

Unlocking Genetic Diversity in Crops for the Resource-Poor

A proposal for a CGIAR Challenge Program

Presented by

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Program Summary

The exciting discoveries of molecular biology are not being used in ways to realize their maximum benefit for the world's poor; neither are the rich pools of genetic resources that exist in collections held by national agricultural research systems (NARS) and the Future Harvest Centers of the Consultative Group on International Agricultural Research (CGIAR). The products of the genomics revolution will not address the needs of the resource poor unless strong coalitions are made by institutions dedicated to alleviating poverty. **The Challenge Program "Unlocking Genetic Diversity in Crops for the Resource-Poor" will produce a new, unique public platform for accessing and developing new genetic resources using new molecular technologies and traditional means.** An unprecedented array of genomic and genetic resources, ready for direct use in plant improvement, will be made available as public goods, first to the national agricultural research systems (NARS) of developing countries, small and large, that have plant improvement programs, and later to any other entities that have crop improvement goals, especially those dedicated to the resource-poor farmers. These products will be in the form of enabling technologies and intermediate products for crop improvement programs in NARS and elsewhere.

The Challenge Program is presented by a founding group, the Consortium, of three CGIAR Centers (CIMMYT, IPGRI, and IRRRI), two NARS (CAAS, China and EMBRAPA, Brazil), and five advanced research institutes (ARIs) (Cornell University, USA; AGROPOLIS, France; John Innes Centre, UK; National Institute of Agrobiological Sciences, NIAS, Japan; Wageningen University, the Netherlands). Additional institutions, both private and public, will join the Challenge Program, once it becomes operational. The Consortium has been formed because the desired outcomes of this Challenge Program will not be achieved by organizations working alone.

This Challenge Program will serve as a platform to assemble and use the intricacies of applied genomic sciences for the benefit of crop improvement efforts by NARS and others. The key feature of the platform is its applicability to any crop and any trait, thereby ensuring that all 22 CGIAR mandate crops may be supported by the platform. The platform will also be applicable to the Water and Food, Biofortification, and Sub Saharan Africa Challenge Programs.

One central objective of this Challenge Program is to demonstrate the application of the platform. The application of comparative genomics to increase tolerance to drought will be a case study or proof of concept. Drought was chosen as the case study trait because drought affects all of CGIAR mandate crops. This effort will be reinforced by the long history of drought research and by current drought research. Furthermore, drought has been identified as a high-priority trait in many regions, especially Africa, where there is high potential to increase crop yields in marginal environments through drought tolerance.

This Challenge Program's development goal is to increase food security and improve livelihoods in developing countries by unlocking the genetic potential and enhancing the use of public genetic resources in plant breeding programs through the concerted generation, management, dissemination, and application of comparative biological knowledge. The Challenge Program contributes to this goal by creating an integrated platform for dissecting genetic diversity in crop plant genetic resources, identifying important genes to reduce the impacts of environmental and biotic stresses on crop productivity, enhancing yield, and improving nutritional quality of crop products. Beyond this, the Challenge Program will identify, manipulate, and validate gene expression resulting in plants with potential value far beyond present-day crops. These plants, through seeds or vegetative propagules, will be transferred to breeding programs. The Challenge Program will generate new, science-based enabling and intermediate technologies. A technology transfer plan will be designed to ensure that the products of research undertaken by the Challenge Program will be delivered to and used by plant breeders and farmers; such a plan will include consideration of *inter alia*: joint venture agreements; licence agreements with humanitarian clauses and market segmentation provisions; and, material transfer agreements. The management of the intellectual property will be consistent with the Guiding Principles for the CGIAR on Intellectual Property Rights Related to Genetic Resources, the

Convention on Biological Diversity, and the International Treaty on Plant Genetic Resources for Food and Agriculture. The principle aim of intellectual property management in the Challenge Program will be to ensure that research outcomes remain accessible in the public domain for the benefit of NARS and other plant breeders, and ultimately, the resource poor farmers in developing countries.

Development of this Challenge Program was motivated by several factors, among them:

- The rate of increase in potential and realized productivity of key crops under favourable conditions is leveling off.
- Rural and urban populations continue to grow.
- Chronic environmental stresses continue to limit productivity.
- Catastrophic events, such as floods, sustained drought, and fire, periodically cause nearly total losses in crops, which, in most countries, are not buffered by food reserves.
- New technologies are now available and accessible for use in enhancing crop productivity.
- New technologies have been proven effective in identifying traits, producing new varieties, but largely in the private sector; a public research platform is needed.
- Productivity gains for dryland cereals and grain legumes appear to be increasing and new technologies offer scope for further increases in genetic gain.

The Challenge Program is taking advantage of a timely opportunity: The genomics revolution is contributing very large quantities of information about biological systems, while the information age is providing unprecedented abilities to store, access, and process data; together they offer the ability to uncover new biological phenomena at the gene level. All of this information can be made available through the new public platform created by this Challenge Program. New molecular-based approaches, as well as traditional ones, will allow plant breeders to easily transfer these genes to crops for resource-poor farmers, especially farmers in marginal agricultural environments, to alleviate chronic and acute deficiencies in food production and quality.

The Challenge Program has proposed a strategy that emphasizes applied aspects of genomics, largely adopting information and materials arising from basic molecular biology research. It will marshal the resources and competencies of the CGIAR, NARS, ARIs, and the private sector into a global public network. It will seek the most effective collaborations to achieve the best scientific outcomes. At the same time, it will build human capacity, especially of NARS scientists, through exchanges of researchers and advanced capacity-building for scientists from the research systems of developing countries. The research of the Challenge Program will not produce and release finished crop varieties for farmers. It will produce new genetic resources, make the initial gene transfers to locally adapted germplasm, and then transfer the derived materials to crop improvement programs, especially of the NARS and CGIAR Centers.

The technical strategy for the Challenge Program is relatively simple. The platform stands on four technological legs (“the table”) with a covering emphasis on human resource development (“the table cloth”). The components are developed as interdependent Subprograms as follows:

- SP1: Genetic diversity of global genetic resources
- SP2: Comparative genomics for gene discovery
- SP3: Gene transfer and crop improvement
- SP4: Genetic resource, genomic and crop information systems
- SP5: Capacity-building

And, the Challenge Program will work across four crop groups:

- Cereals
- Root and tuber crops
- Legumes
- *Musa* and forage species

The inclusion and exploration of a strategic range of source and target crops in the Program from its outset will capture and capitalise upon the unique advantage possessed by the CGIAR system i.e., the

power of comparative biology, physiology and genomics across a broad range of germplasm sets. Exploration at the allelic/functional and structural genomic level will elucidate the diverse mechanisms underlying a priority trait and facilitate the recognition of general and crop specific patterns and models which in turn will generate novel hypotheses for complex trait performance.

A Program Steering Committee (PSC) will serve as a Board of Directors and comprise the Chief Executive Officers, or their designees, of the consortium members with additional representation invited from GFAR and the CGIAR Executive Council; the latter in an *ex-officio* role. The PSC, chaired by an independent chairperson, will receive independent advice from a Program Advisory Committee (PAC) and a GFAR Stakeholders' Committee. The Challenge Program will be guided by an internationally recruited eminent scientist as Program Director who will also provide leadership for Subprogram 5. The Program Director will be assisted by a Lead Scientist for each of the four research Subprograms; together, this team will guide the operation of the Challenge Program. They will provide reviews of proposed research for the PAC and PSC and will conduct quality and progress evaluations of research projects.

Anticipated outcomes in the first five years include, but are not limited to:

- A fully defined platform for accessing, identifying, and utilizing genetic resources for crop improvement.
- Accessions in genetic resource collections identified with variants of genomic regions or alleles of candidate genes having a favorable impact on priority traits that can be transferred to germplasm for resource-poor farmers in accordance with internationally agreed arrangements for access and benefit sharing for genetic diversity.
- A better understanding of the genetic structure of genebank collections that enhances the value of genetic resource collections.
- Candidate genes and genomic regions underlying critical traits identified; functional characterization of those candidate genes or genomic regions accelerated.
- An information network established for genomic and phenotypic data integrating advanced genetic resources, genomic, and crop information systems, which will increase the efficacy of public and private plant breeding programs for the international community.
- Capacity among research centers greatly expanded through collaboration and advanced capacity-building of scientists.
- An extended global network of CGIAR Centers, NARS, public ARIs, and private institutes established for the effective utilization of advanced technologies for crop enhancement for developing countries.
- The Challenge Program integrated approach validated by the case study on drought tolerance.

Anticipated outcomes in the second five years include:

- Information and genetic resources derived from this research available for use in research and in crop improvement programs.
- The understanding of the genetic control of priority traits greatly enhanced and made available to the global research community.
- Breeding materials containing new alleles that will directly improve productivity or quality developed and available to crop improvement programs. These lines, with further breeding and selection, will enhance productivity and quality of food crops for resource-limited farmers worldwide.

Financial resources required for this Challenge Program are rather considerable and require sustained availability. In-kind contributions from the initial consortium members already indicate sustained commitment to the Program (i.e., the equivalent of 25 full-time researchers per year—a total value of US\$ 5.726 million—access to laboratories, and genetic resources) and this is expected to increase significantly with the addition of new partners. The full implementation of this Challenge Program requires funding of US\$ 14 million per year. This includes project or grant funds that will be allocated based on the merit of individual projects. All research activities will be funded on the basis of relevant, and high-quality proposals with performance reviews as noted above.

Introduction and Overview

A powerful coalition to use advanced technologies and plant genetic diversity to address the continuing problems of hunger and poverty, especially among the resource-poor farmers of the developing world

The Challenge

For hundreds of millions of malnourished people throughout the world, agricultural research and development offers perhaps the only means of escaping an existence circumscribed by poverty and hunger. With their research partners worldwide, the Future Harvest Centers of the Consultative Group on International Agricultural Research (CGIAR) have been major players in conducting and stimulating research and adoption of new crop varieties and practices in countries where the production of staple foods is limited and where agriculture is often the primary livelihood. Most of these advances have been achieved using traditional plant breeding procedures.

While these advances have averted starvation among millions of people, many experts – and poor farmers themselves – believe that the pace of improvement is too slow. The causes for concern are many.

- The rate of increase in potential and realized productivity of key crops under favourable conditions is leveling off; productivity gains for dryland cereals and grain legumes appear to be increasing and new technologies offer scope for further increases in genetic gain.
- Rural and urban populations continue to grow.
- Chronic environmental stresses continue to limit productivity.
- Catastrophic events, such as floods, sustained drought, and fire, cause nearly total losses in crops, which in most countries are not buffered by food reserves.
- The development of state-of-the-art molecular biology has been primarily a private initiative, and owing to access and ownership issues, this technology may never be fully available to help those who need it most.

Despite the fact that agricultural research has addressed many important problems with notable gains, generally it has not attained more than moderate levels of tolerance to stresses, such as those induced by limited water or high temperature, and it has yet to devise biologically or physically sustainable solutions to many problems. Why is this so? Are genetic resources at fault, or methods? Perhaps both, but the limitations they presently impose may yet be overcome.

As the reader will observe, *Unlocking Genetic Diversity in Crops for the Resource-Poor* offers radically new approaches to crop improvement that will significantly alleviate the global challenges outlined above. The Challenge Program described here also ensures that those challenges are met with technology that remains in the public domain. The pages that follow outline how the CGIAR Centers and their partners will enable the world's poorest people to break the seemingly intractable barriers to raising the productivity of their food crops and improving their livelihoods.

The Opportunity

The genomics revolution is contributing unprecedented quantities of information about biological systems, while the information age is providing unprecedented abilities to store, access, and process data; together they offer the ability to uncover new biological phenomena at the gene level. Genetic homology (synteny) among widely different species and across species, genera, families, orders, and kingdoms unlocks genetic diversity in ways that enable diversity to be used in crop improvement with a precision never before achieved. Developing countries want to be involved with this revolution, and to use new technologies in the fight against hunger and malnutrition.

There is no better time to adopt and adapt a new paradigm of gene discovery and use it in plant breeding to eliminate the genetic barriers that limit food production, particularly in difficult, marginal agricultural environments. Many believe that the gene revolution, properly harnessed and vigorously applied, will take crop performance to new levels, just as hybrid vigor, crop morphology, mechanization of field research, computers, and crop management interventions have done over the past eight decades.

This Challenge Program marshals the unique expertise of three groups of partners who have undertaken to unlock genetic diversity with molecular tools and use it to improve the productivity and sustainability of farming systems throughout the world.

- The CGIAR Centers, in addition to their molecular research, hold in trust for the world vast amounts of plant diversity, the basic resource for crop improvement.
- The national agricultural research systems (NARS) of developing countries are the primary experts on assessing and breeding plants under their own conditions, in consultation with the farmers for and with whom the work is undertaken.
- The advanced research institutes (ARIs), both public and private, of the developed world are developing the novel molecular techniques and strategies to decode diversity, such as that held by the CGIAR Centers and NARS.

By capturing the synergies that result from this type of broad-based collaboration, the Challenge Program will contribute to increasing the rate of potential and realized productivity for keystone crops in marginal environments.

Mission

The Challenge Program on *Unlocking Genetic Diversity in Crops for the Resource-Poor* will realize the potential of plant genetic resources to improve livelihoods and increase food security in developing countries. It will do so by enhancing the use of genetic resources in breeding programs through a concerted effort to generate, manage, and apply genomic information derived from comparative studies. It will enhance the public domain as the best means to ensure fair access and benefit sharing for resource-poor farmers.

Rationale

The publication in 2001 of two drafts of the human genome, the complete DNA sequence that encodes the instructions to build and operate an organism, represented a critically important leap forward in the understanding of biology. Even before the sequence was available, medical scientists were making use of the huge similarities shared among animal species. For example, they would identify differences in human patients at the DNA level, use those differences to detect similar mouse sequences using available databases, isolate the gene(s) from the mouse genome, and then use the mouse gene(s) to pinpoint the human homologue. The time has come to take this approach and these techniques, broadly called comparative genomics, to agricultural plants in the service of agriculture for impoverished people.

In some respects, agricultural scientists are in a better position than their biomedical colleagues. Whereas medical scientists painstakingly have to acquire informative pedigrees that can be used to track the inheritance of genes of interest, the CGIAR Centers and NARS already hold huge numbers of segregating lineages, the results of crossing known parents. These “families” hold vital information about the inheritance of important traits and associated genes. Moreover, the segregating lineages are just a small element in the general package of diversity held. The Centers alone currently conserve over 650,000 samples of landraces, traditional varieties, wild species, old cultivars, new cultivars under development, and breeding lines (Appendix 1). These samples represent roughly 40% of the world’s holdings of unique accessions of major crops and forages of global and regional importance. They are unique because they are held in trust for humanity and therefore can be considered a global public good. A wealth of information has been generated over the years as these collections have been researched and used (Fuccillo et al. 1997), but truly unlocking the potential of that

diversity requires the application of genomic technology with new strategies in plant breeding. That is the approach of this Challenge Program (Figure 1).

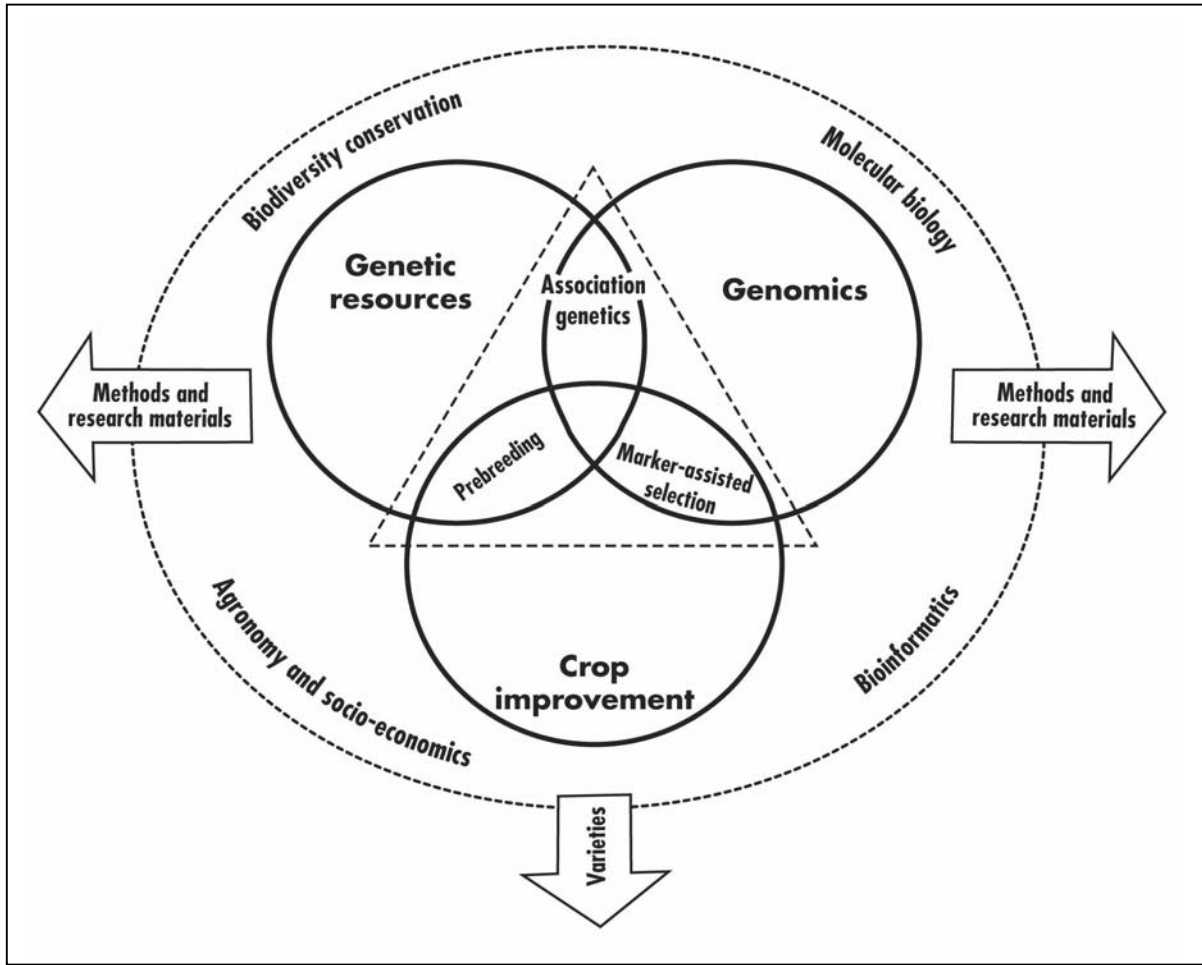


Figure 1. Conceptual basis for the Challenge Program on Unlocking Genetic Diversity in Crops for the Resource-Poor.

The three components of this first Challenge Program are separate but interconnected: (1) genetic resource collections provide the raw materials, (2) genomic science provides the means to exploit genetic resources (i.e., identify new alleles), and (3) crop improvement applies traditional and modern methods of gene/allele transfer into functional crop varieties. The Challenge Program will address the interfaces of these three basic components, as represented by the area bounded by the triangle. This boundary indicates that crop improvement and the management of genetic resource collections remain on-going activities. It also indicates that the Challenge Program will emphasize applied aspects of genomics, largely by adopting information and materials arising from basic research in molecular biology. The larger circle surrounding the smaller ones represents other materials and disciplines upon which the Challenge Program will draw and to which it can contribute, such as bioinformatics. The arrows represent the Challenge Program's outputs.

Further refinement of the intermediate products and dissemination of improved varieties to the resource-poor will be undertaken through close partnerships with NARS, NGOs and farmers' organizations. These will build on the many such partnerships already established in the CGIAR.

Plant sequences that have already been decoded show that, as with animals, many plant genes have counterparts in all species. Furthermore, in a group such as the grasses, which includes all the cereals on which people depend for food, the physical organization of the genes is broadly similar across barley, maize, rice, sorghum, wheat, other (minor) cereals, and wild grasses. An understanding of how a gene functions in

one species is thus likely to enhance the understanding of how it works in others. In legumes and solanaceae, gene organization among species is being elucidated. Functional gene homology for root and tuber crops provides the basis for explaining similar physiological processes. Rapidly developing, large-scale molecular technologies, such as DNA microarrays (also known as gene chips), make it possible to ask, for example, how thousands of genes (even the entire genome set of genes) change their activity when a plant is stressed by drought. Even more exciting is the possibility of comparing gene expression at the entire genome level in response to a common stress across several species – a strategy not feasible until the advent of large-scale molecular genomics. Such information leads to an understanding of the complete range of responses to a particular stress, not just those of an individual species or variety. This knowledge, in turn, leads to the identification of novel response mechanisms that can be induced and/or introduced into any species, thus broadening the genetic diversity within a species for almost any trait.

The ARIs – public and private, North and South – are key elements of this Challenge Program. They have the (often expensive) equipment for undertaking genomic analyses and/or have undertaken the more basic research necessary to develop the tools and techniques. When applied to the tremendous diversity of genetic resources available in the CGIAR Centers, these molecular tools will rapidly reveal much about the basic molecular biology of crop plants.

With the goal of providing information, associated genetic resources, and molecular tools as international public goods, the partnerships within this Challenge Program ensure that all scientists will have access to the rich resources and strategies necessary to meet the objectives of their own particular programs. Information, tools, and strategies will be developed through full partnerships with NARS. Some NARS have advanced research capabilities in genomics that will considerably further the agenda of this Challenge Program, and all NARS have the experience of working with farmers under their conditions. The NARS are thus ideally placed to assess and characterize the plants whose genomes are being investigated. This collaborative work links genotypic information to phenotypic expression and is essential to the success of the overall effort. Aside from participating in the research, scientists from NARS will be trained by the many partners in the Challenge Program, thus building the capacity of developing countries to address their problems directly. Finally, collaboration between NARS and farmers themselves will be vital to ensure that new varieties meet farmers' needs and are adopted rapidly.

The outputs (biological constructs, tools, techniques, and strategies) of this Challenge Program can be used to address almost any germplasm-based problem in agriculture, and we expect that many problems will be addressed.

Demonstrating the Concept: Drought Tolerance

A problem of global importance has been chosen to demonstrate the application of the Challenge Program's outputs. In choosing a problem to use as a proof-of-concept of the Challenge Program's approach, several factors were considered. Foremost was the universality of a problem among crops and locales. This criterion assures the involvement of a broad spectrum of scientists and institutions within and outside the CGIAR. Other criteria included the progress achieved through more conventional plant breeding efforts, the possibilities for future gains, the level of past and current investment in research, and the likelihood that a comparative genomic approach would result in a positive outcome.

The abiotic stresses that limit agricultural productivity meet all of these criteria, with drought being the most important. In agriculture, scarcity of water is a concern for farmers around the world – rich and poor, subsistence and commercial, in the North and the South. In tackling drought stress, we are taking on one of the oldest and most pervasive threats posed to agriculture by the environment. Almost every country and every crop faces water-limiting situations at one time or another, and this occurrence is likely to increase as the world's water resources decline (Seckler et al. 2002), as demand for water for non-agricultural uses rises, and, in the longer term, as climate change accelerates.

Breeding for drought tolerance in many of the major crop species has produced important advances and even improved cultivars, but progress has been slow and the prospects for future gains uncertain (Blum 1998; www.plantstress.com; Grando et al. 2000; Winter et al. 2001). Plants' responses to drought stress are complex, varied, and involve interactions between many different molecular, biochemical, and physiological processes (Ingram and Bartels 1996). Our understanding of these processes even at the genetic level is still in its infancy, although it is advancing rapidly in several species, especially the cereals and *Arabidopsis*. Most of these efforts focus on a single species and are not yet taking advantage of results obtained from other species, although a few collaborations do strive to bridge the gap between species. As a proof-of-concept, the Challenge Program proposes to build on these previous and on-going alliances by applying genomic tools and technologies to a better understanding of drought tolerance mechanisms across a subset of the crop species important to the CGIAR. For example, the CGIAR Technical Advisory Committee funded a project between CIMMYT and IRRI that focused on identifying candidate genes by sharing results obtained in maize at CIMMYT and rice at IRRI. The Rockefeller Foundation funds a number of projects focused on drought stress in the major cereals. Results from these projects were discussed recently at a meeting in May 2002 hosted by IRRI. CIMMYT has established a joint project with Pioneer Hi-Bred on drought tolerance that provides CIMMYT access to the vast amount of information Pioneer possesses in several species (e.g., rice, *Arabidopsis*, maize). From 1991 to 2002 IFAD funded IITA, CIAT and EMBRAPA to explore the potential of increasing productivity of cassava germplasm through drought tolerance in north-east Brazil and west Africa, and a new BMZ- funded project will support CIAT and a NARS network to study bean genomics for improved drought tolerance in Latin American El-Nino-affected regions. A major emphasis in this Challenge Program is to demonstrate how synteny and comparative genetics among plant/crop groups (cereals, roots and tubers, legumes, *Musa* and forage species) can be used to take drought tolerance and other traits to new levels of expression for productivity enhancement. The Challenge Program will build on existing activity; for example, many NARS, such as CAAS, have established national programs and networks to study drought in field crops.

As genes and gene systems are identified in the target crops, and as genes from other plant groups (e.g., *Arabidopsis*) are demonstrated, they will be made available to all other crop species. We are hopeful that they can be used without significant further investment in developing tools or technologies.

Challenge Program Overview

The Challenge Program operates over two phases of approximately five years (Figure 2); Phase 1 is described in most detail here. In Phase 1, the Challenge Program will acquire and/or develop the tools and techniques needed to identify useful genetic variation among the collections held by the CGIAR Centers and elsewhere. It will identify genes and pathways to use in crop improvement programs, identify marker systems to speed selection for these, and develop integrated crop genetic resources, improvement, and bioinformatics systems to facilitate and optimize implementation of the results. The feasibility of this integrated, collaborative approach will be demonstrated by the case study on drought tolerance.

In Phase 2, optimal alleles and novel genes identified in Phase 1 will be incorporated into elite breeding materials and locally adapted landraces in the most efficient way and in partnership with NARS. The new lines will ultimately be passed to farmers for comprehensive assessment in concert with NARS. New systems for producing and disseminating seed will also be tested and promoted. Improvements gained in some crops will be transferred to other crops, which are vital for better nutrition and for the economic health of farming systems. In both phases, information and materials developed will be freely available to the resource poor. Fair access and benefit sharing will be in harmony with the Convention on Biological Diversity and the International Treaty on Plant Genetic Resources for Food and Agriculture.

It is important to emphasize that the applications of the Challenge Program are generic (Figure 3). They can and will be used for any crop, any gene, and any trait, although, as noted, the Challenge Program proof-of-concept will focus initially on studying the tolerance of the major food crops to drought-stressed environments.

The Challenge Program is composed of five Subprograms (Figure 4):

- Subprogram 1: Genetic Diversity of Global Genetic Resources
- Subprogram 2: Comparative Genomics for Gene Discovery
- Subprogram 3: Gene Transfer and Crop Improvement
- Subprogram 4: Genetic Resource, Genomic, and Crop Information Systems
- Subprogram 5: Capacity Building

And, the Challenge Program will work across four crop groups:

- Cereals
- Root and tuber crops
- Legumes
- *Musa* and forage species

The inclusion and exploration of a strategic range of source and target crops in the Program from its outset will capture and capitalise upon the unique advantage possessed by the CGIAR system i.e., the power of comparative biology, physiology and genomics across a broad range of germplasm sets. Exploration at the allelic/functional and structural genomic level will elucidate the diverse mechanisms underlying a priority trait and facilitate the recognition of general and crop-specific patterns and models which in turn will generate novel hypotheses for complex trait performance.

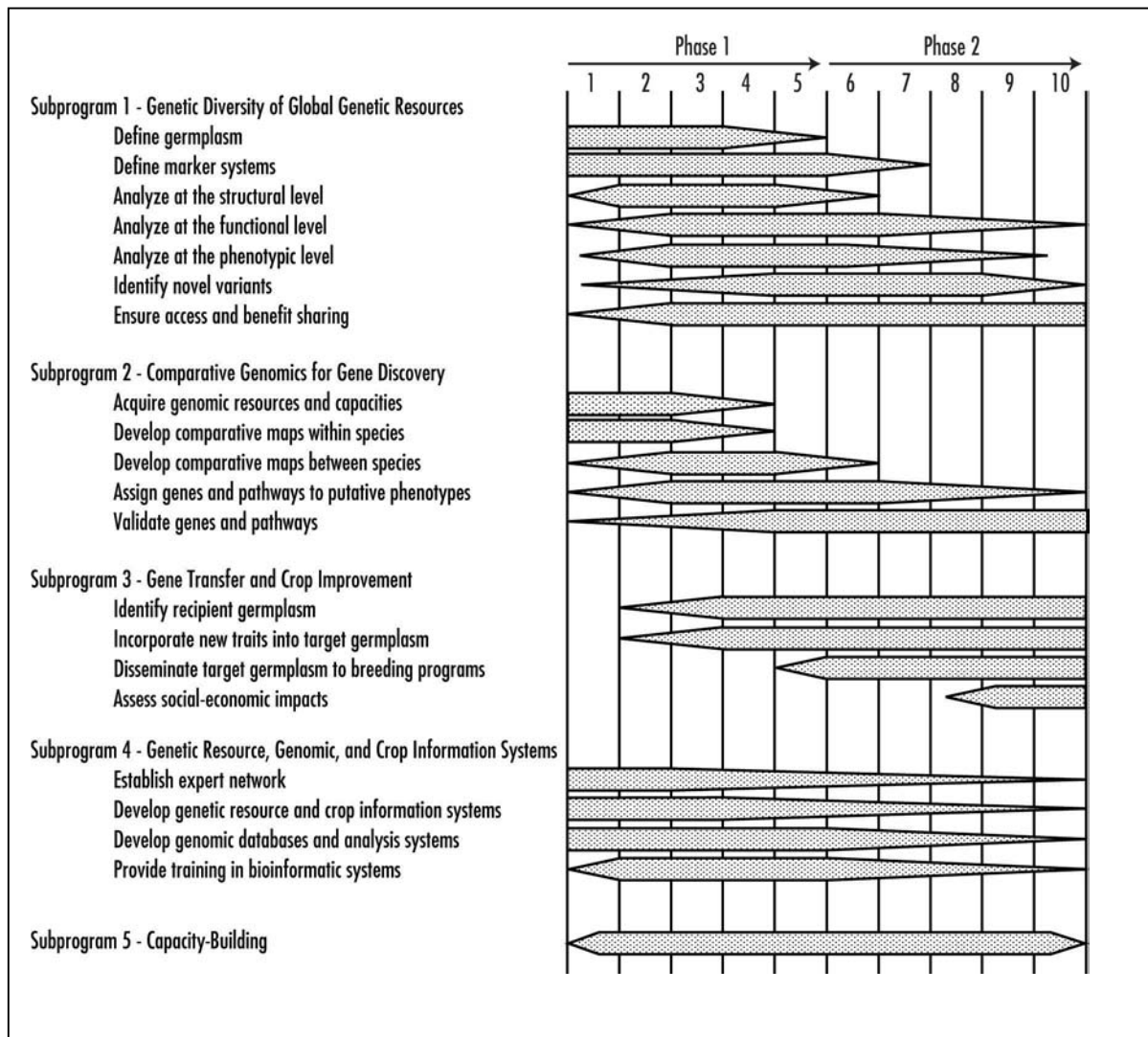


Figure 2. Outputs of the Challenge Program on Unlocking Genetic Diversity in Crops for the Resource-Poor, by Year and Subprogram.

The Challenge Program is divided into two phases of approximately five years. In Phase 1, the Challenge Program will acquire and/or develop the tools and techniques needed to identify (1) useful genetic variation among the CGIAR Center collections of genetics resources; (2) genes and pathways to use in crop improvement programs; (3) marker systems to speed selection for those genes and pathways; and (4) bioinformatics tools to make all data and genetic materials publicly and easily available for research and plant breeding. In Phase 2, optimal alleles and novel genes identified in the first phase will be incorporated into elite breeding materials and locally adapted landraces for comprehensive assessment by national research programs and farmers. The relative emphases placed on each activity may be seen in the figure. In Phase 2, many of the activities in Subprogram 1 and Subprogram 2 decrease, whereas Subprogram 3 activities increase. Activities in Subprogram 4 remain relatively constant throughout the life of the Challenge Program. Capacity-building (5) will be a constant theme of the Challenge Program throughout.

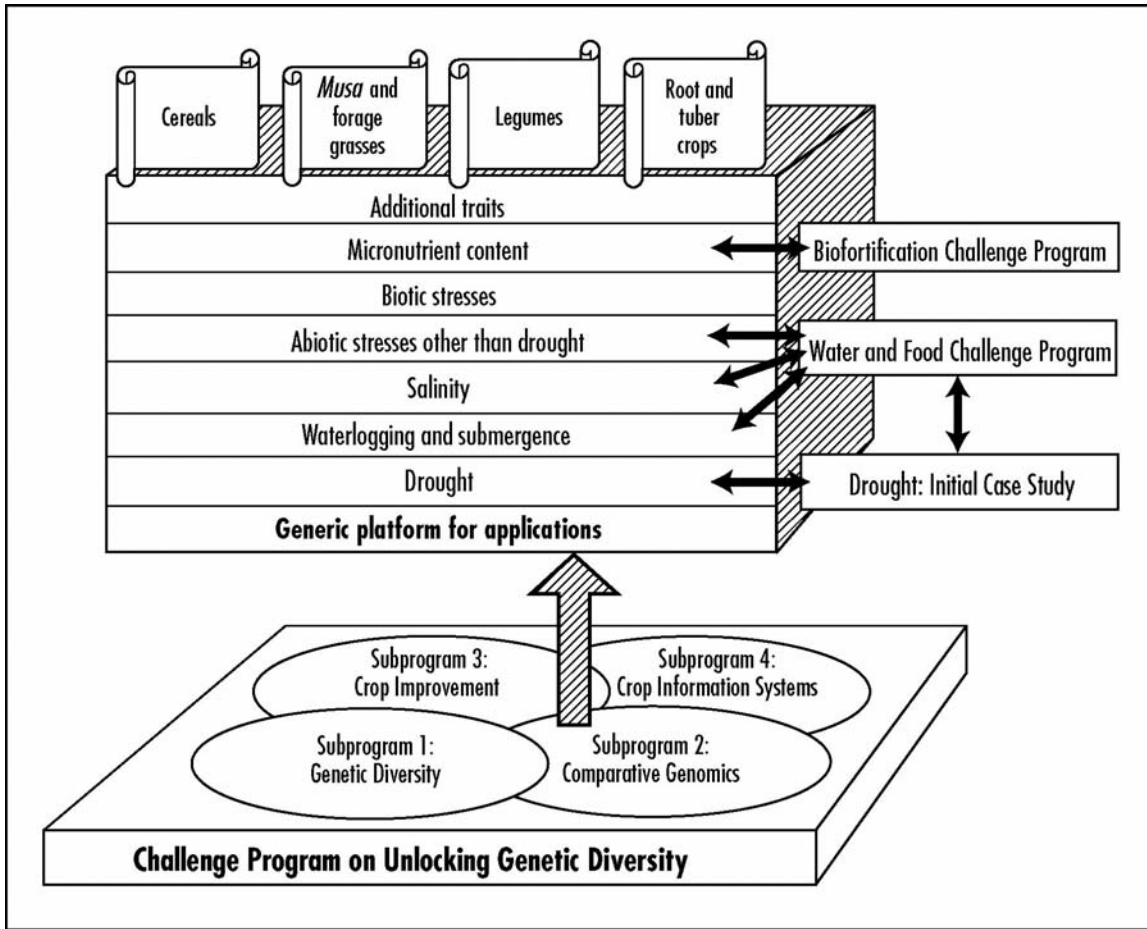


Figure 3. The Challenge Program *Unlocking Genetic Diversity in Crops for the Resource-Poor* is designed to function across crop species and traits of interest and to help achieve the goals of the other Challenge Programs.

The four overlapping circles at the bottom of the figure, representing the four research Subprograms of this Challenge Program, from the main platform for tapping genetic diversity. Four crop groups of great importance in developing countries appear in the boxes at the top of the figure to illustrate that the Challenge Program is applicable work for any crop species or related set of species. Likewise, the Challenge Program provides a means of working on many traits of interest, as illustrated by the examples below the species boxes. The products developed by working on these species and traits can help achieve the goals of other Challenge Program – e.g. Biofortification, Water and Food, Sub Saharan Africa – and help overcome drought (the initial case study of this Challenge Program).

become available; other activities may be developed by other parties, either in response to calls for proposals by the Challenge Program or independently. The latter may often be the case, especially given that other Challenge Programs that would benefit from the outputs of this Challenge Program will be established.

Each Subprogram requires inputs from and provides outputs to other Subprograms. Ultimately, the output of the Challenge Program is improved germplasm that is derived from the successful application in plant improvement programs of the tools and technologies developed by the Challenge Program.

The Subprograms are described in detail later in this document, but they are introduced briefly here to provide an overview. Additional details can be found in the various appendices.

Subprogram 1: Genetic Diversity of Global Genetic Resources

At the core of the Challenge Program is the extensive characterization at the structural and functional level of the vast genetic resources (including wild relatives, landraces, breeding lines, cultivars, mapping populations, and genetic stocks) held by the participating institutions (see Appendix 1). Together with the comparative genomic gene discovery component, the functional and structural characterization of diversity in these collections will provide the raw materials (i.e., the genes) for novel solutions to virtually any breeding objective for the 22 mandate crops of the CGIAR.

The ultimate goal of the Challenge Program is to analyze genetic diversity on a large number of accessions, up to 3,000, from each crop, using from 300 to 500 genes already identified from prior research as probes. This effort will identify DNA sequences that are similar in the crop plant to the known genes used as probes. This provides the allelic variation for study in Subprogram 2, Comparative Genomics for Gene Discovery. In addition, phenotypic data will be collected and analyzed with the genetic data by new methods of detecting associated characters and genes. From these analyses, accessions within a crop will be identified for direct transfer to breeding programs as outlined in Subprogram 3, Gene Transfer and Crop Improvement. The main objective of the Challenge Program is to create a public platform and databases that are not specific to crops or traits. The information available can be used for high-priority traits in any of the crops.

Although the ideal platform would have a complete genetic characterization of a representative sample of all of the 22 CGIAR mandate crops, this cannot all happen at once. Priorities will be established in the technical planning workshops to determine which collections will provide the maximum benefit to the information in the platform. Selection criteria for target crops in each crop group may include (among others): importance of the crop, amount of genetic analysis available, and availability of sufficient accessions for study. Note that these crops will comprise cereals, legumes, *Musa* and forage species, and roots and tubers.

Organization of this key element of the Challenge Program will include joint consultation by crop and genomic specialists to set priorities and select genes for use in the diversity assays. Agronomists, agroecophysicologists, and social scientists will participate in the strategic planning. The genetic diversity analyses will be done cooperatively in laboratories at several institutions and will include NARS scientists who will adopt methodologies for their own laboratories. A critical element for Subprograms 1 and 2 is having an appropriate source of phenotypic data and plant tissues for DNA and RNA analysis. This will require accessions from collections to be grown in the field or under controlled growth conditions, and in some cases under contrasting treatments, such as well-watered and drought-stressed conditions.

Agronomists and physiologists will participate in these studies and provide key methodologies. NARS scientists are expected to participate directly as well. For example, accessions from the national, CGIAR, and ARI genebanks may be grown at NARS facilities that are representative of the target environments of this Challenge Program. Appropriate data and tissue samples will be collected and analysed by NARS scientists in collaboration with scientists working in Challenge Program laboratories. This provides continuity of the research with NARS scientists and their direct involvement in the analysis and interpretation of the results.

The genetic resources used in the Challenge Program will be available through agreement among all participating institutions in accordance with the principles for access and benefit sharing of genetic diversity as described within the framework of the Convention on Biological Diversity, the International Treaty on Plant Genetic Resources for Food and Agriculture, and the Trade-Related Aspects of Intellectual Property Rights (TRIPS) agreement. An intellectual property management policy will be developed that ensures NARS have ready access to technologies and products arising from the Challenge Program.

Structural characterization of genetic diversity

Comparisons of genetic diversity of individuals within a species and among related species historically have been done via the use of phenotypic traits or, more recently, molecular genetic markers. These markers quantify the differences in specific loci in the genome. These loci may or may not be within genes; depending on the marker type, these loci may or may not be mapped in the genome. Molecular markers do have a great advantage in characterizing germplasm as they do not suffer as greatly from two of the major drawbacks of phenotypic characterization: (1) large effects of the environment on the expression of many traits and (2) a limited number of possible traits that can be measured, coupled with a limited number of distinct polymorphisms in these traits. These two drawbacks lead to the inevitable poor classification of many lines, which will look similar (or different) owing to reasons other than genotype. The information gained from characterization studies using molecular markers can help to better predict shared pedigree or geographical origin of individuals and to find population structures that influence the analysis of functional characterization, such as associations between markers and phenotypes. Structural characterization with molecular markers is a critical first step in any detailed genomic study, as the information gained can be used to narrow down the number of individuals used in further (and more detailed) analyses.

Functional characterization of genetic diversity

Molecular genetics of model species, including *Arabidopsis*, tomato, rice, and *Medicago* have revealed and isolated hundreds of genes having specific functions. Remarkably, a large proportion of genes from one species are identical to those from another species. This information has spawned a whole new field of comparative genetics (Bennetzen and Freeling 1997; Devos and Gale 1998, 2000). This conservation of sequence identity between and within species across large regions of the genome (synteny) or in coding regions (microsynteny) serves as a means both to assay genetic diversity and to discover new alleles of important genes for use in crop improvement programs. Many accessions can be assayed and their allelic diversity characterized. The analysis of associations between phenotypic data on these accessions that relate to traits of interest under specified conditions and their molecular characterization will detect patterns or clusters of accessions related to geographic and evolutionary origins and trait differences – thereby providing access to previously undetected sources of useful genetic variation (e.g., for drought tolerance).

Subprogram 2: Comparative Genomics for Gene Discovery

The second Subprogram of the Challenge Program focuses on the tools, technologies, and approaches to achieve an understanding of gene systems across many species of importance to developing country agriculture.

Comparative genetics across crop species

The CGIAR and NARS as a whole have the unique advantage to develop universal maps across economically important species. For almost all of the CGIAR mandate crops, quite extensive genetic maps within the species are already available (Appendix 2). Comparative maps are also available for many CGIAR crops with their models. These are most advanced for the cereals (rice, sorghum, maize, barley, millet, wheat), but potato-tomato and some inter-legume comparisons are also available.

Conserved orthologous sets of genes (COS) (Fulton et al. 2002) are groups of conserved markers across large families of plant species. The COS markers for dicots are already available from Cornell University, and it should be feasible to develop a similar set for the monocots.

Functional genomics for candidate gene discovery

With sequences of an entire genome such as *Arabidopsis* and rice, and extensive sets of expressed sequences for many other crops available, sets of genes for these species can now be spotted on a slide or chip (gene or DNA arrays). The arrays can be used to view the coordinated expression of the genes (Brown and Botstein 1999; DeRisi et al. 1997). By examining the expression of many genes simultaneously under a specific condition, e.g., under drought stress (Seki et al. 2001; Oztur et al. 2002), the complex interactions of different biochemical pathways can be understood and genes identified that are responsible for improving a complex trait. Finer discrimination of the effects of a particular stress on gene expression in plants may come from comparative microarray analysis featuring cDNA derived from plants subject to different stresses (Kikuchi et al. 2002).

The resulting information facilitates the dissection of genetic and metabolic systems of the organism. Structural and functional conservation in gene regulatory circuits is particularly relevant for identifying genes with large effects on phenotypes. Transcriptional factors control genetic switch points that affect multiple downstream genes. Manipulation of such regulatory elements can bring about dramatic changes in phenotypes that are often viewed as being controlled by many genes with minor effects. The dramatic effect of transcriptional factors is well illustrated by the CBFs (C-repeat binding factors) and the related DREB (dehydration responsive element binding) factors. These factors control multiple downstream genes that confer tolerance for cold, salt, and drought stress (Stockinger et al. 1997; Jaglo-Ottosen et al. 1998; Thomashaw 1999; Kasuga et al. 1999) and are already being tested by several CGIAR Centers. The available sequence databases of rice, *Arabidopsis*, maize, wheat, potato, tomato, soybean, and *Medicago* will make it possible to mine regulatory elements and translated genes in other genomes.

Subprogram 3: Gene Transfer and Crop Improvement

The ultimate development goal is to provide new crop varieties that are selected and adopted by the target communities and farmers in resource-limited regions. Through Subprograms 1 and 2, this Challenge Program will identify new germplasm with genes/traits that will be valuable if incorporated into adapted varieties. This new germplasm will be found in raw germplasm that requires considerable plant breeding effort to transfer to locally adapted types by traditional plant breeding methods.

The Challenge Program will define protocols (e.g., with case studies) for more efficient gene transfer. This will include marker genes that are closely genetically linked to the genes for the desired trait (marker-assisted selection), rapid tests for phenotype recognition, and genetic transformation of new genes into locally adapted genetic materials, such as improved varieties and landraces. The scope for the Challenge Program is to identify genes, develop ways for detecting them in plant breeding programs, and to make initial gene transfers by hybridization and transformation into several locally adapted genotypes (varieties). Therefore, the Challenge Program will not produce finished varieties. Materials developed by the Challenge Program will be made available to breeding programs of NARS, CGIAR Centers, ARIs, and private breeding programs utilising many of the networks that already exist for this purpose.

Protocols for selecting the desired traits will be produced and demonstrated to NARS breeders and others through the Challenge Program. The new genetic materials that are produced will be distributed to breeders under material transfer agreements (MTAs) and assurance of adherence to biosafety standards. These transfers will require the recipients to guarantee that the materials will be used to develop locally adapted varieties and will be readily available to farmers. The MTAs will be modeled after those currently used by the CGIAR Centers and other institutions.

The transfer of genes by hybridization or transformation will be done in collaboration with NARS scientists who participate in the Challenge Program capacity-building activities. Selection protocols using marker-

assisted selection, or in some cases functionality, may be assayed to detect specific gene products or pathways that have been correlated with improved performance (Ribaut et al. 2002).

While the vast genetic resources available are likely to provide the majority of the optimal gene systems, in some cases the optimal or critical gene or gene system may be entirely lacking in a species. In this case, genetic engineering will be employed to introduce the required gene into the target species. For example, modifications of gene expression by manipulating promoters by gene insertion will be studied. Genetic engineering may also be used for gene discovery and validation. The ability to target a single gene and modify both its expression and resulting products confers unparalleled power for better understanding the role of a specific gene in a biological context. Transgenic materials will be developed and made available only in strict accordance with biosafety regulations and ethical principles. The capacity for biosafety handling will be enhanced in the context of Subprogram 5.

Following gene transfer, it will be necessary to validate the expression of the desired traits, both from the standpoint of the genetic background to which they were transferred and under field conditions representative of the farms in the targeted regions. In the Challenge Program, validation will be done by agronomists, breeders, physiologists, and social scientists. The participating institutions will provide scientists for this step, but NARS scientists have a principal role because the validation is most appropriately done under representative conditions of the targeted farmers' environments.

Many of the CGIAR Centers and NARS have crop improvement programs that are well established and have made significant contributions over the past decades. The products of these breeding efforts are appropriate genetic resources for introducing new genes and gene combinations to build upon or enhance already productive materials. Protocols for optimizing gene and trait expression, in particular for drought tolerance, will be provided to the breeding programs so that they can efficiently select for the desired genes and/or traits. In most cases, molecular markers will be available so that the gene(s) can be followed most efficiently by simply assaying for the associated marker.

Subprogram 4: Genetic Resource, Genomic, and Crop Information Systems

Clearly, the Challenge Program will involve the capture, storage, integration, analysis, and dynamic dissemination of substantial volumes of diverse and dispersed genomic, genetic resource, and crop improvement information. The challenge of linking and integrating these information components into a coherent information gateway will therefore play a central role within the Challenge Program and forms the basis of Subprogram 4. The strategic alliance between bioinformatic, biometric, and advanced data management techniques will contribute to the development of a "gold standard" integrated genetic resources, genomics, and crop improvement information network that will be the basis of genetic resource management and use for the coming century. It is highly appropriate that information describing the in-trust collections of genetic resources held by the CGIAR Centers should be the initial focus of this "gold standard." In addition, this networking of expertise will provide the foundation for an integrated research program for the Challenge Program, addressing critical questions concerning the methodologies for linking gene discovery with genetic resource characterization and crop evaluation data. The design of the information network will be driven by the specific requirements of the research activities outlined in Subprograms 1-3.

Subprogram 5: Capacity-Building

Capacity-building is a major goal of this Challenge Program, and it is appropriate to dedicate considerable resources to capacity-building. The platform developed in this Program provides the materials and technology for application to research and applied plant breeding. For NARS scientists to utilize the materials and technology in their own research and plant breeding programs, considerable capacity-building will be needed. NARS are particularly interested in genetic diversity analysis of their landraces and in optimizing the potential for finding new traits for their breeding programs. Once traits are found, they will wish to develop markers for use as indirect selection tools. They will also want to access data about genes and traits, so they

must be able to browse the databases. Finally, and perhaps most important, NARS scientists will gain experience with gene transformation and state-of-the-art conventional hybridization /selection techniques for variety development targeted to their own local environments.

Each of the four research Subprograms will engage in capacity-building activities. These activities will be conducted at any of the research institutions participating in the Challenge Program. CGIAR scientists as well as NARS scientists will need to gain experience in particular areas, such as microarray analysis, bioinformatics, genetic mapping, and biosafety. Exchanges of scientists and sabbatical leaves will be encouraged. The CGIAR Centers and other participating institutions will support the research of students seeking advanced degrees and that of postdoctoral fellows; these researchers may work at more than one institute. Finally, summer internships for young students from NARS will be provided. The Challenge Program offers an attractive venue for building the skills of students from NARS and advanced institutions. The formulation of the capacity building activities will be based on a needs assessment, and will reflect NARS requirements, more generally.

Research facilities and capabilities will be developed according to an organized plan for how various participating institutions can provide research support to each other. It is envisaged that not all partners (CGIAR Centers, NARS, and ARIs) will need, or will be able to afford, to have the full range of instrumentation for genomics/genetic resources research.

The Challenge Program will have annual research meetings for participants and will organize other conferences. It is also expected that the Program will organize a website. The website will provide up-to-date news of research results, research protocols, and links to publications and other websites.

The various capacity-building initiatives of this Challenge Program will be directed by the Challenge Program Director with the aid of a full-time Training Coordinator. Lead Scientists in Subprograms 1- 4 will plan capacity-building activities and present those plans to the Director for review and submission for funding. The activities of the Capacity-Building Subprogram will continue for the duration of the Challenge Program.

In Summary

The more this Challenge Program achieves, the more it can achieve, because information gathered from any source can be used to illuminate other questions. For example, knowing about drought tolerance in *Arabidopsis*, a model dicot, could enhance yields in upland rice, a monocot and seed crop, which might then be used to solve problems associated with water-logging in taro, another monocot but a root crop. Because the Challenge Program provides information through an integrated network, the value of the information grows as a power function of the amount of information.

Finally, none of the partners on its own could undertake the effort envisaged in this Challenge Program. Quite apart from the prohibitive costs, the synergies expected from a wide collaboration to unlock genetic diversity with molecular tools are a novel aspect of this initiative. The 11 Future Harvest Centers that hold the in-trust collections have much to contribute. The ARIs need access to diversity to advance their basic comparative plant genomics research efforts. The NARS in particular need access to the variability under study, the technologies necessary to best tap that variability, so that they can meet the needs of farmers. Most of all, the resource-poor farmers of the developing world need the products of this Challenge Program to give them better and more sustainable livelihoods that will enable them to remain on their land and thrive.

Expected Outcomes

Phase 1: First Five Years

- Accessions in genetic resource collections identified with variants of genomic regions or alleles of candidate genes having a favorable impact on priority traits that can be transferred to germplasm for

resource-poor farmers in accordance with internationally agreed arrangements for access and benefit sharing for genetic diversity.

- The genetic structure of genebank collections characterized, thus leading to enhanced value of genetic resource collections.
- Candidate genes and genomic regions underlying critical traits identified; functional characterization of those candidate genes or genomic regions accelerated.
- An information network established for genomic and phenotypic data integrating advanced genetic resources, genomic, and crop information systems, thus enhancing the efficacy of public and private plant breeding programs for the international community.
- Capacity among research centers and NARS of the South greatly expanded through collaboration and advanced capacity-building of scientists; the capacity building activities to be based on a needs assessment.
- An extended global network of CGIAR Centers, NARS, public ARIs, and private institutes established for effective deployment of advanced technologies for crop enhancement for developing countries.
- The Challenge Program integrated approach validated by the case study on drought tolerance.

Phase 2: Second Five Years

- Information and genetic resources derived from this research deployed for use in research and stakeholder crop improvement programs.
- The understanding of the genetic control of priority traits greatly enhanced and made available to the global research community.
- Breeding lines containing new alleles that will directly improve productivity or quality developed. These lines, with further breeding and selection, will enhance productivity and quantity of food crops for resource-limited farmers worldwide.
- The most promising materials advanced to on-farm trials for evaluation of productivity and acceptability to growers and consumers.
- Assessment of socio-economic impact completed.

Strategy

The conceptual basis for this Challenge Program consists of three separate but interconnected components (Figure 1): (1) genetic resource collections provide the raw materials, (2) genomic science provides the means to exploit these genetic resources (i.e., identify new alleles), and (3) crop improvement applies traditional and modern methods of gene/allele transfer into functional crop varieties. The Challenge Program therefore addresses the interfaces of these three basic components, as represented by the area in Figure 1 bounded by the triangle. This boundary indicates that traditional crop improvement and the management of genetic resource collections remain on-going activities. It also indicates that the Challenge Program will emphasize applied aspects of genomics, largely by adopting information and materials arising from basic research in molecular biology. The larger circle surrounding the smaller ones represents other materials and disciplines upon which the Challenge Program will draw and to which it can contribute, such as bioinformatics.

Together these components form a generic platform for accessing and using genetic resources (Figure 3). The protocols for each of the components are also generic; they can be adapted to any crop or trait.

Implementation

This proposal lays out a *program* approach that provides the general strategy, types of approaches, and data needed, but not the specific workplans. These will be developed during technical workshops planned for the first half of 2003, immediately upon approval by the CGIAR of the Challenge Program. The workshops will be attended by scientists representing the institutions/organizations who participated in the Alexandria Stakeholder Meeting, and others. These workshops will identify high-priority *projects*; providing details including specific objectives, locations for the research, collaborating scientists, required research materials,

and genetic and phenotypic assay protocols. Project proposals will be developed and will provide specific workplans, timelines, milestones, and budgets. These proposals, which will be addressed by some commissioned research and a competitive grants program, will be reviewed and presented to the Program Steering Committee (PSC) for endorsement. Funding will be made available based on the PSC recommendations from Challenge Program funding and/or via additional, competitive funding sources. The Business Plan provides additional details on the operational aspects of the Challenge Program.

***Collaboration among Centers, Institutes, and NARS:
Essential for Success***

An essential element of the strategy for this Challenge Program is collaboration. The importance of multidisciplinary teams has been well demonstrated as the science of molecular biology has advanced to rapid nucleotide sequencing of whole genomes (as with the human and rice genomes) and linkage of human disease syndromes to specific genes, including issues of implementation in medicine and health and pharmaceutical industrial policies. Crop genomic sciences build on the fundamental discoveries demonstrated by the human genome efforts mentioned in the introduction to this document. Unfortunately, crop genomics laboratories often work in isolation from each other and other disciplines. This is inefficient and in some cases futile. This Challenge Program will seek the most effective collaborations to achieve the best scientific outcomes and also to advance human capital through inter-institutional exchanges of scientists. Attention will be given to social and policy issues throughout the duration of the Challenge Program.

Challenge Program Description

Subprogram 1: Genetic Diversity of Global Genetic Resources

Rationale and Goals

This Subprogram has two principal goals: (1) Developing a functional platform for general application to genetic diversity and gene discovery and (2) genetic characterization of the collections of genetic resources held by CGIAR Centers, national programs, and special collections of ARIs (including crop wild relatives, landraces, breeding lines, cultivars, mapping populations, and genetic stocks), with emphasis on the 22 CGIAR mandate crops.

This Subprogram will define a core subset of up to 3,000 accessions per crop in the target crops for each crop group. The accessions included in the subset will be chosen on the basis of existing information on origin, traits, and past diversity studies. Although the subsets ideally will encompass an entire range of genetic diversity of each crop, emphasis will be placed on identifying accessions with high-priority traits within each crop (e.g., tolerance to drought based on geographical origin, phenotypic characterization, or pedigree, as consistent with the drought case study).

The core subsets will first be analyzed using molecular genetic markers to find the structural genetic diversity present within the subset. This step will allow a smaller number of accessions to be identified for further (and more detailed) analyses (those not similar by markers and thus probably containing the highest number of unique alleles at other loci as well). The reduced subset will then be analyzed for functional diversity at known genes of interest. These genes will be assembled from sequences known to be conserved across many different species, and from genes identified in Subprogram 2. As the drought case study identifies genes related to drought tolerance, these genes will also be included in the functional marker set, and diversity for response to drought can be identified in some of the entries of the reduced subset. These novel variants will be characterized further to provide new alleles, genes, and pathways for the Challenge Program and ultimately for dissemination to breeders.

Approach

Selection of genetic resources for diversity analyses

The number of accessions will vary by crop, the current status of knowledge, and the relative importance of the crop; however, as noted, as many as 3,000 accessions will be assembled per species in the target crops for each group as a core subset of the larger collection(s). The entries will include representative cultivars, landraces, and wild relatives from the crop collections, as well as precise genetic stocks, such as aneuploids, congenic and contig lines, and segregating and mapping populations and their parents, particularly those already developed for drought structural genomics studies. The composition of a set of accessions for a single crop will be made by consultation among collaborators, including genebank curators, breeders, geneticists, agronomists, agroecophysicologists, and social scientists from NARS, CGIAR Centers, and ARIs.

Selection of marker systems

Markers for structural diversity assays. The marker systems most commonly used among the CGIAR crops at present are simple sequence repeats (SSRs). Reasonably extensive pre-mapped sets are available for many of the CGIAR mandate crops (Appendix 2). However, the consensus among molecular geneticists is that single nucleotide polymorphisms (SNPs) will become the preferred system over the next few years. In principle, SNPs provide additional flexibility by accessing haplotypes within marker genes, and the limited variability (i.e., only two alleles) at each base-pair may be an advantage.

The Challenge Program will exploit all available types of markers for genotyping and will assemble a suitable marker system for the target crops. If no marker systems exist in a particular species, and there are no plans in the public or private sector to develop them, the possibility of developing a new marker system for that species can be considered within the scope of the Challenge Program. If new markers are to be developed, preference will be given to SNPs. The Challenge Program will, in general, avoid use of any marker that is subject to a proprietary use policy that could limit its use for crop improvement for resource-poor farmers. Challenge Program policy will ensure rapid publication and distribution of newly discovered markers.

Markers for functional diversity assays. Following structural characterization, the original sample of 3,000 lines may be narrowed to as few as 10% of the original number, depending on the crop and the specific trait(s) emphasized. This subset of genetic resources will be screened with as many as 500 genes. These 500 genes will be assembled into a panel of genes for functional diversity and gene discovery assays. The panel will comprise a number of anchor markers (around 100), which are conserved across different species, for comparative genetic studies. For some crops these are already available; for others, COS are likely to be derived from ongoing sequencing programs. To achieve full map coverage, a further 30 to 50 crop-specific genes may be needed. The remaining genes will be chosen because they are candidate genes controlling traits of interest in the individual crop. Initially, genes found to be important to drought tolerance in the species to be characterized will be included, or we will include drought-responsive genes from a closely related species where work has been done in this area. Almost certainly research on all of the CGIAR crops will target one or two other cross-cutting traits, whereas other traits, particularly those related to end-use quality, may be crop-specific. The gene set should not be considered static. New candidates will be identified through Subprogram 2, particularly from microarray experiments, and some genes previously included may be recognized as being less relevant.

The assembly of gene sets will, in the first instance, be a Challenge Program-wide activity, undertaken as the first priority activity in Subprogram 2, particularly in the identification for comparative mapping genes. Although some trait-related candidates are likely to be species-specific, consultation between crop groups will lead to selection of the most appropriate candidate set. It is envisioned that drought-related genes will be identified and included quickly, especially in the gene sets for the cereals, as the drought case study gets underway.

For the comparative genetics goal in Subprogram 2, there should be coordination of the traits and genes that will be addressed in each of the crops selected for study. Intellectual property issues are unlikely to arise with genes used for screening, in contrast to traditional hybridization or transgenic breeding. Nevertheless, the Program may adopt a standard procedure of informing inventors of the Challenge Program's proposed use of their genes.

High-throughput genotyping. To complete the functional characterization of germplasm, high-throughput genotyping capability is envisioned because of the large number of assays required. Automated liquid handling, polymerase chain reaction (PCR), and separation systems are available for SSRs and have been established within the CGIAR. Detection systems for SNPs are still under development but are likely to achieve massive throughput rates soon.

Phenotypic analyses

Phenotyping, the characterization of sets of accessions for various physical and chemical attributes of plants, is an essential complement to genotyping. This activity will include characterization of groups of accessions for a set of traits of importance for production and end-uses and, depending on the crop, a set of specific traits targeted for the work within the Challenge Program. The involvement of NARS in this Subprogram is essential for identifying environments that will provide a range of expression of the various traits and information on genotype x environment interaction. The NARS scientists, in collaboration with Program agronomists and physiologists, will conduct experiments with groups of accessions in their own fields that represent the targeted farmer environments. In these experiments, contrasting treatments will be included to produce data and tissue samples relevant to the goal of the gene discovery. The phenotypic data and tissue

samples (or RNA or DNA extracted from them) will be taken by the NARS scientist to the relevant participating institution's laboratory for analysis. This critical role of the NARS in the Program will assure that relevant data are evaluated, provide a capacity-building component for the NARS scientists, and facilitate total involvement of NARS from the initiation of research through data analysis and publication of results.

The collections held by the CGIAR Centers and other organizations are generally well characterized for some traits. These data will be extremely useful for association analysis with genetic data. This Challenge Program will develop new ways to discover new relationships among traits and will most likely find new modes of character expression.

For DNA collection, DNA must be extracted from the accessions grown under standardized conditions. Both genomic and complementary DNA will be required to complete the genetic diversity assessments and to use in functional genomics studies for accessions showing contrasting phenotypes.

Identify novel variants

New techniques and tools are becoming available for the identification of novel (and potentially useful) variants, as detailed below.

Association genetics. A primary application of the genotypic and phenotypic data will be the discovery of genes and markers, which are found in linkage disequilibrium (LD) among the selected genotypes, on the assumption that this disequilibrium has resulted from natural and farmer selection during domestication and from breeders' selections on adaptive traits (Pritchard and Rosenberg 1999; Pritchard et al. 2000; Nordborg et al. 2002). Linkage disequilibrium means that complexes of traits or genes do not occur at random. Linkage disequilibrium is higher in self-pollinated crops than in cross-pollinated crops because linkage blocks are held intact as a result of low recombination rates. The development of the theory and the necessary software for analysis of crop plant species (Remington et al. 2001) is still in its infancy and will be addressed in Subprogram 4.

Association analysis by various statistical methods produces graphic displays of groups of genotypes or accessions that provide clues about new traits or how groups of traits (hence genes) have come together for adaptive significance (Rosenberg and Nordborg 2002; Nordborg and Tavare 2002; Hagenblad and Nordborg 2002). The selection of accessions from such groups will most likely reveal previously unknown genes that, upon further study, will be available for plant breeding. It is assumed that markers linked to genes of interest will be identified in the same manner and that these markers will be useful for marker-assisted selection (MAS) in Subprogram 3. The resulting genotype-phenotype databases will allow breeders to address any trait in their crop. Within the Challenge Program, the methods will be demonstrated with single-gene traits of significance, such as semidwarfism in wheat or grain color in maize, determinant or indeterminate growth habits in legumes, and with important traits under more complex genetic control, such as drought tolerance and other abiotic stresses.

Discovery and use of new alleles. The discovery and accessing of alleles that cause a particular gene function and their selection by DNA hybridization tests with SNPs or other markers is referred to as "allele mining." The term "mining" can be misleading, because alleles are a renewable genetic resource and allele mining is not extractive, nor does it exhaust the supply of alleles in an accession or population of plants. It is this mining that unlocks new variation from genetic resource collections for crop improvement. With the molecular methods to be used in this Challenge Program, previously undisclosed but useful alleles can be identified, characterized, and isolated for further study and transferred to plants of the same species from which they were derived by classical breeding or to other species by means of genetic engineering.

Unique alleles will be subjected to study in Subprogram 2, where the relationships between allelic variation and phenotype will be addressed as an essential gene function discovery tool within the Challenge Program. Candidate genes will be identified through quantitative trait loci (QTL) mapping, association genetics, microarray analyses, and comparative genetic analysis from model plant systems. Genomic DNA stocks, as a

by-product of the genotyping analysis, will be immediately available for allele mining. The CGIAR, ARI, or NARS groups working with any crop may propose candidates.

Databases. It is important that all laboratories participating in the Challenge Program, including those of CGIAR Centers, NARS, and ARI partners, use an automated laboratory information management system (LIMS). Although each laboratory need not have an identical LIMS, it should be compatible for direct communication and information transfer, as well as quality control components of the high-throughput genotyping system and all other aspects of handling genomic resources and information. The same will apply to other genomics facilities, such as microarray and DNA sequences. These issues will be addressed in Subprogram 4.

Access and benefit sharing

Both the Convention on Biological Diversity and the International Treaty on Plant Genetic Resources for Food and Agriculture underline the importance of fair access to biodiversity for the world community, and of sharing the benefits associated with the use of that diversity. Ensuring fair access and benefit sharing will be particularly challenging for this Challenge Program, given that it is focused on the inventory and use of diversity at the gene level, whereas until now experience with access and benefit-sharing arrangements has been at the level of accessions. The Challenge Program will develop protocols to facilitate access and benefit sharing for its products. These protocols will be in line with the major conventions, including WTO-TRIPS, while taking into account the interests of the various stakeholders, particularly those of the target farming communities.

Outputs and milestones (timeline) for Subprogram 1: Genetic Diversity of Global Genetic Resources

Activity and output	Timeline (year)									
	1	2	3	4	5	6	7	8	9	10
Define genetic resources										
Composite sets of accessions determined by collaborators for genetic characterization and use in genomics and comparative genetics										
Select marker systems										
Identification and assembly of a set of structural markers for target crops										
Identification and assembly of a set of up to 500 candidate functional genes (many of them associated with drought) for diversity and gene discovery studies on the refined core subset, for target crops										
Continuous refinement of candidate gene sets, taking into account results of Subprogram 2 and the development of COS										
Analyze at the structural level										
Comparative genetic analyses and mapping of several disparate crop groups to find synteny and orthologous gene systems										
Analyze at the functional level										
Application of high-throughput genotyping to refined core subset of germplasm, initially focusing on drought genes identified in the case study										
Analyze at the phenotypic level										
Targeted phenotyping of accessions for particular traits based on allelic variation (focusing initially on drought)										
Identify novel variants										
Identification of alleles at candidate gene loci or markers having positive correlations with target traits										
Tools for efficient identification of useful genotypes from the composite sets of germplasm										
Discovery of new alleles (differences in DNA sequence and/or expression patterns) of genes involved in drought tolerance in specific genotypes from the composite sets of germplasm										
Access and benefit sharing										
Protocols for access and benefit sharing of derivatives of accessions, developed in line with the Convention on Biological Diversity and the International Treaty on Plant Genetic Resources for Food and Agriculture										

Subprogram 2: Comparative Genomics for Gene Discovery

Rationale and Goals

The overall goal of Subprogram 2 is to discover functions of economically important genes and to make them available for the crop improvement needs in Subprogram 3. The approach will apply to any of the CGIAR mandate crops and is based on the premise that many genes in plants are shared and that there is functional conservation. By building upon the comparative genetics approach, through genetic mapping and assays for genetic complementarity among crop plants, it will be possible to discover gene functions and how these functions relate to character expression.

The first task for Subprogram 2 will be to prepare and assemble panels of known sequences, including those that will be used in the genetic diversity assays in Subprogram 1. The subset of stocks identified by structural characterization in Subprogram 1 will be assayed by gene expression analyses to discover potential variation for desirable traits. The interesting genes will be subjected to detailed functional analyses to determine if they do encode useful new traits that can be incorporated into new source germplasm in Subprogram 3. As a focus of this Subprogram, the first genes and phenotypes to be studied in depth will be those involved in drought tolerance, across the four crop groups.

Because these approaches are dependent upon available sequence information, this Subprogram will select representative crops that are under intensive research within the CGIAR System and, in a coordinated multi-Center approach, develop a strategy for identifying genes of common interest in the CGIAR mandate crops. *Arabidopsis* (a dicot) and rice (a monocot) will serve as anchor species for sources of known genes and reference genetic maps.

Approach

Acquisition of genomic resources and capacities

Collectively, the NARS and CGIAR Centers have the world's best-characterized, most diverse genetic resources of food crops. Several Centers have produced special genetic stocks (mutants, isogenic lines, and mapping populations) that further strengthen their ability to discover gene functions using sequence information. Several collaborative networks and consortia have been developed to leverage international cooperation and access to technologies, such as:

- CIMMYT-IRRI collaboration on genomics of drought
- CIMMYT-Pioneer Hi-Bred collaboration on functional genomics of drought
- Global *Musa* Genomics Consortium- INIBAP (International Network for the Improvement of Banana and Plantain)/IPGRI, IITA)
- Rice Functional Genomics International Working Group (IRRI)
- International Triticeae Mapping Initiative and US Wheat EST Consortium
- Cereal Genomics Consortium (US universities and CGIAR Centers)
- Legume Genomics Initiative (international institutes and CGIAR Centers)
- Cooperative Research Centre for Molecular Plant Breeding (CIMMYT)
- Cassava Biotechnology Network (IITA-CIAT)
- *Phaseolus* Genomics Network (CIAT and a number of international institutes)

This Challenge Program will fully utilize existing genomic resources, including sequence data, cDNA libraries, ESTs, SSRs, SNPs, BAC clones, RFLP probes, and cloned genes, among others. Collaborations with ARIs and NARS will be developed to produce additional genomic resources specifically needed for the Challenge Program. These resources are largely available in the public domain, but in some instances agreements on the use of genomic resources must be obtained from the private sector. Most often agreements are needed for research or derived product use of specific genomic materials. The CGIAR Centers already have considerable experience in accessing and utilizing protected genomic materials, but this Challenge Program will pursue

innovative models to broaden access to intellectual property and modern tools developed by the public and private sectors (see the Business Plan).

The goals of this Subprogram are to use existing resources in the public domain to develop comparative genetic maps within crop species; to extend these comparative maps between species; to identify new candidate genes using microarrays; and to validate the functions of these candidate genes. The outputs of this Subprogram will feed into all of the other Subprograms and ultimately lead to promising new breeding lines containing previously untapped genes and pathways.

Development of comparative maps within crop species

Genetic mapping has been done for many crop species for many years; this has been one of the main uses of molecular genetic markers practically since their conception. References on genetic maps for crop species are too numerous to list. For almost all of the CGIAR mandate crops, quite extensive genetic maps within the species are already available. Consensus maps, or the combination of genetic mapping information from many different crosses, have also been made for many of the major species, and a comparative mapping tool to generate these consensus maps has been developed in conjunction with the National Center for Genome Resources (NCGR) and four CGIAR Centers (CIAT, CIMMYT, CIP, and IRRI). This comparative mapping tool will work on any crop species for which more than one genetic map exists, providing a few of the markers, at least, are in common between the two maps.

Development of comparative maps between crop species

The CGIAR System as a whole has the unique advantage and resources necessary to develop a universal map across economically important species. For almost all of the CGIAR mandate crops, quite extensive genetic maps are already available. These frameworks will underpin an SSR-SNP assay service as developed in Subprogram 1 for genetic resource collections and segregating populations. Comparative maps are also available for some CGIAR crops with their models. These are most advanced for the cereals, but potato-tomato and some inter-legume comparisons have been published. Linkages between crop groups within the Challenge Program will exploit and extend these maps to predict the location of candidate genes from model species to crops. The resulting comparative maps will greatly enhance the understanding of genetics for less-researched crops, for which few (or no) genetic maps have been previously developed.

This activity will create consensus maps within the monocots and dicots using available sequence information in *Arabidopsis* and rice, existing genetic and physical maps of crop species, and phenotypically well-characterized genetic materials that show clear genetic variation relevant to the target traits, particularly drought (mutants, advanced breeding lines, RIL, backcross lines). The COS concept recently developed by Fulton et al. (2002) will be applied to identify sets of conserved markers across monocot or dicot crops of interest to this Challenge Program. The COS markers for Solanaceae are already available and posted on the Tanksley laboratory website at Cornell University (www.sgn.cornell.edu). The COS marker approach involves using rice gene sequences to screen *in silico* for single-copy sequences in another distantly related species with a sufficient pool of genomic or EST sequences already in a database (e.g., *Musa*). The selected sequences are expected to yield robust hybridization probes that connect the genetic maps of distant species, and at the same time identify SNPs within the species. We will aim for a collection of about 800 COS markers that will serve as universal anchors for building a consensus frame map in each syntenic crop grouping.

Due to the challenges of accurately measuring physiological parameters in field conditions, QTLs for physiological parameters are generally less significant compared to those obtained for morphological traits, and the total phenotypic variance is rarely greater than 25% for any given parameter. Even so, this QTL information is extremely valuable. It provides an essential bridge between the data emerging from functional genomics and morphological plant responses, which will allow us to identify and characterize the major pathways related to drought response and tolerance across crop species. The Challenge Program will assemble the QTL results both within a species as well as across species to determine consensus regions related to various drought response parameters. While breeders and geneticists explore the benefits of gene pyramiding,

physiologists will determine the cellular and developmental mechanisms that determine each phenotype. Molecular geneticists will identify and test candidate genes through comparative analysis or positional cloning methodologies. The 'best' genes for a wide array of drought-prone environments will be discovered and made available for the benefit of poor farmers in the world's dry areas.

Assignment of genes and pathways to putative phenotypes

Functional genomics and microarrays for candidate gene discovery. The Challenge Program will use a common gene array platform for discovering genetic networks and candidate genes responsible for drought tolerance, as well as targeting other traits such as resistance to major pests and diseases, tolerance to environmental stresses, crop quality, or plant growth responses. Such an approach takes advantage of the model species with rich sequence information and also species with rich phenotypic data and unique characteristics. For example, many indigenous crop plants although genetically poorly understood, have a diversity of plant traits that are useful for enhancing stress tolerance. Gene expression of these crop species could lead to the discovery of novel genes that are not possible to identify in species where the phenotypes are not so dramatically expressed nor so easily discernable.

Within the first phase of the Challenge Program, we envision two categories of arrays to be used by different research partnerships. First, through a consortium approach, arrays will be developed, or accessed, with near-genome wide coverage for a comprehensive survey of gene expression patterns. Second, based on the data from the large arrays, we will develop arrays with a subset of genes designed for diagnostic and more in-depth analysis of drought tolerance. Furthermore, there is the possibility of developing arrays for discovering functions of specific categories of genes, such as transcription factors with potentially large phenotypic effects. Chen et al. (2002) recently demonstrated the use of gene chips containing 402 transcription factor genes in *Arabidopsis* to assess the regulation of plant responses to multiple environmental stresses. Development of similar gene chips is within reach for some species using publicly available sequence information. Such gene arrays can serve the needs of discovering regulatory pathways in multiple species. Depending on the efficiency and economy of scale, arrays will be selected from commercial sources or developed with collaborators to meet the specific needs of the Challenge Program. Recent work by Pioneer HiBred International, in collaboration with Curagen Corporation, demonstrates the utility of the development and use of Rapid Analysis of Gene Expression (RAGE) for gene discovery and optimization of plant breeding processes for maize traits of mid-low range heritability (Guo et al. 2001; Bruce et al. 2002; Bruce et al. 2000).

Arrays will be made and shared among Challenge Program partners for use in expression analysis using well-characterized genetic stocks. Complementary DNA (cDNA) is used as targets for hybridization to the known sequences on the chips and will be obtained from populations and stocks developed for studying drought tolerance. These plants will be grown in contrasting conditions (well watered versus drought stressed) and sampled at appropriate times throughout the life cycle. Another approach will involve the use of genetic stocks with contrasting phenotypes for a trait of interest. Congenic (or near-isogenic) lines obtained via induced mutation or backcrossing are ideal for this purpose. Some are already available for certain traits and new stocks can be produced specifically for this Challenge Program. The arrays will be analyzed to identify genes by their differential or correlated expression. They will be used to identify common genes involved in a phenotypic response, both in intra- and inter-specific comparisons, thereby identifying potentially orthologous genes and multigene families. By this means, it is possible to identify genes in a crop plant that could not be discerned by phenotypic or traditional genetic analysis, thus expanding the genetic resource base for crop improvement.

Validation of genes and pathways

To provide useful selection tools to breeding programs, it is important that any candidate gene (inferred from sequence information or expression analysis) be confirmed with additional functional evidence. Ideally, specific gene markers should be associated with a phenotypic value in such a way that breeding gains can be predicted through the introduction of the genes into varieties.

Appropriate biological context. Microarray or DNA chip experiments generate a large amount of data through a single hybridization. The greatest challenge is how to organize and interpret these data to identify the most informative changes in gene expression and evaluate their associated phenotypes. Unfortunately, most of the profiling experiments reported thus far provide little biological information that can be used in interpreting the results, apart from the fact that large numbers of candidate genes or pathways were associated with plant response under given experimental conditions. A major activity will be the germplasm characterization at the morphological, physiological, and biochemical levels to provide the suitable information that should facilitate the interpretation of changes in expression for the genes involved in the regulation of target traits. Because the QTL location can also be used as a validation step for the candidate genes when they map at the same genomic regions, the measurements of a new set of morphological traits and physiological parameters should be initiated to correlate key target traits, identify the corresponding QTLs, and facilitate the interpretation of changes in expression of the genes involved in the regulation of those target traits. For example, if sucrose synthase gene presents changes in expression under water-limited conditions and maps at the same genetic region as a QTL for sucrose content identified under the same conditions, in the same segregating population, and in the same target tissue, such a result would strongly reinforce the hypothesis that this gene has an impact on the plant phenotype via changes in sucrose concentration, especially if this change in sucrose concentration is related to ear growth and grain yield. Therefore, well-characterized germplasm, considering a broad spectrum of measurements, from grain yield to the quantification of the target physiological parameters, would be crucial for the validation and interpretation of the results obtained from profiling experiments.

Reverse genetics. The CGIAR Centers have a range of genetic resources that can be used to lend support to or confirm the predicted functions of candidate genes. For example, reverse genetics based on TILLING (Colbert et al. 2001) and insertion tag lines (Parinov et al. 1999, Jeon et al. 2000) can be used to identified mutants or natural variants in specific sequences. Once knock-out or activation lines are available, the corresponding function of the gene can be ascertained phenotypically. When a direct gene disruption or activation is not possible, a combination of correlated expression data, QTL position, and analysis of common promoter sequences can provide accumulated evidence to support the hypothesized function of a gene.

Gene discovery and validation using genetic engineering. The diversity of genetic resources available to the Challenge Program will provide much of the germplasm necessary to further identify useful genes and to validate those found in the various gene discovery efforts. There may also be circumstances where the most effective diversity does not exist within the species of study. In these cases, genetic engineering will be an effective tool to confirm gene function *in planta*. Transformation of most of the major crop species is routine and many of the Challenge Program members already have in-house capacities. When necessary, genetic engineering will be used to produce plants that have new genes for a particular trait (usually these will be derived from related species), or an existing gene(s) that is under new developmental control (e.g., continuously expressed, or expressed under the response to stress). These materials can then be subjected to detailed studies to analyze the specific effect(s) that a single gene, or group of genes, has on a particular trait. As indicated in Subprogram 3, transgenic varieties are not expected to be a major output of the Challenge Program, but their use as a research tool in this Subprogram is invaluable.

Drought case study

Genetic dissection to identify QTLs related to drought tolerance has been conducted extensively in various crops for morphological traits (Agrama and Moussa 1996; Austin and Lee 1998; Frova et al. 1999; Sari-Gorla et al. 1999) or physiological parameters (Lebreton et al. 1995; Tuberosa et al. 1998; de Vienne et al. 1999). Such genetic dissection has been conducted in different crosses, at different inbreeding levels (hybrids, F2:F3 families, and recombinant inbred lines – RILs), under different water regimes (well-watered, intermediate stress, and severe stress conditions) and in several different environments. This effort has generated large phenotypic data sets, and many QTL profiles have been produced for morphological traits and physiological parameters. As the morphological traits studied are complex and regulated by several genes, with yield being among the most polygenic and complex trait, no major QTL (more than 25% of the phenotypic variance) has

been identified. The majority of single QTLs express up to 10% of the phenotypic variance, and total phenotypic variance expressed by combining all of the significant QTLs was generally only a total of 40%.

The recent development of genomic technologies that provide structural and functional information for gene characterization (i.e., the localization, sequence, and expression framework of a gene) has received a significant boost during the last few years. Profiling experiments generate a large amount of data in a short period of time, and the greatest challenge is how to organize and interpret these data to identify the most informative changes in gene expression and evaluate their associated phenotypes. It is not an easy task, as tolerance to abiotic stresses is associated with a host of morphological and physiological traits, including root morphology and depth, plant architecture, variation in leaf cuticle thickness, stomatal regulation, osmotic adjustment, antioxidant capacity, hormonal regulation, desiccation tolerance (membrane and protein stability), maintenance of photosynthesis, and the timing of events during reproduction (Bohnert et al. 1995; Shinozaki and Yamaguchi-Shinozaki 1997; Bray 1997; Nguyen et al. 1997; Edmeades et al. 2001).

To provide a biological framework for the interpretation of changes in expression for genes involved in the regulation of target traits/pathways, germplasm must be extensively characterized at the morphological and physiological levels. Changes in hormone, carbohydrate, and water status are the examples of pathways that will be targeted to better understand the response of cereals under drought. The quantification of abscisic acid, carbohydrates (sucrose, glucose, and total sugar), and key water parameters such as osmotic adjustment, osmolite (proline), and relative water content will also be analyzed. By combining this information, the QTL locations can be used as a validation tool for the candidate genes when they map at the same genomic regions, thus confirming the involvement of these genes to drought tolerance.

The list of candidate genes for drought tolerance based on gene function can range in the hundreds of genes (Skriver and Mundy 1990; Bray 1993; Ingram and Bartels 1996; Bohnert et al. 2000). The question now is how to prioritize research aimed at characterizing the genes involved in the drought-tolerance process, and once those genes are characterized, how to identify and efficiently manipulate the elite alleles at those target loci to improve a given variety. The functional genomics approach undertaken in the Challenge Program will comprise two basic types of activities. The first one is to use microarray expression analyses to identify genes that are either up-regulated or down-regulated in target tissues collected from segregating populations under water-limited conditions. The main objective is to broadly identify significant differences in gene expression involved in plant response at different periods of water stress and in different target tissue. Identified ESTs can be mapped in segregating populations, and the map locations can be compared to QTL positions identified for the corresponding physiological parameters. The second approach is to study the expression patterns of candidate genes reported in the literature as involved in the response of a plant under water stress (Seki et al. 2001; Reddy et al. 2002). Special attention will be given to candidate genes that have been mapped in genomic regions corresponding to QTLs previously identified as being of interest for drought tolerance. This approach acts as a screen, first to determine if these genes show differential expression in drought segregating material, and second to assess the relative importance of the genes in the overall response of the plant to water stress. This will provide a validation tool for the microarray work and in addition will provide information on genes that may not yet be available on microarrays.

Outputs and milestones (timetable) for Subprogram 2: Comparative Genomics for Gene Discovery

Activity and output	Timeline (year)									
	1	2	3	4	5	6	7	8	9	10
Assembly of genomics resources										
Consolidate existing (and develop new) framework genetic marker systems for target crops										
Universal anchor markers (COS markers) developed for monocots and dicots										
Develop comparative maps within species										
Develop and deploy comparative mapping tools to Challenge Program partners, linked to the Challenge Program consensus map repository and major international plant databases										
Develop comparative maps across species										
Integration of comparative maps with available sequence and functional genomics data										
Assign genes and pathways to putative phenotypes										
Production of EST, gene-specific oligo arrays for model species and other crops depending on information developed at the DNA sequence and EST levels										
Gene expression profiles established for selected phenotypes and crop genotypes										
Identification of common and unique genes (orthologs) correlated with phenotypic expression across species										
Validate genes and pathways										
Function of >100 candidate genes for stress tolerance and regulatory control of stress-response pathways validated using over-expressing constructs or variants (induced or natural) of the target genes										
Databases established based on gene array and proteomic analyses (linked with bioinformatics in Subprogram 4)										

Subprogram 3: Gene Transfer and Crop Improvement

Rationale and Goals

This Subprogram provides the ultimate tool for the Challenge Program to achieve its mission, which is to make new alleles – identified in Subprogram 1 and proven to provide phenotypes in Subprogram 2 – available in agronomically or horticulturally superior varieties that are selected and adopted by targeted agricultural communities of farmers in resource-limited areas.

The CGIAR Centers and NARS have crop improvement programs that often have been underway for decades. These programs have been breeding and selecting for plant characteristics appropriate to most of the resource-limited agricultural regions, and therefore germplasm has been developed to respond to most of the abiotic and biotic stresses. Due to the nature of the target environments, genetic gains have been obtained at high cost, considering the time and the resources invested, specifically in developing the appropriate screening tests under stress environments. New opportunities to improve plants now exist with recent developments in molecular technology and genetics allowing the genetic dissection and the discovery of genes involved in the regulation of target traits under specific environments. The germplasm coming out of ongoing breeding efforts is the appropriate genetic platform for introducing new genes and gene combinations to build on or enhance these already productive materials. It has been proven (at least in tomato and rice) that the transfer of superior alleles from wild relatives to elite germplasm can significantly improve crop performance. These superior alleles would never have been identified via traditional breeding methods, but such alleles will be identified in CGIAR genebanks under Subprograms 1 and 2, validated, and transferred to new source germplasm by Centers and NARS via hybridization with, or genetic engineering of, improved varieties and landraces.

A given phenotype is the result of the accumulation of favorable and unfavorable alleles at a large number of genes most likely located at the same position in a given genome and independent of germplasm performance. It is the nature/quality of the alleles at those genes that will generate phenotypic differences across germplasm and make some genes more important in a given genetic background compared to others. A major output of

Subprogram 2 will be the construction of consensus maps that should allow the identification of genetic regions involved in the expression of target traits across crosses, considering different genetic backgrounds, and across environments. The different components (and therefore the nature of this consensus map) will evolve over time, as more information from QTL and gene discovery studies is incorporated. Marker-assisted selection experiments based on the regions of interest reported on the consensus map will not be the most efficient approach, because only some, rather than all, of those regions will have a significant impact on the plant phenotype, depending on different allelic composition of the crosses. Nevertheless, this type of MAS can be conducted at very low cost, with a potentially large throughput, and therefore MAS strategies based on the regions of interest reported on the consensus map will be developed and tested.

The goal of this Subprogram is to develop new elite germplasm by integrating new alleles developed and validated in other Subprograms into the best current elite breeding materials. This goal will be achieved quickly and efficiently by integrating molecular technologies into breeding schemes (i.e., by developing efficient MAS strategies aimed at plant improvement and by making use of genetic transformation if needed). When doing so, Challenge Program members will adhere to policies for access and benefit sharing for alleles derived from accessions in the public domain, as developed within the framework of the Convention on Biological Diversity, the International Treaty on Plant Genetic Resources for Food and Agriculture, and Subprogram 1.

Approach

Identification of recipient germplasm

For each crop, breeders will select elite germplasm, varieties, or landraces as candidates to receive new genes for the selected traits, depending on the targeted environments. The selection of the germplasm to be improved is crucial, and the balance between germplasm presenting broad adaptability versus germplasm that is outstanding under specific environmental conditions needs to be considered carefully. Depending on the elite germplasm available, transfer of elite alleles from a donor to a recipient line or the pyramiding in one genetic background of favorable alleles coming from several outstanding lines can be considered.

Incorporation of new traits into source germplasm

The breeding system chosen for genetic enhancement is, to some extent, crop dependent and is dependent on whether the gene selected for transfer can be introduced by sexual hybridization or whether genetic transformation is necessary. For sexual hybridization, several options can be considered, depending on: (1) the nature of the germplasm available, as mentioned above; (2) the nature of the target trait/environment (simply inherited versus polygenic traits); and (3) related to the second point, the nature of the elite allele to be transferred. Most of the strategies will be based on the development of molecular markers identifying the gene of interest or directly assaying products related to specific gene function. As demonstrated extensively in the literature, the use of markers will allow the breeders to trace favorable alleles in the genetic background of interest and identify individual plants in large segregating populations that carry the favored alleles.

At the same time as the genetic enhancement activities are underway, field trials will be established to validate the expression of the new genes in relation to the trait of interest. Improved germplasm developed in this third Subprogram will be distributed to collaborators for selection in targeted field environments. Data will be interpreted over all sites using well established CGIAR Center protocols for international trials. The data will be collected in the integrated database management system developed in Subprogram 4.

Disseminate source germplasm to breeding programs

After initial hybridization and selection, or some cases after genetic transformation of the new genes, the derived populations must be put to the acid test of use in farmers' fields. These activities will be coordinated by NARS or NGOs with collaboration from regional offices of the various CGIAR Centers. A participatory method that involves farm families and communities in testing and ultimately selecting new varieties will

provide immediate acceptance or rejection of the new materials. End-use evaluations, such as food preparation, post-harvest storage, and marketing will accompany the research in farmers' fields. Farmers will be introduced to seed production and distribution systems, if none are readily available. Thus farmers, associations of farmers, or communities can develop a system for seed distribution, such as seed banks, for-profit cooperative seed companies, or other systems, including the participation of private industry, where appropriate.

Outputs and milestones (timeline) for Subprogram 3: Gene Transfer and Crop Improvement

Activity and output	Timeline (year)									
	1	2	3	4	5	6	7	8	9	10
Identify recipient germplasm										
Candidate varieties identified and promoted to wide testing in targeted sites for productivity and acceptability for end-users	■	■	■	■	■	■	■	■	■	■
Incorporate new traits into source germplasm										
Development and testing of new MAS strategies	■	■	■	■	■					
Genes and traits transferred to agronomically acceptable genetic backgrounds				■	■	■	■	■	■	■
Disseminate source germplasm to breeding programs										
Advanced materials transferred to national programs for field validation of trait expression						■	■	■	■	■
Potential varieties or populations advanced to on-farm participatory evaluation and selection						■	■	■	■	■

Subprogram 4. Genetic Resources, Genomic, and Crop Information Systems

Rationale and Goals

Subprogram 4 provides access to analytical tools for all data generated in other Subprograms by all partners. The goals include systems, research, and capacity-building elements, which are detailed below. The drought tolerance case study will provide an ideal test for the utility of the information systems development.

Systems

The systems component is designed to strengthen expert information networks in bioinformatics, biometrics, and genetic resources. These networks will facilitate the biological objectives of the Challenge Program by establishing agreed information standards and developing the methodologies and protocols for information flow among the Challenge Program partners and with other relevant information systems. The main task of the networks will be to enhance the current genetic resources and crop information systems in a decentralized manner so as to further integrate existing systems and to expand their coverage to the genomics and genetic information required for Challenge Program activities. This activity will require the development of information exchange mechanisms to integrate existing systems used by Challenge Program partners and to interface with key international plant databases (e.g., the *Arabidopsis*, rice, and *Medicago* genome and genetic databases).

Research

An integrated research program will be undertaken, involving experts on bioinformatics, association genetics, genetic resources, and crop improvement to provide the methodologies needed for Challenge Program activities and to make them available to other end-users (especially NARS). These research activities will be coordinated with other groups working in the same area. Informatics research will cover comparative genetic and genomic mapping, functional genomics, proteomics and metabolomics, high-throughput genotyping and phenotyping, and association genetics.

Capacity-building

Training capacities and materials will be developed in bioinformatics, biometrics, and genetic resources for use in crop improvement; courses will be delivered to Challenge Program partners and other NARS end-users.

Approach

A variety of international information system and software engineering initiatives will provide starting points of references for the design and implementation of proposed Subprogram 4 networks and systems. These will or could include the following:

- The System-wide Information Network for Genetic Resources (SINGER; www.singer.cgiar.org)
- The International Crop Information System (ICIS; www.icis.cgiar.org), including crop specific implementations such as the International Rice Information System (IRIS; www.iris.irri.org)
- Global genetic resources information networks for wheat (CIMMYT) (the International Wheat Information System (IWIS) (www.cimmyt.org/Research/Wheat/IWISFOL/IWISFOL.htm) and barley (ICARDA), as well as databases in NARS Challenge Program partner sites
- International genetic resources databases such as the European crop genetic resources catalog (www.ecpgr.cgiar.org/epgris), the Germplasm Resources Information Network (GRIN; www.ars-grin.gov) and Shigen (www.shigen.nig.ac.jp)
- Partnerships with international plant genetic and genomic databases such as Gramene (www.gramene.org), MaizeDB (agronomy.missouri.edu), the Arabidopsis Information Resource (TAIR; www.arabidopsis.org), the MIPS Arabidopsis database (mips.gsf.de/proj/thal/); the Japanese Rice Genome Project (RGP) In Rice Genomic database (rgp.dna.affrc.go.jp/giot/INE.html); and The Institute for Genomic Research (TIGR) databases (www.tigr.org)
- The comparative mapping tool pilot project completed in January 2002, between National Center for Genome Resources (NCGR) and several CGIAR Centers; the NCGR is also the host of functional genomics databases relevant to the Challenge Program, such as PathDB
- The European Gene-Mine project (www.gene-mine.org)
- International consortia for the development of controlled vocabularies and ontologies for molecular (the Gene Ontology (GO) Consortium; www.geneontology.org), higher plant functions (Plant Ontology Consortium; www.plantontology.org), and agriculture (FAO Agricultural Ontology Service; www.fao.org/agris/aos/)
- International consortia and projects for the development of biological database interoperability, such as the Distributed Annotation System (DAS; www.biodas.org) and BioMOBY (www.biomoby.org) projects
- Bioinformatics open source software communities (see www.open-bio.org)
- Plant databases constructed by commercial concerns (e.g., Syngenta; Pioneer; Biobase) could also, pending appropriate negotiations, be exploited by the Challenge Program

Members of this Challenge Program consortium already participate actively in several of the above information systems and activities.

Strengthening and integration of networks

Genetic resource and crop improvement information networks will be strengthened and capacities increased to improve linkages between partners' informatics projects and to develop the capacity to manage and integrate genomic and genetic information generated by the Challenge Program. The CGIAR Centers will increase their expertise in bioinformatics and biometrics, especially in the areas of genomics and association genetics. The Challenge Program will serve as a vehicle to strengthen and integrate expert networks in genetic resources, bioinformatics, and association genetics for efficient communication of data and information transfer among the CGIAR Centers and other partners.

Standards, methodologies, and protocols

A critical element of an integrated genetic resource and genomic research program is the standardization of information exchange protocols. This Challenge Program will take the lead in furthering the harmonization of information systems across centers and institutes.

Substantial new developments are needed in five areas, described below.

- First, improved standardization of passport, characterization, and evaluation data across species will be needed to facilitate the data mining process required by the Challenge Program's bioinformatics and genomic research. A common data descriptor dictionary will be developed for genetic resource and crop improvement information systems to facilitate the exchange of data within the information network. This activity will also integrate statistical, geographical information system, and quality control tools to improve the accuracy and availability of information.
- Second, an extremely important activity will be the development of a workflow management system linked to the laboratory information management system (LIMS) in Challenge Program partner sites for tracking and quality control of experimental reagents and high-throughput data outputs of the Challenge Program. The workflow management system will be linked with passport, characterization, and evaluation data in genetic resource and crop information systems to facilitate data mining. Particular attention will be given to standardizing molecular characterization data (fingerprinting and diversity at candidate gene loci) and to making the changes in existing information systems that will be needed to accommodate these new data.
- Third, suitable map construction tools and databases will be identified, developed, and used (including data exchange standards) to construct syntenic consensus maps for different crop groupings.
- Fourth, candidate, orthologous loci for priority traits (such as those relevant for the case study on drought tolerance) will be identified and annotated, including mapping of such loci onto the comparative (syntenic) maps of various crops of the Challenge Program. This catalog will be linked to associated cDNA clone resources used for microarray expression analyses.
- Finally, information exchange protocols will be required to facilitate distributed, on-line retrieval and analysis of information. Particular attention will be given to integrating Challenge Program data with international information sources relevant to Challenge Program objectives and to adopting agreed standards for database interoperability based on current advances in distributed web services.

Development of integrated genetic resource and crop information systems

Crop improvement and genetic resource information systems are generally linear growth datasets, primarily serving genetic resource and plant breeding communities. These systems are somewhat mature in design and currently focus on passport, pedigree, and phenotypic data for genetic resources. In contrast, sequence datasets in genomic and molecular information systems, which primarily serve molecular biologists, show exponential growth. These rapidly evolving systems need to deal with heterogeneous, dynamic data. A particular challenge will be the enrichment of these systems with molecular information generated by this Challenge Program (SSRs and SNPs), which will be linked to crop improvement and genetic resource information to promote the further use of genetic resources held in the CGIAR collections and also available in NARS collections.

A distributed network of information systems based upon agreed interoperability protocols will be developed. These databases will be curated locally and contain all available project data as well as catalogue all information providers, standards methods. The network will facilitate public on-line access to and exchange of comparative genomic, crop improvement and genetic resource information and may be mirrored at various sites to improve accessibility.

Development of genomic databases and analysis systems

Comparative genetic and genomic mapping. Stand-alone analytical tools, such as the Comparative Mapping Tool developed by NCGR in collaboration with several CGIAR Centers, will be integrated into information systems for comparative genetic, physical, and sequence-level mapping. These will be used to develop maps

anchored on sequence information and COS markers across model species and related crops studied within the Challenge Program. This system will include enhanced Challenge Program partner capacity for general management of genetic marker data and related information on mapping populations especially supporting the genetic resources systems.

Functional genomics, proteomics, and metabolomics. A methodology will be developed to construct a functional biology platform of gene discovery, focusing on critical plant gene families, such as signal transduction pathway and transcription factor genes that could have a high impact on target traits across many species. In collaboration with ARIs, analysis and representation tools with associated databases subsystems will be developed that integrate gene and gene interaction data into biological systems models for biochemical pathways, cell signal transduction, genetic networks, and gross plant physiological mechanisms.

High-throughput genotyping and phenotyping. New database technologies will be developed to improve the capacity of existing genetic resource and crop improvement information systems to handle data from high-throughput genotyping and phenotyping systems. New data-mining systems and statistical support for association genetics will be needed for integrating molecular and field characterization data across genetic resource collections and for integrating candidate gene information from the genomics activities of the Challenge Program.

Capacity-building in bioinformatics systems

The development of an integrated bioinformatic and genetic resource/crop improvement training activity for scientists will be included in the Challenge Program to ensure that new scientific information produced by its research can be shared efficiently. This activity will include the production of training materials, such as web-based manuals and on-site short courses for geneticists and breeders from collaborating institutions.

Outputs and milestones (timeline) for Subprogram 4: Genetic Resources, Genomic, and Crop Information Systems

Activity and output	Timeline (year)										
	1	2	3	4	5	6	7	8	9	10	
Establish expert network											
Coordinated expert networks spanning bioinformatics, association genetics, and genetic resources established											
Develop integrated genetic resource and crop information systems											
First draft information management standards, methodologies and protocols are agreed upon by Challenge Program information scientists based upon consultation with external technical experts in the field											
Information systems participating in the Challenge Program are harmonized based on agreed standards, methodologies, protocols and the Challenge Program requirements											
Use cases and design requirements for information networks completed											
Genetic resource and crop improvement information networks integrated											
Develop genomic database and analysis systems											
An inventory of existing and proposed new tools and protocols to be used in the Challenge Program											
Use cases, design requirements, and prototyping/adoption of comparative genetics, genomics, proteomics, metabolomics, and systems biology platform completed											
High-throughput genotyping and phenotyping information incorporated in the genetic resources and crop information systems											
New genetic resource analysis and management tools (i.e., integrating genomics and association genetics into genetic resources systems)											
Provide capacity-building in informatic systems											
An integrated training program in bioinformatics, association genetics, and genetic resources information management is designed											
Training materials are developed											
Courses in bioinformatics, association genetics, and genetic resources are developed and delivered											

Subprogram 5: Capacity-Building

Rationale and Goals

Institutional capacity building in the south is of critical importance as it provides a niche for skilled personnel to work effectively on biodiversity management and conservation and to provide training and research opportunities, rather than NARS scientists going for research or training mainly in the north or CGIAR centres.

To ensure sustainability of the Challenge Program activities and to build long term training and research capacity and capabilities in the NARS, the Challenge Program will identify strong institutions in regions and sub-regions able to serve as training and capacity building hubs. Complementary infrastructure such as equipment may be required to strengthen the capacity of the “Centres of Excellence” to fully play their role beyond the lifespan of the Challenge Program.

A comprehensive survey on existing strengths and weaknesses of institutions participating in the Challenge Program and a systematic needs assessment of NARS is a pre-requisite to the implementation of the capacity building subprogram.

The recent GFAR regional priority setting exercise will be used as a reference in combination with other assessments made at regional and sub-regional levels (e.g., the CORAF study on capacity building for biotechnology in West and Central Africa). In addition, an inventory of needs assessment, training capacities and opportunities will be sought to ensure that the Challenge Program is consistent with NARS demand. Additional partners will be sought if gaps in expertise are identified. Synergies with other Challenge Programs will be explored in developing capacity building activities.

Since capacity-building is a major goal of this Challenge Program, it is appropriate to dedicate considerable resources to capacity-building. The genetic resources platform developed in this Program provides the materials and technology for application to research and applied plant breeding. Considerable capacity-building is needed for NARS scientists to utilize these genetic materials and technologies in their own research and plant breeding programs. NARS are particularly interested in genetic diversity analysis of their landraces and optimizing the potential for finding new traits for their breeding programs. Once traits are found, NARS researchers will wish to develop markers for use as indirect selection tools in breeding programs. They will also want to access data about genes and traits, so they must be able to browse the databases. Finally, and perhaps most important, NARS scientists will need to gain experience with gene transformation and traditional hybridization /selection techniques for variety development targeted to their local environments.

It is the goal of the Challenge Program to provide training opportunities in applications of genomic sciences to genetic resources and plant breeding to NARS. The Challenge Program will be guided by the relevant regional and sub-regional networks and organisations in the choice of laboratories and programs to be supported on the basis of need, capacity, potential and commitment to apply the training. The Capacity-Building Subprogram will be budgeted at a sufficient level to provide an orderly training effort, prioritized by needs of the NARS. In some cases this capacity-building will be complementary to on-going activities at the participating institutions.

Approach

Each of the four research Subprograms will engage in capacity-building activities. These activities will be conducted at any of the research institutions participating in the Challenge Program. CGIAR scientists as well as NARS scientists will need to gain experience in particular areas, such as microarray analysis, bioinformatics, genetic mapping, and biosafety. Exchanges of scientists and sabbatical leaves will be encouraged. The CGIAR Centers and other participating institutions will support the research of students seeking advanced degrees and of postdoctoral fellows; these researchers may work at more than one institute.

Finally, summer internships for young students from NARS will be provided. The Challenge Program offers an attractive venue for building the skills of students from NARS and advanced institutions.

Research facilities and capabilities will be developed according to an organized plan for how various participating institutions can provide research support to each other. Not all partners (CGIAR Centers, NARS, and ARIs) need, or can afford, to have the full range of instrumentation for genomics/genetic resources research.

The Challenge Program will have annual research meetings for participants and will organize other conferences. It is also expected that the Program will organize a website. The website will provide up-to-date news of research results, research protocols, and links to publications and other websites.

The various capacity-building initiatives of this Challenge Program will be directed by the Challenge Program Director with the aid of a full-time Training Coordinator. Lead Scientists in Subprograms 1- 4 will plan capacity-building activities and present those plans to the Director for review and submission for funding. The activities of the Capacity-Building Subprogram will continue for the duration of the Challenge Program.

Assessment of Socio-economic Impacts

The socio-economic aspects of this Challenge Program extend throughout its life and, initially, have helped to inform the development of Program goals and outputs. Social scientists will be directly involved in planning the dispersal and diffusion of the new genetic materials to farmers. This activity is important, because the Challenge Program will produce different types of genetic materials through crop improvement, some of which will be derived from conventional hybridization and selection and others that will be developed through breeding with transgenic parents; still others may be the direct products of transgenic events. Starting at an early stage and continuing throughout the life of the Challenge Program, it will be important to engage policymakers, regulators, NGOs, manufacturers, and farmers in a dialogue about the Challenge Program's goals and the nature of the materials it produces. Stakeholders will be consulted and they will regularly contribute to the setting and refinement of the Program's goals and objectives.

Business Plan

Overview

This Challenge Program will bring together the resources and competencies of CGIAR Centers, developing country national programs (NARS), and advanced research institutes (ARIs) to form a powerful, global, and public platform providing a suite of products for research and plant breeding programs throughout the world. This goal will be achieved through the development of effective collaborations, resulting in high-quality scientific outcomes and extensive human capacity building with exchanges of researchers and advanced capacity-building of NARS scientists.

The business plan for this Challenge Program has been developed on the principles of public access to research products, especially for NARS; strategic research and development linkages; adherence to international agreements on germplasm; an efficient governance and management structure; responsible intellectual property management; and transparent mechanisms for allocating resources.

Principles of Involving Consortium Members

This Challenge Program brings together a diverse range of prestigious research institutions involved in a range of research and plant breeding programs. The founding members of the consortium have helped to shape the direction, strategy and governance of the Challenge Program. Other CGIAR centers (in addition to CIMMYT, IPGRI, and IIRRI) will be confirmed as members of the consortium, based on a willingness to make a

commitment (relevant germplasm collections, scientific capability, dedicated in-kind contribution of at least \$400,000 pa) to the Challenge Program. Furthermore, NARS, ARIs and others will become participants in the Challenge Program through either commissioned research or competitive grant programs. Research priorities and work plans for the Challenge Program will be detailed during technical workshops in the first half of 2003. Organisations/interests represented at the Alexandria Stakeholder Meeting and others will be invited to participate in these research planning workshops to help identify research priorities and to consider their involvement with the Challenge Program in specific research areas.

Links to Other Initiatives

The Challenge Program will build on existing networks such as SINGER, the Global *Musa* Genomics Consortium, the International Rice Functional Genomics Working Group, the International Crop Information System (ICIS), the US Cereals Comparative Genomics Initiative, and the Cassava Biotechnology Network. It will also establish links with related initiatives such as the Australian Centre for Plant Functional Genomics, the Cooperative Research Centre for Molecular Plant Breeding, and the Dutch Government initiative on the genomics of Solanaceae. A comprehensive assessment will be made of the results of these various consortia to ensure that the most relevant and up-to-date outputs are used in the Challenge Program.

This Challenge Program will also provide enabling technologies and intermediate products to the Biofortification Challenge Program, and information and germplasm for the Water and Food Challenge Program. Furthermore, the Sub Saharan Africa Challenge Program, currently under development by FARA, presents opportunities for collaboration on technology development, germplasm development, and capacity building, especially in biotechnology.

Contributing Strengths of Consortium Members

The structure, activities, and outputs of the Challenge Program are summarized in Figure 2. The following sections describe the strengths of the contributors.

Initial Consortium Members

The initial founding members bring a wide range of expertise to the Challenge Program; this will be further complemented as others such as the CGIAR germplasm centres join the consortium.

Chinese Academy of Agricultural Sciences (CAAS)

- Largest collection of cereals in Asia, totaling more than 160,000 accessions (wheat, 40,000; rice, 70,000; maize, 12,000; millet, 20,000; sorghum, 10,000; and barley, 12,000)
- Recognized leadership for agricultural biotechnology and breeding programs in China
- Recognized leadership in using genetic resources to explore new genes
- Host of the National Grand Science Program for Crop Genetic Resources and Gene Improvement, the only such facility for life sciences in China (10,000 sq.m research facilities, 6,000 sq.m greenhouse area, state-of-the-art equipment (US\$ 10 million) such as FPLC-TOF, proteomics work systems, high-throughput sequencing facilities, and microarray facilities)

Cornell University

- Cornell genomics initiative
- Institute for Genomic Diversity – molecular diversity of plants
- USDA-ARS Center for Comparative Genomics and Bioinformatics houses the single largest cluster of plant genome databases in the USA, including GrainGenes, RiceGenes, SolGenes, and RiceBlast DB
- Leading public research/training program in plant proteomics
- Recognized world leader in comparative plant genomics and certain aspects of developmental plant biology

Brazilian Agricultural Research Corporation (EMBRAPA)

- The National Center for Genetic Resources and Biotechnology Research (CENARGEN)
- Genebank with more than 60,000 crop accessions

AGROPOLIS

- Several research units specialized in crop genome analysis, genetic diversity and adaptation to environmental stresses of Mediterranean and tropical crops
- Comprehensive multidisciplinary force allying genetics, molecular biology, ecophysiology, agronomy and modelling
- Extensive experience in rice, wheat, sorghum, maize and banana genetics
- Entry point to collective expertise on wheat, maize and rice genomics coordinated within the national Génoplante initiative
- Access to regional (often in-house) and national sequencing, genotyping, plant genetic transformation, phenotyping platforms within the French network of Génopoles
- Germplasm core collections of hard wheat, maize, sorghum and rice seeds as well as banana plants in Guadeloupe, permanent segregating populations (recombinant inbred lines, doubled haploids), rice insertion mutants (over 30 000 T-DNA lines)
- Several BAC libraries in each of wheat, sorghum, rice and banana
- Extensive interaction with partners in Mediterranean, subtropical and tropical agriculture

International Maize and Wheat Improvement Center (CIMMYT)

- Maize and wheat genebank collections totaling more than 160,000 accessions
- Strong biotechnology program, including studies of molecular genetic diversity and abiotic stress tolerance using molecular markers and genetic engineering
- Biotechnology service laboratory that provides DNA sequencing, fingerprinting, single marker analysis, and transformation services
- Recognized leadership in the development of drought-tolerant maize and wheat varieties
- Extensive network of partnerships that includes more than 100 developing countries
- Developers of International Wheat Information System (IWIS), providing pedigree and phenotype information with links to SINGER and the International Crop Information System (ICIS)
- Mirror site for MaizeDB, with links to IWIS

International Plant Genetic Resources Institute (IPGRI)

- World's largest international institute dedicated solely to the conservation and use of plant genetic resources
- Coordinator of the CGIAR System-wide Genetic Resources Program through which the centers coordinate their policies and practices in managing the in-trust plant collections, and collaborate on research, information, and capacity-building in genetic resources.
- Coordinator of the CGIAR's System-wide information network for genetic resources (SINGER), which establishes and links databases on germplasm collections
- Coordinator of Promusa, the global banana improvement network and the global *Musa* genomics consortium
- Extensive network of partnerships

International Rice Research Institute (IRRI)

- Largest collection of rice genetic resources in the world
- Recognized leadership in the development of multiple stress tolerant, adaptive rice varieties through an extensive collaborative network in developing countries
- Strong biotechnology and bioinformatics capacity for studies of molecular genetics, gene expression, gene discovery, and allele mining for agronomically important traits
- Coordinator of the International Rice Functional Genomics Working Group, which plays a key role in bridging ARIs and NARS in the application of rice genome sequence information for gene discovery

- Coordinator of the International Crop Information System (ICIS; www.icis.cgiar.org) project to develop systems to integrate genetic resource, crop improvement, and molecular information on germplasm for any crop
- Bioinformatics expertise and experience in developing the International Rice Information System (IRIS; www.iris.irri.org), including components for laboratory information management, genetic resources, international germplasm testing, functional genomics, and genetic improvement of rice, as well as links to international plant databases

John Innes Centre (JIC)

- A major crop genetics research group, with UK leadership in wheat, legume, and brassica crops
- Genome research, genetic and molecular analysis of key traits, and comparative genetics are major thrusts of the group, which also specializes in millet (*Pennisetum*, *Setaria*, and *Eleusine* spp.) molecular research
- Extensive crop genetic transformation capability, with experience of wheat, barley, rice, maize, peas, and bananas
- Extensive germplasm resources, including: the UK National Collections of small grain cereals (wheat, barley, oats; approximately 48,000 accessions), and European collections of peas; collections of cereal wild relatives; special collections, including the Watkins' Collection; defined wheat and barley genetic stocks (e.g., isogenic lines, recombinant inbred lines, recombinant doubled haploid lines, wheat aneuploids, inter-varietal chromosome substitution lines, alien-wheat chromosome addition and substitution lines)
- Interaction with leading-edge international research into model species and other cognate science carried out by the 800 researchers at JIC and the Sainsbury Laboratory in the Norwich Research Park
- The John Innes Centre Genome Laboratory, opened in January 2002, houses a wide range of genomics equipment (e.g., high-throughput DNA sequencing, automated SNP and microsatellite analyses, micro-array facilities)
- Extensive field (the JIC 300 ha farm), glasshouse, and controlled environment facilities

National Institute of Agrobiological Sciences (NIAS), Japan

- NIAS has the leadership for decoding the entire sequence of the rice genome within the framework of an International Consortium. Decoding of the rice genome sequences is being done by an International Consortium comprising 10 countries. Japan (NIAS/STAFF) plays a leading role among these countries and is engaged in the decoding of the sequences of six of the twelve chromosomes of rice (No.1, 2, 6, 7, 8 and 9). As of 18 December 2002, 366Mb of the rice genome (92% of 400Mb) was sequenced as minimum tiles of PACs/BACs by the International Rice Genome Sequencing Project (IRGSP) and 205Mb (57%) of this was a contribution from Japan. IRGSP announced the completion of phase 2 level sequencing of the rice genome on 18 December 2002.
- NIAS leads the Millennium Genome Project's Rice Genome Program. The Millennium Genome Project is a large national project that started in 2000 and encompasses all of the projects known as the Rice Genome Program. In these projects, besides sequencing, NIAS has a leading role in the isolation and characterization of agriculturally useful rice genes, coordinating research with about 100 institutes and universities nationwide.
- NIAS maintains the genome and bio resources resulting from the Rice Genome Program, e.g., 28,000 full length cDNAs, 3,267 RFLP marker clones, 7,606 YAC filter clones, 50,000 BAC clones, 70,000 PAC clones, 50,000 gene deletion rice plants and about 1,000 recombinant inbred and chromosome segment substitution lines. These resources are useful tools for isolating and characterizing the genes.
- To produce transgenic plants with value-added traits, NIAS is conducting gene discovery research and developing gene transformation systems. So far, NIAS has isolated and characterized the genes related to, for example, morphology, photosynthesis, and flowering. NIAS has also developed transgenic plants resistant to bacterial and fungal diseases, absorbing soil and air pollutants, and having added nutritional value.
- NIAS participates in the collection, preservation, and evaluation of genetic resources and clarification of bio-diversity. NIAS maintains and evaluates a wide array of genetic resources (plants: 225,000; microorganisms, 19,683; animals, 239; silkworms, 646) collected worldwide. NIAS genetic resources

scientists are conducting research on these genetic resources and actively collaborating with institutes worldwide.

Wageningen University

- Wageningen Plant Sciences Centre for education and fundamental, strategic, and applied plant research (1,600 employees)
- Key site for new Dutch government initiative on genomics of Solanaceae
- Facilities for molecular sequencing
- Center for nutrigenomics, fundamental genomics and proteomics, and bioinformatics
- Genebank with crop accessions of vegetable crops
- Capacity-building, such as special courses and learning on the job
- Novel techniques for measuring plant responses to stress

Partnerships

EMBRAPA (Brazil) and CAAS (China) are the two NARS that have been part of the group of institutions that have proposed this Challenge Program. They both have important plant genetic resources collections and high-level relevant scientific infrastructure and capacity for the Challenge Program. In addition, since there are more NARS that have invested in building up genomics expertise, the Challenge Program will seek to broaden the participation of NARS with relevant interests and capacity.

Apart from seeking the participation of NARS which have already invested in molecular genetics and genomics capacity, the Challenge Program will actively stimulate NARS capacity building. This will be coordinated through Subprogram 5. There are four important building blocks of this approach:

- Needs assessment- the priority setting for capacity building will be done in partnership with NARS to ensure that the activities are consistent with NARS demands;
- Capacity building through research- the emphasis of the capacity building subprogram will be on training through research. This will involve many of the research projects carried out within the subprograms and PhDs and postdoctoral fellowships with the aim to strengthen in particular NARS that have initiated programs to build up such capacity;
- Ensuring proper implementation through breeding programs - most of the subprograms involve upstream research. In particular within the framework of Subprogram 3 and the drought case study it will be very important to strengthen and enable the links to the breeders and the breeding programs to ensure that the intermediate products developed by the Challenge Program will eventually lead to new and significantly improved varieties and genotypes for farmers' fields;
- Centres of Excellence- it is envisaged that the involvement of NARS will not only be strengthened by means of North-South collaboration, but will also foster South-South collaboration through an emphasis on the development of regional centres of excellence for capacity building and regional networks. The NARS with the stronger scientific infrastructure and capacity will be acting as regional hubs, with facilitated access for surrounding countries.

Unlocking genetic diversity using molecular tools and comparative genomics, i.e. the work envisaged by this Challenge Program, is among the most important priorities of the NARS for agricultural research. A recent regional priority setting exercise related to research issues for genetic resources management, conducted by GFAR, is entirely congruent with the aims and objectives of the Challenge Program and will serve to inform priorities for the Program. GFAR will be invited to participate in the Challenge Program at the governance level (through the Program Steering Committee) and an annual meeting with the GFAR Stakeholders' Committee is proposed.

Partnerships will also be developed through an open competitive grant process. In this way, the best scientific ideas to serve the objectives of the Challenge Program will be solicited. At least half of the research funds available in the Program will be used for competitive grants with most of the remainder of the research funds to be assigned to an open commissioned research process. As with all competitive grant programs, the review

and decision process must be transparent, independent, and clear of conflicts of interest. To ensure scientific quality and impartiality, the Program Advisory Committee (PAC) will be asked to oversee the review of all research proposals. The PAC may elect to assemble a review panel of top calibre scientists to provide additional scientific review of the submitted proposals. The Program Research Management Team (PRMT) will evaluate each proposal along with the external reviews and make a recommendation to the Program Advisory Committee regarding which proposals should be approved. Final approval will be made by the Program Steering Committee. External agencies (e.g., US Department of Agriculture (USDA), US National Science Foundation (NSF), EU Sixth Framework Program, the World Bank) with rich experience in competitive grant programs will be consulted in developing and operating the grant program.

All grant proposals must clearly contribute to the scientific scope and goals of the Challenge Program and should be time-bound. The proposal should involve one or more institutes among at least two of the different groups of partners (NARS, CGIAR, ARI). Some donor funding may require specific partners to be involved and the Program Steering Committee will be responsible for ensuring that all research projects involve proper and adequate partners. To expand the resource base of the Challenge Program, matching in-kind contributions or co-financing arrangements will be preferred. There are opportunities to link with existing and proposed programs such as the proposal "Plant genomics for food security and health using rice as a model plant" under the EU 6th Framework (Tuberosa, University of Bologna) and the US Cereals Comparative Genomics Initiative (Zeigler, Kansas State University), to name but two. Proponents will need to demonstrate that IP will be managed to ensure that results are available for the benefit of the resource poor in developing countries.

A Request for Proposals (RFP) will be prepared by the scientific staff of the subprograms coordinated by the Program Research Management Team (comprising the Challenge Program Director, subprogram Lead Scientists and the Training Coordinator) with input from the Program Advisory Committee, and approved by the Program Steering Committee.

The Request for Proposals (RFP) will define criteria for participation such as subject area; eligibility; partnership requirements; size of grants; and submission requirements, as well as evaluation criteria and a timeline for project implementation.

The proponents of the Challenge Program acknowledge that certain research is well positioned to launch a full-scale effort whereas some studies require initial testing of concepts and ideas. Both types of research are important for delivering timely milestones and promoting innovation. Thus, it is intended to provide two categories of grants: a) small start-up grants of one to two years at up to \$100,000 and b) standard grants of three years at \$300,000-500,000 for multiple partners (e.g., collaborative proposals between two or more institutions). To cast a wider net of research ideas and to avoid unnecessary investment in preparing full proposals, a call for pre-proposals for the standard grants will be instituted. Pre-proposals meeting the Program requirements and considered meritorious will be invited to prepare full proposals.

Clearly, various funding opportunities will develop during the course of the Challenge Program. Therefore, the competitive grant program should have sufficient flexibility to accommodate a variety of funding sources and stipulations (restricted versus unrestricted funds) from donors provided that the broad goals and the principles of the Program are served. An RFP involving one or more of the subprograms will be implemented on an annual basis. Such a regular and continuous granting process will help maintain the momentum and interest of the research community.

Private-sector participation

The Challenge Program will develop a strong partnership with the private sector, both large and small enterprises. The participation and contribution from agricultural biotechnology and information technology companies will be important, in particular to Subprograms 1, 2, and 4 (technical capacity in the field of genomics; experience with regulatory and IP matters; communication software and integrating of electronic systems; marketing). There is an emerging network of private breeding and seed companies in many developing countries, often closely associated with NARS. These will be instrumental through Subprogram 3

to make sure that improved varieties reach farmers' fields. The Challenge Program will seek ways in which the business interests of the private sector can be combined with the objective of the Program to enhance the public domain.

The CGIAR Private Sector Committee, companies represented on that committee, and others have expressed a keen willingness to be involved with the Challenge Program. In addition to participation at the research and development level, the Challenge Program will seek input from the private sector to the Program Advisory Committee and expert panels for independent review of competitive grant applications. It is likely also that larger companies may provide grants to Subprogram 5, for training scholarships within the framework of capacity building.

The participation of the private sector is likely to be expedited through clear, uncomplicated rules of engagement and well-articulated calls for proposals and all research for the Challenge Program will be the subject of research collaboration agreements.

The Challenge Program will assess potential private-sector partnerships on a case-by-case basis and will be guided by the goal of making products freely available, preferably in the public domain but, if not, with provisions for availability to the resource poor through mechanisms such as royalty-free licences for humanitarian purposes, and market segmentation.

Governance and Management

Governance and management of the Challenge Program are shown in Figure 5. The Challenge Program will be governed by a Program Steering Committee consisting of the Chief Executive Officers (or their nominees) of the consortium members and an independent Chairperson, Dr. Ismail Serageldin, former Chairman of the CGIAR and Vice-President, ESSD, World Bank. The Program Steering Committee will meet once- twice per year. Its role will include:

- determining strategic directions for the Challenge Program;
- establishing performance criteria to determine the progress of the Challenge Program in achieving its objectives;
- approving annual workplans and budget;
- approving the annual report of the Challenge Program;
- approving guidelines for the inclusion of new participants and related research projects, including the competitive grants portfolio;
- appointing and evaluating the performance of the Challenge Program Director, and Subprogram Lead Scientists;
- establishing and ensuring adherence to intellectual property management guidelines for Challenge Program activities;
- receiving reports from the Challenge Program Director and the Program Advisory Committee;
- ensuring that contributions to the Challenge Program from the consortium members are consistent with those committed, and meet the needs of the Subprograms; approving commissioned research projects;
- approving an overall strategy for the interface of the Challenge Program with donors and other external agencies; and
- Final approval of competitive grants and commissioned funding.

It may be seen from the above-mentioned points that the Program Steering Committee will have both the authority and the responsibility to make decisions for the consortium members. This model is based on experience with similar research consortia such as the Rice Wheat Consortium for the Indo-Gangetic Plains and Australia's Cooperative Research Centre for Molecular Plant Breeding. Consortium members will sign a joint venture agreement outlining the conditions under which they participate in the Challenge Program.

As previously mentioned, the PSC will be expanded to include other CGIAR centres with a commitment to the work of the Challenge Program. This commitment will be evaluated on the basis of: relevant germplasm

collections; scientific capability; and, in-kind contributions of at least \$400,000 pa. The PSC will also invite GFAR and the CGIAR Executive Council (ExCo) to nominate representatives; in the case of GFAR, this will provide an excellent coordinating mechanism for working with NARS, regional fora, farmers’ groups, and NGOs and, in the case of ExCo, appropriate representation at this level provides light oversight for the CGIAR. The ExCo representative will serve in an *ex-officio* capacity.

Along similar lines to the other two Challenge Programs already approved, this Program will comprise three lead centres (CIMMYT, IPGRI and IRRI), who will manage and execute the Challenge Program in accordance with the strategic guidance provided by the Program Steering Committee and the approved annual work plans, and also provide fiduciary responsibility on behalf of the consortium.

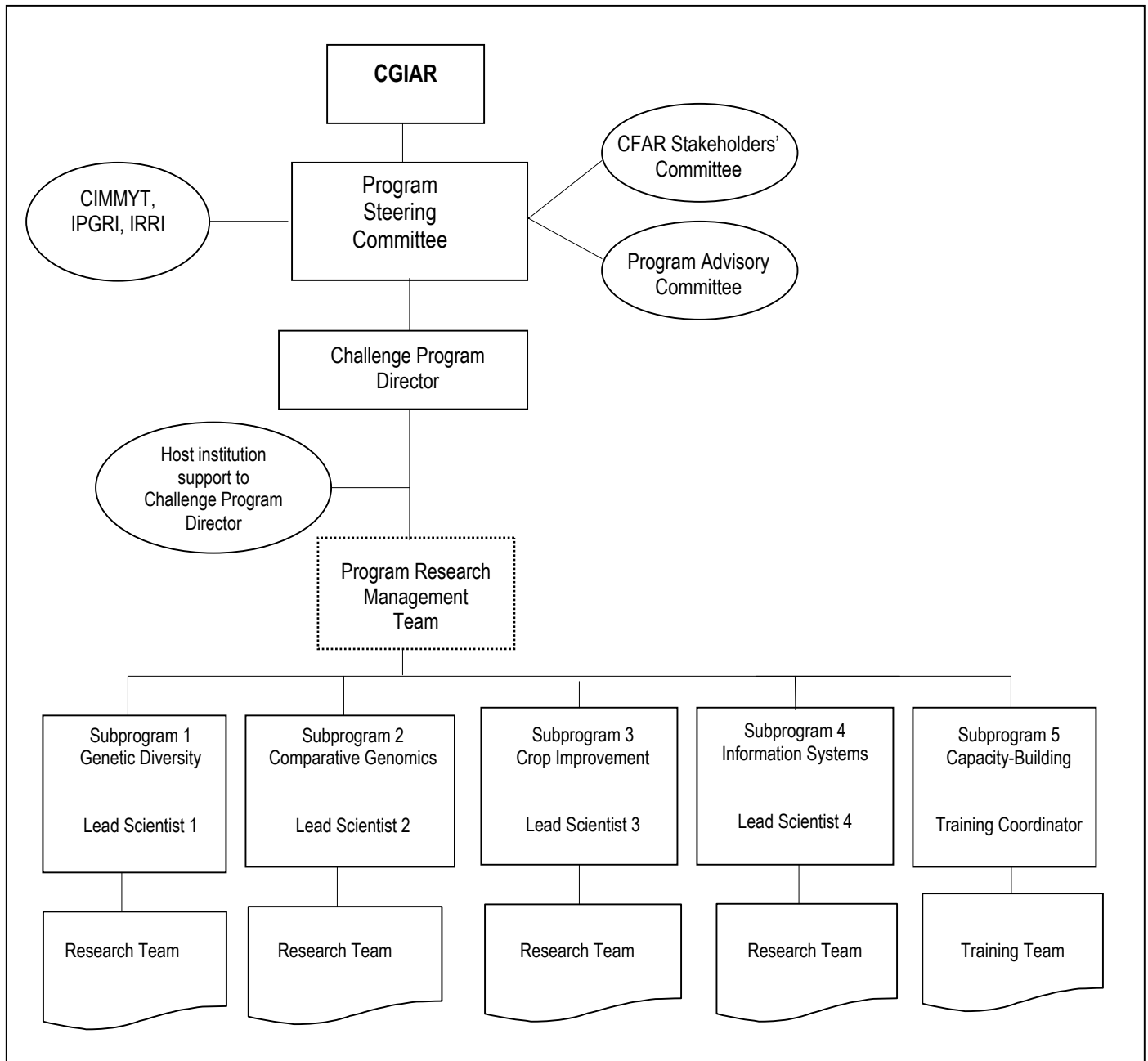


Figure 5. Overall governance and management structure of the Challenge Program.

Program Advisory Committee

The Challenge Program will be advised by a Program Advisory Committee, which will provide independent scientific advice to the Program Steering Committee. Membership of this group will be decided by the Program Steering Committee in a consultative process with stakeholders.

Stakeholders' Committee (GFAR)

A suitably representative Stakeholders' Committee for this Challenge Program will be proposed under the auspices of GFAR. It will meet once annually, probably at the CGIAR AGM, to be updated on the progress of the Challenge Program, and to provide feedback to the Program Steering Committee on issues that impact on the beneficiaries of the research.

Challenge Program Director

The Challenge Program will be managed by a Director who will be directly accountable to the Program Steering Committee in much the same way that a Center Director General is accountable to a Board of Trustees. The Challenge Program Director will be recruited through an international search process and appointed by the Program Steering Committee through one of the CGIAR consortium members. The appointee will be full-time Director of the Challenge Program.

If the Challenge Program Director is chosen from one of the founding consortium CGIAR institutes, it is proposed to locate the appointee at an institute different to that where he or she is currently employed, to help ensure that the business of the Challenge Program is managed in a fair and equitable manner. Further details will be resolved during the recruitment process that will be initiated as soon as the Challenge Program is approved by the CGIAR.

The Director will play a major role in ensuring coordination, integration, and communication across research activities as well as providing a public interface to the Challenge Program, especially as this relates to fundraising and seeking new research partners. The Director will focus his/her attention on outputs from the scientists involved in the Challenge Program, whereas day-to-day management will be provided at the institutional level.

In summary, the Challenge Program Director will:

- provide leadership to the Challenge Program;
- liaise with participants, funding agencies, and other initiatives compatible with the goals of the Challenge Program;
- ensure that the Challenge Program budget is used in accordance with the annual budget and any direction of the Program Steering Committee;
- monitor and keep the Program Steering Committee informed of the Challenge Program's performance;
- oversee preparation of an annual report for approval by the Program Steering Committee;
- prepare draft annual budgets and workplans and submit these to the Program Steering Committee for approval;
- act as a focal point for interaction between Lead Scientists and key researchers from Members of the Consortium;
- identify new research opportunities, including potential research partners;
- identify new funding opportunities, interact with funding agencies, and develop new research proposals consistent with the objectives of the Challenge Program; and
- assist with evaluation of Lead Scientists.

The Challenge Program Director will be assisted by administrative and other support at the host institution; the direct cost (including overhead) of this support will be charged to the Challenge Program budget, based on actual expenditure.

Program Research Management Team

Research coordination across the Challenge Program will be achieved through a Program Research Management Team (PRMT), which will focus on the conduct, integration, and coordination of research activities. Each of the Lead Scientists will be responsible for ensuring that the work of the Program is coordinated and contributing to Challenge Program milestones and agreed outputs. Lead Scientists will be recruited to the Challenge Program upon its approval in an open selection process. Final decisions on these positions, which are expected to account for at least 50% of a scientist's time, will be made by the Program Steering Committee in July-August of 2003.

The PRMT will comprise the Challenge Program Director (convener), the Lead Scientist for each of the four research Subprograms, and key researchers for specific research projects. The Challenge Program Director will convene the team at least four times per year (using electronic means as much as possible). This model is similar to that which has proven successful in the Cooperative Research Centres in Australia and is a feature of a number of research consortia in Europe, the USA, and elsewhere.

Within the four research Subprograms of the Challenge Program, Lead Scientists and the Training Coordinator will convene team meetings as appropriate.

Outputs and Outcomes

Anticipated activities and outputs of the Challenge Program are shown in Figure 2. Additional considerations related to outputs and outcomes are discussed next.

Stewardship

A key to the success of this Challenge Program will be the sharing of structural and functional genomic information across species and for a specific abiotic stress trait: drought. Success therefore requires the collaboration of all consortium members, since no single group has sufficient research scope, resources, or in-house expertise to bring all the information and technologies together in a comprehensive manner. The genetic materials and data will be made readily available for research and plant breeding programs. Subprogram 4 (Genetic Resources, Genomic, and Crop Information Systems) is specifically designed to extend and develop information management systems to assure accessibility and for user-friendly data analysis systems.

Experience with the SINGER network, together with the consortium members' expertise in other specialized networks (e.g., in genetic resources, association genetics, and bioinformatics) will be utilized to ensure that the needs of developing country researchers and plant breeding programs in NARS will be met.

In addition to the research outputs shown in Figure 2, the Challenge Program will strengthen the capacity of scientists in NARS to conduct modern, relevant science by:

- exchanging expertise through advanced training, graduate studentships, and visiting scientist programs;
- providing ready access to a public platform for genomic research;
- providing access to tools for gene discovery;
- providing access to high-throughput analytical tools for genetic resource characterization;
- providing access to universal anchor markers, consensus maps for QTL or candidate genes, and databases;
- improving the capacity to practice functional gene and MAS for producing improved varieties;
- exchanging advanced plant breeding materials with improved alleles for drought tolerance; and
- sharing high-throughput genetic resources genotyping and phenotyping information.

Although the main aim of this Challenge Program is to generate a public platform that will deliver international public goods, the private sector may also have unique opportunities to pursue intellectual property arrangements on innovations and derivatives produced by the Challenge Program. Such

arrangements will be negotiated to provide fair access and benefit sharing, particularly for non-commercial markets in developing countries.

To fully utilize the synergies of the research approach—comparative genomics across the CGIAR mandate crops—the Challenge Program will:

- identify accessions in genetic resource collections with variants of genomic regions or alleles of candidate genes having a favorable impact on priority traits;
- enhance the understanding of the genetic control of priority traits;
- identify candidate genes or tightly linked genomic regions underlying those traits;
- develop a gene management system, both from a technical and a policy point of view;
- provide advanced genomic and crop information systems to enhance the efficacy of plant breeding programs globally;
- develop and share breeding lines containing new alleles that will directly benefit crop improvement programs; and
- provide incentives through an intellectual property position on innovations and derivatives, for the private sector to invest in research that will benefit the resource-poor.

Each of the Subprograms has consulted extensively and developed research approaches, milestones (timelines), and outputs for its work. Further technical workshops will be held in the next few months to refine priorities and work plans.

All materials required for research and development under the four research Subprograms- as identified during the technical workshops- will be exchanged with a Material Transfer Agreement (MTA) that fully conforms with current and future requirements under the In-Trust Agreements between International Agricultural Research Centers and the FAO, the Convention on Biological Diversity, and International Treaty on Plant Genetic Resources for Food and Agriculture.

Intellectual Property

The Challenge Program will aim to generate new, science-based enabling and intermediate products that will be freely accessible to developing countries. If the technologies used to develop these products are in the private domain, the Challenge Program will negotiate access to these technologies through research alliances with the technology owners.

This Challenge Program aims to apply a comprehensive comparative analysis of genes across the major crop species to give the public sector access to, and the freedom to operate with, modern tools of crop improvement. In markets for which the CGIAR does not have a mandate, the private sector will also have incentives to develop and deliver new technologies arising from the work of the Challenge Program. These may be developed-country markets or emerging commercial markets in developing countries.

The Challenge Program will develop an IP management plan based on a set of Guiding Principles agreed among the consortium members at the initiation of the Program. These Guiding Principles will be complementary to the IP policies of the consortium members and will be specific to the work of the Challenge Program. The overriding principle will be to share the outputs of the Program for research purposes but also to offer potential users opportunities for commercial development in accordance with specific IP agreements. At the same time, strategies will be developed to ensure direct benefits and free access for the resource poor. The Guiding Principles will form part of the joint venture agreement between the Challenge Program consortium members. Implementation of the Principles will be the overall responsibility of the Challenge Program Director who may wish to call upon consortium members with appropriate expertise and upon expert assistance from the CGIAR Central Advisory Service (CAS) based at ISNAR in providing information and tools to track and manage Program IP, as needed.

The Guiding Principles will also be used to assist the development of effective partnerships with the private sector.

The detailed IP management plan to be developed during 2003 will be based on the specific anticipated outputs and intellectual assets to be generated by the Program. Technical workshops in the first part of 2003 will develop detailed research workplans and identify the methodologies and associated proprietary technologies that may impact on the ability of the Challenge Program to share products with NARS and other partners. The Challenge Program will seek partnerships that assure the accessibility of its outputs.

All commissioned research and competitive grants will be the subject of a research agreement that includes an IP management plan and a technology transfer strategy that outlines the IP assets, target users, and mechanisms to implement the transfer.

Stewardship of intellectual property under this Challenge Program will provide the following benefits:

- maintain the flow of genetic diversity to the crop improvement programs of the CGIAR and NARS for resource-poor farmers;
- provide NARS with diverse germplasm that contain priority traits within the public domain;
- provide NARS with the opportunity to commercialize intellectual property;
- provide the private sector with opportunities to develop partnerships with NARS in the delivery of improved varieties to farmers; and
- provide a public platform for access to information; technologies and products in the continuum from genetic diversity to improved varieties.

Biosafety

All Challenge Program research will be conducted under National biosafety regulations. Transboundary movement of transgenic materials (if developed) will strictly follow National and International regulations and will strictly adhere to the principle of “prior consent” of the Cartagena Protocol on Biosafety. As a component of Subprogram 5: Capacity Building, the Challenge Program will assist NARS to gain expertise in biosafety and related issues relevant to the Program.

Performance Evaluation and Impact Analysis

The structure and management of the Challenge Program provide opportunities at different levels for rigorous review and assessment of its performance. As noted, the Program Steering Committee will have primary responsibility for the performance of the Challenge Program in meeting its goals and objectives. Independent advice will be provided to the Program Steering Committee by the Program Advisory Committee and the GFAR Stakeholders’ Committee to ensure both the excellence and relevance of the research. The Challenge Program Director will be directly accountable for the outputs of the Challenge Program. He or she will address concerns over progress of specific research activities with the relevant Consortium Member (in the event that an issue cannot be resolved with the appropriate Lead Scientist).

Each of the four research Subprograms will be headed by a Lead Scientist from one of the consortium members, and this person will have responsibility for ensuring that objectives and milestones for his/her Subprogram are on target. The Challenge Program Director will provide leadership for Subprogram 5, and will be supported in this by a Training Coordinator.

The Lead Scientists and key researchers of the consortium will meet regularly (at least four times per year) to discuss research issues and progress; these meetings will be convened by the Challenge Program Director, in electronic format as much as possible.

Approval of all commissioned research, competitive grants awarded, and additional research projects will be referred to the Program Steering Committee. This will guarantee that decisions will be taken with full knowledge and authority and that the research and capacity building of the Challenge Program are clearly focused on the CGIAR mission.

An annual research meeting will be held for participants in the Challenge Program to review research progress and to discuss related issues. This forum will be an important opportunity for research groups within and across the Challenge Program's Subprograms to meet and develop workplans for the coming 12 months. The annual meeting will also be an opportunity for stakeholders to interact with Challenge Program researchers and help ensure that the beneficiaries of the work of the Challenge Program contribute to its research planning. In addition, there will be an annual meeting with the GFAR Stakeholders' Committee where the Challenge Program will report to, and receive feedback from, this committee.

The Program Advisory Committee will assist the Program Steering Committee to develop performance indicators that will form the basis for *ex ante* and *ex post* impact assessment. It is expected that the Program Advisory Committee will provide regular advice on scientific issues, and assess progress. A subgroup of the Program Advisory Committee may also be constituted in year 4 for a more formal review in consultation with the CGIAR Science Council.

The impact of the Challenge Program may be measured at different levels. At the research level, time-based milestones offer a verifiable means of assessing progress. It should be noted that in the early stages of the Challenge Program, in addition to intermediate research products and enabling technologies, strategies for the use of new technologies will be an important output. An important aspect of these intermediate products- and part of the IP management plan- will be tracking the intellectual assets that have contributed to their development.

Impact analysis will also occur at the development level, when decisions about using new technologies and products are taken, and at a social level when the impacts of improved varieties may be measured in farmers' fields. It is likely that the newly formed Science Council panel on impact assessment will be strongly placed to assist in the development of impact analysis.

Budget and Resources

The consortium members bring considerable resources to the Challenge Program by providing personnel, research infrastructure, and major facilities. In addition, a number of relevant on-going activities will complement the activities of the Challenge Program.

Contributed personnel are summarized in Table 1.

Table 1. In-kind contributions (per annum) to the Challenge Program on Unlocking Genetic Diversity in Crops for the Resource-Poor.

Institution	Full-time equivalent researchers (US\$ 000s)	Allocation by Subprogram (%)			
		Genetic Diversity	Comparatives Genomics	Gene Transfer, Crop Improvement	Information-Systems
CGIAR Centers	2,328	40	30	20	10
NARS	1,357	20	20	40	20
ARIs	2,041	10	50	10	30
Total	5,726				

In addition to the contribution of consortium members listed above, additional resources will be added as other partners join the consortium and with implementation of the commissioned research and competitive grants program. The level of new funding that is required for this Challenge Program is listed in Table 2.

Table 2. Annual new funding (US\$ 000s) needed for full implementation of the Challenge Program on Unlocking Genetic Diversity in Crops for the Resource-Poor.

Activity	Year					Total
	1	2	3	4	5	
Governance and management	1,000	1,000	1,000	1,000	1,000	5,000
Genetic diversity	4,500	4,000	3,500	3,000	2,000	17,000
Comparative genomics	1,500	1,500	2,500	2,500	2,500	10,500
Gene transfer, crop improvement	--	1,500	2,000	3,000	4,000	10,500
Information systems	4,000	4,000	3,000	2,500	2,500	16,000
Capacity building	2,000	2,000	2,000	2,000	2,000	10,000
Total	13,000	14,000	14,000	14,000	14,000	69,000

In terms of resourcing, the central thesis of this Challenge Program is that a number of discrete research activities currently underway will benefit from coordination and integration. Furthermore, new areas of work have been identified; additional funding of this work is considered essential for the Challenge Program to achieve its objectives. There are firm indications that a number of donors will support this Challenge Program upon its approval by the CGIAR and these contributions are expected to amount to more than \$4M in 2003. Together with the projected income from the World Bank of \$3M, it can be seen that the Challenge Program has a very strong launching pad (\$7M) for attracting additional funds.

Additional funding for the Challenge Program will be sought on the basis of donors' interests. For example, there will be separate and varied opportunities to "market" aspects of this Challenge Program, such as genetic diversity, genomics, crop improvement, information systems, and the drought case study. Appropriate donors will also be sought for the spectrum of Challenge Program activities, ranging from basic to applied research and to development work. It should be emphasized that the Challenge Program will provide a range of opportunities for donors to invest in its work; there will be sufficient flexibility to accommodate a variety of funding sources and stipulations (restricted versus unrestricted funds) from donors provided that the broad goals and principles of the Challenge Program are served.

In particular, it is likely that the drought case study will provide opportunities for fund raising, as drought is widely recognized as a major constraint on crop production in developing countries. For example, Lantican et al. (2002) have shown that there is enormous potential (up to 3.5% yearly) to improve wheat productivity in marginal (drought-prone) environments, and the losses to drought in rainfed rice systems amount to more than 4% per year or, the equivalent of almost \$3B of lost production.

The proponents of the Challenge Program acknowledge that the envisaged Program activities are too large for a single centre or combination of centres and that a critical mass of researchers is needed to assure the quantity and quality of work that will be undertaken. Moreover, only a partnership that goes beyond the CGIAR, encompassing both ARIs (private and public) and NARS can achieve the goals set for this Challenge Program and provide access to (proprietary) technologies developed in the North and necessary for the challenges of the South. The Challenge Program links but goes beyond the core mandates (genetic conservation and crop improvement) of the CGIAR centres.

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Appendix 1

Size and Structure of Germplasm Collections at the CGIAR Centers, 2001

Center and location	Crop	Number of accessions		
		Held in trust	Other	Total
CIAT (International Center for Tropical Agriculture, Colombia)	Cassava	5,728	2,332	8,060
	Common bean	30,590	810	31,400
	Forages	16,339	7,845	24,184
	Total	52,657	10,987	63,644
CIMMYT (International Maize and Wheat Improvement Center, Mexico)	Wheat	79,912	75,000	154,912
	Maize	20,411	4,675	25,086
	Total	100,323	79,675	179,998
CIP (International Potato Center, Peru)	Potato	5,057	2,582	7,639
	Sweet Potato	6,413	1,246	7,659
	Andean roots/tubers	1,112	383	1,495
	Total	12,582	4,211	16,793
ICARDA (International Center for Agricultural Research in the Dry Areas, Syria)	Cereal	54,218	5,795	60,013
	Forages	24,581	5,947	30,528
	Chickpea	9,116	2,103	11,219
	Lentil	7,827	2,135	9,962
	Faba bean	9,074	1,671	10,745
	Total	104,816	17,651	122,467
ICRAF (International Center for Research in Agroforestry, Kenya)	Agroforestry trees (total)	25	10,000 ^a	10,025
ICRISAT (International Crops Research Institute for the Semi-Arid Tropics, India)	Sorghum	35,780	941	36,721
	Pearl millet	21,250	142	21,392
	Pigeon pea	12,698	846	13,544
	Chickpea	16,961	289	17,250
	Groundnut	14,357	985	15,342
	Minor millets	9,050	202	9,252
	Total	110,096	3,405	113,501
IITA (International Institute of Tropical Agriculture, Nigeria) ^b	Bambara groundnut	2,029	---	2,029
	Banana	---	400	400
	Cassava	2,158	1,371	3,529
	Cowpea	15,001	1,000	16,001
	Soybean	1,909	1,144	3,053
	Wild <i>Vigna</i>	1,634	50	1,684
	Miscellaneous legumes ^c	---	400	400
	Yam	2,878	822	3,700
	Total	25,609	5,187	30,796
ILRI (International Livestock Research Institute, Kenya)	Forages (total)	11,537	1,667	13,204
IPGRI/INIBAP (International Plant Genetic Resources Institute/International Network for the Improvement of Banana and Plantain, Italy) ^e	<i>Musa</i> (total)	914	229	1,143
IRRI (International Rice Research Institute, Philippines)	Cultivated rice	77,827	16,737	94,564
	Wild rice	2,790	1,778	4,568
	Total	80,617	18,515	99,132
WARDA (West Africa Rice Development Association, Côte d'Ivoire) ^d	Rice (total)	14,917	460	15,377
Total		514,093	151,987	666,080

Source: In-trust figures provided by IPGRI and totals provided directly from genebanks during 2001.

a Estimate provided by manager of ICRAF genetic resource program.

b In addition to this material, IITA holds about 2,500 accessions of maize and multipurpose trees.

c Includes African yam bean, Kersting's groundnut, and various beans (e.g., lablab, jack, and winged beans).

d The WARDA base collection is housed at IITA.

e The *Musa* collection is housed in Leuven, Belgium.

Appendix 2

Genomic Resources Available for CGIAR Mandate Crops

The majority of the CGIAR's mandate crops are well represented by the Core Participants of the Challenge Program. Comparative Model Species are also available to allow for comparative genomic studies and to take advantage of the vast amount of genomic resources available in the model species. In addition, many of the CGIAR mandate crops already have various genomic resources available. Genetic maps (both molecular marker and QTL) are available either at the basic (+) or advanced (++) level. Similarly, various genomic tools are under development (+) or well advanced (++) , such as SSRs (microsatellite markers for mapping), BACs (bacterial artificial chromosomes for gene isolation), ESTs and databases (expressed sequenced tags and databases containing the sequences and associated function), DNA microarrays (DNA chips for expression studies), and transformation systems (to allow for gene discovery, validation and introduction in a species). Note that this list does not include all CGIAR mandate crops but only those for which substantial genomics resources are available.

Crop	Institutes	Comparative model species	Genetic maps	SSRs	BACs	ESTs and databases	DNA microarrays	Transformation system
Barley	ICARDA, JIC	Rice	++	++	++	++	+	++
Cassava	CIAT, IITA	-	++	++	++	++	+	++
Chickpea	ICARDA, ICRISAT	-	+	++	-	+	-	+
Common bean	CIAT	-	++	++	+	+	-	-
Cowpea	IITA	-	+	+	-	-	-	-
Forages	CIAT, ICARDA, EMBRAPA	?	++	++	+	+	+	+
Groundnut	ICRISAT	-	+	++	-	-	-	+
Lentil	ICARDA	Medicago	++	++	++	-	-	++
Maize	CIMMYT, IITA, CAAS, EMBRAPA	Rice	++	++	++	++	++	++
<i>Musa</i> spp.	IITA, IPGRI, Agropolis	-	+	+	+	+	-	+
Pearl millet	ICRISAT, JIC	Rice	++	++	++	-	-	+
Pigeon pea	ICRISAT	-	+	+	-	-	-	+
Potato	CIP	Tomato	++	++	++	++	+	-
Rice	CIAT, IRRI, WARDA, JIC, CAAS, NIAS, Cornell, Agropolis, Wageningen	Rice	++	++	++	++	+	++
Sorghum	ICRISAT, JIC	Rice	++	++	++	++	-	+
Soybean	IITA	Medicago	++	++	++	++	+	+
Sweet Potato	CIP	Tomato	++	++	++	++	+	-
Wheat	CIMMYT, ICARDA, CAAS, EMBRAPA, JIC, Agropolis	Rice	++	++	+	++	+	++
Yam	IITA	Tomato	+	+	-	-	-	-

Appendix 3

Acronyms and Abbreviations

AGROPOLIS	International Complex for Research and Higher Education in Agriculture (France)
ARI	Advanced research institute
BAC	Bacteria artificial chromosome
CAAS	Chinese Academy of Agricultural Sciences
CBR	C-repeat binding factor
cDNA	complementary DNA
CENARGEN	National Center for Genetic Resources and Biotechnology Research, Brazil
CGIAR	Consultative Group on International Agricultural Research
CIAT	International Center for Tropical Agriculture (Centro Internacional de Agricultura Tropical)
CIMMYT	International Maize and Wheat Improvement Center (Centro Internacional de Mejoramiento de Maíz y Trigo)
CIP	International Potato Center (Centro Internacional de la Papa)
COS	Conserved orthologous sets
DNA	Deoxyribonucleic acid
DREB	Dehydration responsive element binding
EMBRAPA	Brazilian Agricultural Research Corporation (Empresa Brasileira de Pesquisa Agropecuaria)
EST	Expressed sequence tag
FAO	Food and Agriculture Organization of the United Nations
ICARDA	International Center for Agricultural Research in the Dry Areas
ICIS	International Crop Information System
ICRISAT	International Crops Research Institute for the Semi-Arid Tropics
IITA	International Institute of Tropical Agriculture
INIBAP	International Network for Improvement of Banana and Plantain
IPGRI	International Plant Genetics Resources Institute
IRIS	International Rice Information System
IRRI	International Rice Research Institute
IWIS	International Wheat Information System
JIC	John Innes Centre, UK
LD	Linkage disequilibrium
LIMS	Laboratory information management systems
MAS	Marker-assisted selection
MTA	Material transfer agreement
NARS	National agricultural research system
NCGR	National Center for Genome Resources
NGO	Non-governmental organization
NIAS	National Institute of Agrobiological Sciences, Japan
PAC	Program Advisory Committee
PCR	Polymerase chain reaction
PRMT	Program Research Management Team
PSC	Program Steering Committee
QTL	Quantitative trait loci
RFLP	Restriction fragment length polymorphism
RIL	Recombinant inbred line
SGRP	System-wide Genetic Resources Programme
SINGER	System-wide Information Network for Genetic Resources
SNP	Single nucleotide polymorphism
SSR	Simple sequence repeat
TRIPS	Trade-Related Aspects of Intellectual Property Rights
USDA	United States Department of Agriculture
WARDA	West African Rice Development Association
WTO	World Trade Organization