatively easily within their breeding programmes. However, the maintenance, characterisation, use and distribution of true genetic stocks exceed the capacity of most country partners.

partners in some specific cases, but on a limited scale in terms of volume and kinds of crops. Realistically they have no particular comparative advantage – particularly in terms of efficiency and cost – over similar activities conducted by respective CGIAR genebanks.

EMBEDDING THE WORK IN A NEW ENTITY AS A RESEARCH ACTIVITY

Moreover, issues of germplasm protection, both of sovereign rights (the International Treaty on Plant Genetic Resources) and of intellectual property (IP) rights, can be major barriers for genetic resource exchange across countries, and are challenging for institutions producing genetic stocks. This has applied particularly to emerging economies such as Brazil, China and India. Attempts to engage the private sector highlight the need for the CGIAR to specify IP rights and access rights much more carefully than has been the case in the past. Developed-country institutes like Agropolis–CIRAD facilitate germplasm exchange as a service among GCP

At present, there appears to be no added value in embedding further development and characterisation of genetic stocks in a new entity post-2014. Reasons include the extensive array of products already developed or under development, the significant resources required to sustain the activity, and the difficulties in handling IP-related issues. In addition, the management of genetic resources is part of the primary mission of the CGIAR crop Centres: all CRPs dealing with genetic gains have as their objectives (working in collaboration with the Global Crop Diversity Trust – see the *In trust for international community* initiative) the exploration, generation and use of genetic stocks.

CONCLUSION

The genetic stocks activity has generated a large and diverse array of resources for GCP's target crops. Certainly, the need to further evaluate and use the genetic stocks stemming from GCP-supported projects, as well as the need to generate new genetic stocks, will both continue beyond December 2014 for all crops. This is due to the continuing and evolving need to identify new alleles and haplotypes to improve cultivated germplasm. However, the future impetus to produce genetic stocks is clearly with the CRPs, in close collaboration with the CGIAR crop Centres, country programmes and the Global Crop Diversity Trust. Alternative suppliers of genetic stocks such as developed-country institutes do not appear to have any comparative advantage over CRPs in terms of mandate, resources, cost and efficiency, but large developing-country programmes will definitely play a key role in genetic stock production, management, use and distribution.

In conclusion, most of GCP's objectives in this research component have been achieved. Genetic stocks and their characterisation will most likely be further developed in a satisfactory manner within CRPs dealing with genetic improvement, thus building on GCP's achievements. These stocks are expected to be managed in a sustainable way, with clear ownership and possible chargeback to generate revenue. Contrary to genetic resources, genetic stocks should be managed as research products and, if there is no demand for the products, be discarded after a clearly defined period of time. Genetic stocks are expected to be mobilised at an increasing rate and hopefully, this will lead to increased food security.

GCP remains committed to its mission and community to the end of the Programme and will work with partners along the delivery chain to maximise successful implementation of the delivery plans developed for each Research Initiative. GCP will also closely engage with its partners until its very sunset to ensure – as far as will be possible – the integration, extension, and expansion of activities, as may be required. The Programme will go a step further and help initiate related new activities that build on GCP's achievements, should there be clear added value and demand for such activities. In this way, the Programme is working to secure broad and sustainable use of its products well beyond 2014, while also mitigating against the loss of gains made thus far.

R Okono

ANNEX 1: CORE REFERENCE SETS DEVELOPED FOR CGIAR MANDATE CROPS

As at June 2012

Crop[a]	Composite or core collection for molecular characterisation	SSR markers (except for cassava)	Number of genotypes per reference set	Lead institute and partners[b]
Bananas & plantains	327	48	96	**Bioversity**, IITA, Agropolis
Barley	2,676	14	300	**ICARDA**, CAAS
Cassava	3,000	36+ DArTs	250	**CIAT**, EMBRAPA, IITA
Chickpeas	3,024	50	300	**ICRISAT**, ICARDA
Coconut	1,014	30	359	**Agropolis**
Common beans	625	36	192	**CIAT**, EMBRAPA
Cowpeas	1,871	16	345	**IITA**
Faba beans	1,000	20	152	**ICARDA**
Finger millet	1,000	20	300	**ICRISAT**
Foxtail millet	500	20	200	**ICRISAT**
Groundnuts	991	21	300	**ICRISAT**, EMBRAPA
Lentils	1,000	24	150	**ICARDA**
Maize	1,775	50	234	**CIMMYT**, CAAS, IITA, Agropolis
Pearl millet	1,000	20	300	**ICRISAT**
Pigeonpeas	1,000	20	300	**ICRISAT**
Potatoes	1,000	50	Analysis in progress	**CIP**
Rice	2,757	50	Analysis in progress	**IRRI**, CAAS, CIAT, AfricaRice, Agropolis
Sorghum	3,393	39	345	**ICRISAT**, Agropolis, CAAS
Sweet potatoes	500	50	Analysis in progress	**CIP**
Wheat	3,000	50	372	**CIMMYT**, Agropolis/CAAS/ICARDA
Yam	350	20	342	**IITA**

[a] Crop species in which molecular characterisation has been supported by GCP

[b] Lead institutes indicated by **bold** above. Full names below

- AfricaRice: Africa Rice Center
- Agropolis: Agropolis International, France1.
- Bioversity: Bioversity International
- CAAS: Chinese Academy of Agricultural Sciences
- CIAT: International Center for Tropical Agriculture
- CIMMYT: International Maize and Wheat Improvement Center
- CIP: International Potato Center
- EMBRAPA: Brazilian Agricultural Research Corporation
- ICARDA: International Center for Agricultural Research in the Dry Areas
- ICRISAT: International Crops Research Institute for the Semi-Arid Tropics
- IITA: International Institute of Tropical Agriculture
- IRRI: International Rice Research Institute

ANNEX 2: CATEGORIES OF GENETIC STOCKS DEVELOPED WITH GCP RESOURCES

As at June 2012

Category (period)	Description	Principal Investigator(PI), Institute Collaborators (name, affiliation)	Target country(ies)/ regions
CSSLs	***Groundnuts*** A cultivated groundnut (variety Fleur11) incorporated segments from wild relatives, using a wild synthetic allotetraploid (*A ipaensis* × *A duranensis*)$^{\times 4}$ that was created in Brazil	*PIs:* Vincent Vadez, ICRISAT, India and Bonny Ntare, ICRISAT, Mali *Collaborators:* • David Bertioli, Universidade de Brasilia • Emmanuel Monyo, ICRISAT, Malawi • Ousmane Ndoye, ISRA, Senegal • Daniel Fonceka, CERAAS, Senegal • Jean-François Rami, Agropolis–CIRAD	Africa • Malawi • Niger • Senegal • Tanzania Asia • India Latin America • Brazil
	Rice Populations of Asian *Oryza sativa* (indica and japonica) rice were introgressed with segments from African rice (*O glaberrima*) and wild relatives (eg, *O meridionalis* and *O rufipogon*)	*PIs:* Mathias Lorieux, CIAT/IRD, Colombia; Joe Tohme,CIAT, Colombia *Collaborators:* • Baboiucarr Manney and Marie-Noelle Ndjiondjop, AfricaRice, Benin • Susan McCouch, Cornell University, USA • Claudio Bondani, EMBRAPA, Brazil • Cesar Martinez, CIAT, Colombia • Miguel Diago Ramirez, FEDEARROZ, Colombia	Latin America • Colombia • Brazil Africa • Burkina Faso • Mali • Nigeria

ANNEX 2: CONTINUED…

Category (period)	Description	Principal Investigator(PI), Institute Collaborators (name, affiliation)	Target country(ies)/ regions
MAGIC populations	***Chickpeas, cowpeas, rice and sorghum*** Populations developed	**Chickpeas** *PI*: Pooran Gaur, ICRISAT, India	Africa • Kenya • Ethiopia Asia • India
		Cowpeas *PI*: Philip Roberts, University California, Riverside, USA	Africa • Burkina Faso • Mozambique • Senegal
		Rice *PI*: Hei Leung, IRRI, Philippines	Global
		Sorghum *PI:* C Tom Hash, ICRISAT, Niger *Collaborators:* • Ian Mackay, NIAB, UK • Mary A Mgonja, ICRISAT, Kenya • Fred Rattunde, ICRISAT, Mali • S Senthilvel, ICRISAT, India • SP Deshpande, ICRISAT, India • R Madhusudhana, DSR, India	Africa • Mali • Niger • Burkina Faso, Kenya • Ethiopia Asia • India
	Common beans Being developed	*PI:* Bodo Raatz, CIAT, Colombia *Collaborator:* Steve Beebe, CIAT, Colombia	Africa • Ethiopia • Kenya • Malawi • Zimbabwe

ANNEX 2: CONTINUED...

Category (period)	Description	Principal Investigator(PI), Institute Collaborators (name, affiliation)	Target country(ies)/ regions
NAMs	***Rice*** Populations developed	*PI*: Mathias Lorieux, CIAT/IRD, Colombia *Collaborator:* Marie-Noelle Ndjiondjop, AfricaRice, Benin	Global
	Sorghum Being developed	*PI:* Jean-François Rami, CIRAD, France Collaborators: • Niaba Teme, IER, Mali • Eva Weltzein, ICRISAT, Mali	Africa • Burkina Faso • Mali • Niger
NILs	***Maize*** Lines introgressed with specific segments from diverse materials, including landrace sources, were donated to CIMMYT by the Syngenta Foundation for Sustainable Agriculture through GCP. These are now being distributed by CIMMYT's maize genebank .	Donated by Syngenta (see Description in previous column)	Global
	Sorghum Lines incorporating the *Alt*$_{SB}$ gene for Al tolerance are being tested in Africa on problematic acid soils	*PI:* Jurandir Magalhaes, EMBRAPA, Brazil *Collaborators:* • *Cornell University, USA*: Leon Kochian, Jiping Liu, Stephen Kersovich, Sharon Mitchell, Martha Hamblin, Theresa Fulton, Alexandra Casa • *EMBRAPA, Brazil*: Claudia Guimãraes, Robert Schaffert, Antonio Marcos Coelho, Vera Alves • *INRAN, Niger:* Soumana Souley, Maman Nouri, Magagi Abdou, Adam Kiari, Fatouma Beidari	Latin America • Brazil Africa • Burkina Faso • Mali • Niger

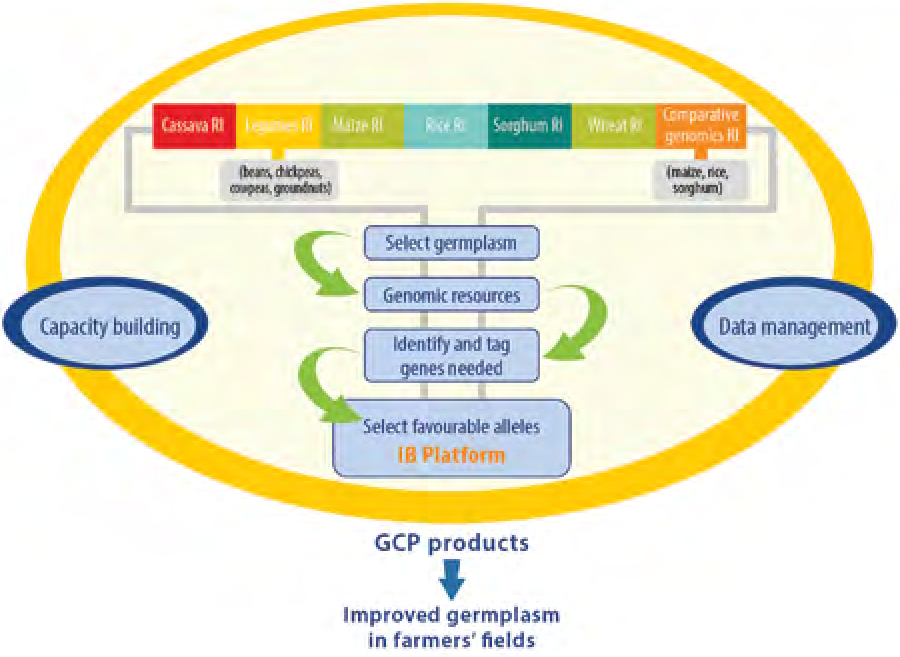
Annex 2: continued…

Category (period)	Description	Principal Investigator(PI), Institute Collaborators (name, affiliation)	Target country(ies)/ regions
RILs	***Most GCP crops*** RILs have been developed to discover QTLs	Various PIs and collaborators	Global
Synthetics	***Groundnuts*** • Amphiploids (incorporating genomes of wild *Arachis* spp selected for their drought tolerance) include: (*A batizocoi* K9484 × *A stenosperma* V10309)$^{\times 4}$, (A batizocoi K9484 × *A duranensis* SeSn2848), (*A batizocoi* K9484 × *A duranensis* V14167)$^{\times 4}$ and (*A ipaensis* KG30076 × *A villosa* V12812)$^{\times 4}$. • Progeny of crosses with domesticated groundnut varieties in Africa are now being evaluated for use in breeding	*PIs:* Jose Valls, EMBRAPA, Brazil; David Bertioli, Universidade de Brasilia, Brazil *Collaborators:* • Wellington Martins, Universidade de Catolica de Goias, Brazil • Ousmane Ndoye, CERAAS, Senegal • Vincent Vadez, ICRISAT, India • Udaya Kumar, UAS, India • Angelique d'Hont, Agropolis–CIRAD, France • Guillermo Siejo, IBN, Argentina • Jens Stoiugraard, AU, Denmark	Africa • Malawi • Niger • Senegal • Tanzania Asia • India Latin America • Brazil

[a] GCP crops include the nine target crops in Phase II (cassava, chickpeas, common beans, cowpeas, groundnuts, maize, rice, sorghum and wheat); with the following nine additional mandate crops also covered in Phase I (barley, coconut, lentils, millet [finger, foxtail, pearl], *Musa* spp, pigeonpeas, potatoes, sweet potatoes and yams), making 18 crops in all.

In 2011, GCP worked with more than 200 partners spread across 54 countries

GCP's Research Initiatives (RIs) and research support activities



Hosted by CIMMYT
(*Centro Internacional de Mejoramiento de Maíz y Trigo*;
the International Maize and Wheat Improvement Center)

Mailing address:
GCP, CIMMYT, Apdo Postal 6–641
06600 Mexico, DF Mexico, Mexico

Physical address:
c/o CIMMYT, Km 45 Carretera Mexico–Veracruz
El Bátan, Texcoco, Edo de México
CP 56237, México

Tel: +52 55 5804 2004
Fax: +52 55 5804 7558

Email: generationcp@cgiar.org or info@generationcp.org

www.generationcp.org

/GCProgramme
www.blog.generationcp.org