

# Challenge Program

for Unlocking  
**Genetic Diversity**  
in Crops for the  
Resource-Poor

**Year 1 Workplan and Budgets**

December 1, 2003

**CIMMYT**  
Apdo. Postal 6-641  
06600 Mexico, D.F., Mexico

# CHALLENGE PROGRAM

## Unlocking Genetic Diversity in Crops for the Resource-Poor

### YEAR 1 WORKPLAN AND BUDGETS

Submitted by the Directors General of CIMMYT (Dr. M. Iwanaga),  
IPGRI (Dr. E. Frison), IRRI (Dr. R. Cantrell) and  
Challenge Program Director Designate Dr. R. S. Zeigler

December 1, 2003



## Letter from the Directors General

The concept for a Challenge Program on crop genetic resources grew out of the widening recognition that the products of agricultural biotechnology are not available to—and, even more alarming, often do not address the needs of—the world’s poor. The CGIAR system is ideally positioned to facilitate a global consortium of organizations dedicated to tapping the genetic potential of staple crops and applying the advances of molecular biology to the specific problems of poor farmers.

From the beginning stages of this Challenge Program, many dedicated scientists and organizations have been involved in its development, evolution, and, now, its execution. The Challenge Program for Unlocking Genetic Resources in Crops for the Resource-Poor has presented the international research community with a unique opportunity to collaborate on issues of global importance, forge strategic partnerships to produce scientific tools and technologies that are publicly accessible, and establish avenues for shaping intellectual property and technology policy to ensure that future advances in biotechnology are accessible and applicable to the needs of the developing world. The Challenge Program unites CG centers, national agricultural research systems of developing countries, advanced research institutes, and private companies from across the globe in these efforts. This expansive partnership will elevate impact-driven research to a new level—global research for local impacts, targeted problem-solving for global applications—and we believe that the whole of our partnership will be much greater than the sum of its parts.

In the early development of the Challenge Program for Unlocking Genetic Diversity in Crops for the Resource-Poor, Masa Iwanaga, Director General of CIMMYT, assumed operational leadership of the Challenge Program while the two other lead Centers (IRRI and IPGRI) provided keen and substantial support in shaping the Challenge Program in consultation with key stakeholders. The three Centers are committed to providing continued support of the Challenge Program and the Challenge Program Director, Bob Zeigler.

The Challenge Program represents a departure from the standard way of doing business within the CGIAR, and without. The success of this Challenge Program will translate into better livelihoods for millions of resource-poor people—and it will certainly spearhead a more streamlined, more efficient, and more effective mode for developing and delivering useful science to the people who need it most.

We hope that this Workplan imbues the reader with the sense of the promise that we believe this Challenge Program holds. Thank you for your support of new initiatives like the Challenge Programs and for your consistent commitment to bringing strong science to bear on the world’s most entrenched problems.

Best regards,

Masa Iwanaga, CIMMYT

Emile Frison, IPGRI

Ronald Cantrell, IRRI



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# EXECUTIVE SUMMARY

## *Program Overview*

The extraordinary discoveries of plant molecular biology have yet to be used in ways that will benefit the world's poor; likewise, 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) have yet to be tapped in a systematic way. Through this Challenge Program, we will create a strong coalition of institutions dedicated to alleviating poverty by applying the recent advances of the biological sciences. This alliance will harness the powerful tools of the genomics revolution to unlock the genetic potential within crop germplasm to address the needs of the resource-poor. **The Challenge Program for 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.** Also known as the "Unlocking Genetic Diversity Challenge Program" (or UGDCP), this Challenge Program will make available as public goods an unprecedented array of genomic and genetic resources, ready for direct use in plant improvement, 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 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 Programs are a new way of doing business within and outside the CGIAR. This Challenge Program grew out of the recognition that the challenges confronting agriculture and the opportunities to address these using the newest tools of biology are beyond the capacities of any single institution, so a small group of institutions with common interests proposed to join forces. The Challenge Program was originally presented by a founding group, the Consortium, of three CGIAR Centers (CIMMYT, IPGRI, and IRRI), 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; and Wageningen University, the Netherlands). Subsequent to a Stakeholders Meeting in Alexandria, Egypt, the following institutions were added to the Consortium and are represented on the Program Steering Committee: GFAR, CIAT, CIP, ICARDA, ICRISAT, and IITA. It is expected that additional institutions, both private and public, will join the Challenge Program as mutual benefits of their membership are identified.

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 for 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 ultimate proof-of-concept of this approach. Drought was chosen as the long-term case study because drought affects all of the CGIAR mandate crops and it has resisted resolution using conventional approaches. This effort will be reinforced by the long history of drought research and by current drought research. Furthermore, drought is widely regarded 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. Along the way, as tools and techniques are developed and refined, other traits—such as disease and pest resistance, food quality, and plant architecture—with a shorter time horizon for impact will be addressed as conditions and opportunities dictate.

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. In pursuit of this goal, the Challenge Program will create 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.

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 straightforward. 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

The Challenge Program will work across four crop groups:

- Cereals, including the grass forages

- Root and tuber crops
- Legumes, including forages
- *Musa* is a special case in that as a monocot it has commonalities with the cereals and as a vegetatively propagated large accumulator of carbohydrates it has commonalities with the root and tuber crops. Thus different issues concerning *Musa* will be addressed within both crop groups.

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

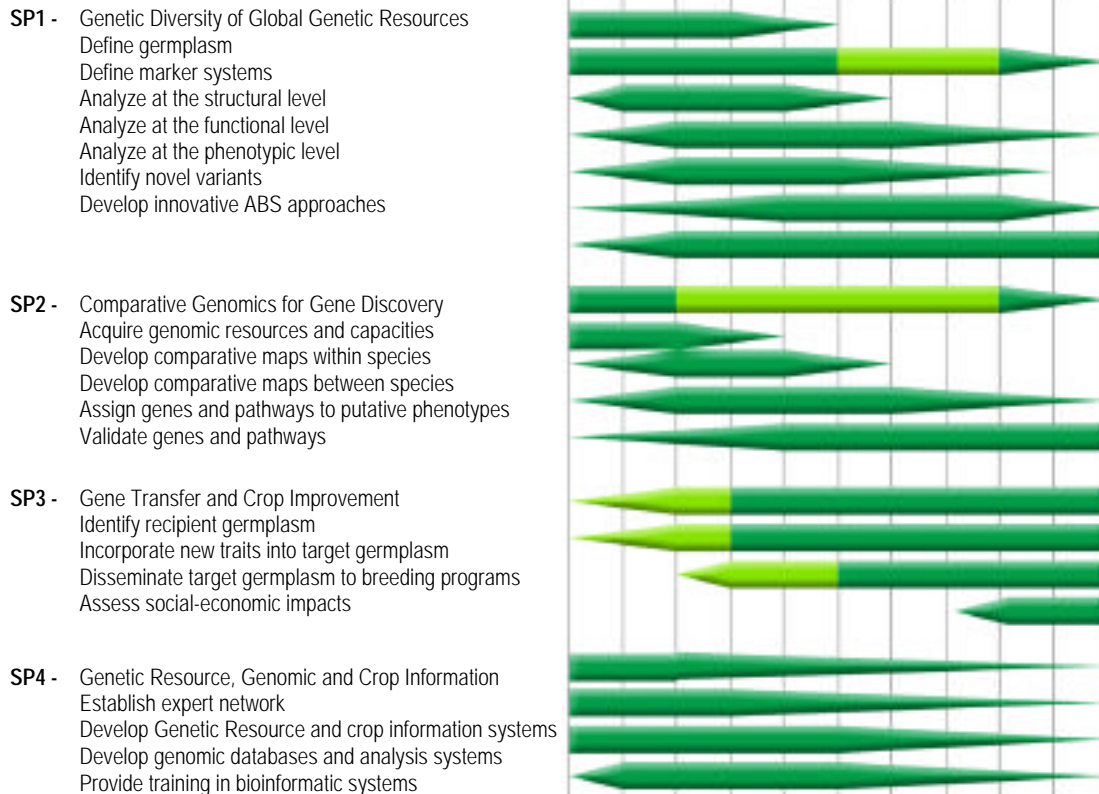
### ***Management and Operations***

A Program Steering Committee (PSC) will serve as a Board of Directors and is comprised of the Chief Executive Officers, or their designees, of the Challenge Program consortium members with additional representation from GFAR and the CGIAR Executive Council (the latter in an *ex-officio* role; see Appendix 1 for PSC membership). The PSC, chaired by an independent chairperson, will receive independent advice from a Program Advisory Committee (PAC) and a Stakeholders Committee convened by GFAR. The Challenge Program will be guided by an internationally recruited eminent scientist as Program Director who will also provide leadership for Subprogram 5: Capacity-Building. The Program Director will be assisted by a Subprogram Leader (SPL) 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 (see Appendix 7 for the terms of reference and recruitment procedure for the SPLs).

The Challenge Program operates over two phases of approximately five years. 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 intermediate products for several traits of interest and demonstrated progress in 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.

**Figure 1.**



**FIVE-YEAR OBJECTIVES.** 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, and 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.

**TEN-YEAR OBJECTIVES.** 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.** Financial resources required for this Challenge Program are 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

**YEAR ONE TECHNICAL WORKPLAN BUDGET.** The financial resources available for year one are approximately €4M (= \$4.6M @ \$1.15 per€) from the EU and \$3M from the World Bank. A work planning meeting was convened in August at Wageningen Agricultural University where it was decided that the funds would be distributed across the Subprograms as shown below. It was further proposed during post-meeting discussions that resources would be allocated among clusters within the Subprogram as shown below. Note that the budget figures approved in Wageningen for each Subprogram only included direct operating dollars. In Table 1, we have added the anticipated \$170,000 in operating funds that will be allocated to each of the four Subprogram Leaders. The remaining funds (~\$900,000) are for capacity-building, initiation of a competitive grants program, CP management, and conferences. Once the Subprogram Leaders are selected they will review allocations with the Program Director. Minor changes may be made within subprograms but major adjustments are not expected. Note that these figures are for Year One only.

Table 1. Agreed resource allocation across Subprograms for Year 1.

SUBPROGRAM	BUDGET
Subprogram 1: Genetic Diversity of Global Genetic Resources	\$2,800,000
Subprogram 2: Comparative Genomics for Gene Discovery	\$1,130,000
Subprogram 3: Gene Transfer and Crop Improvement	\$600,000
Subprogram 4: Bioinformatics	\$2,100,000
Total	\$6,630,000

Table 2. Subprogram 1: Genetic Diversity of Global Genetic Resources

Research cluster	Budget
CL1: Composite Genotype Sets	\$400,000
CL2: Collection of Marker Sets/Genotyping/Data Analysis	\$2,000,000
CL3: Phenotyping Protocols Workshop	\$100,000
CL4: Intellectual Property/Access and Benefit-Sharing (Policy Research)	\$200,000
Subprogram Leader research support	\$100,000*
Total	\$2,800,000

**Table 3. Subprogram 2: Comparative Genomics for Gene Discovery**

Research cluster	Budget
CL1: Germplasm Evaluation	\$300,000
CL2: Marker Development	\$290,000
CL3: Gene Expression Profiling	\$280,000
CL4: QTL Analysis	\$160,000
Subprogram Leader research support	\$100,000*
Total	\$1,130,000

**Subprogram 3: Gene Transfer and Crop Improvement**

Research cluster	Budget
CL1: Marker Assisted Selection (MAS) Training Workshop	\$50,000
CL2: MAS Across Crop Groups	\$350,000
CL3: Crops With Appropriate Gene Technologies (Transformation Across Crop Groups)	\$50,000
CL4: Recurrent Parents	\$50,000
Subprogram Leader research	\$100,000*
Total	\$600,000

**Subprogram 4: Bioinformatics**

Research cluster	Budget
CL1: Expert Networks	\$1,000,000
CL2: Genetic Resources, Crop, and Genomics Analysis and Information Systems	\$1,000,000
Subprogram Leader research support	\$100,000*
Total	\$2,100,000

\* \$100,000 reflects additional operating funds to support Subprogram Leader in research activities of his/her respective Subprogram.

**Subprogram 5: Capacity-Building**

It was decided during the work planning activities that the best use of capacity-building funds would be to build the capacity-building activities into the critical foundation activities that would be initiated immediately. Based on these first year activities, well-focused specific capacity-building programs and activities could be built for the second and later years. Capacity-building activities, while funded within each of the research clusters, can be easily identified and have been extracted here:

*SP1CL1: Composite Genotype Sets.* The process of constructing the composite collections will significantly enhance expertise and understanding of methodologies for the formation of targeted core collections. NARS involved in compilation of composite collections include: National Bureau of Plant Genetic Resources of India (in collaboration with ICRISAT); National Plant Genetic Resources of Syria and Jordan (in collaboration with ICARDA); NARS scientists and students from Peru (in collaboration with CIP); and 2-3 NARS scientists will be trained (through CIAT).

*SP1CL2: Collection of Marker Sets/Genotyping/Data Analysis.*

- Cassava: Two NARS scientists from developing countries will genotype accessions using Dart markers at CAMBIA (CIAT/IPGRI). At IITA, a laboratory technician and database manager will be trained in data capture and automated fragment analysis at IITA's Plant Biodiversity Genomic Facility in Kenya.
- Chickpea: Two NARS scientist (India and Syria) will be trained in genotyping as well as data analysis.

- Common bean: NARS scientists from Bolivia, Colombia, and Mexico (and likely Kenya) will be trained in fluorescent microsatellite technology with lab exchanges between these institutions to standardize technology (CIAT/EMBRAPA).
- Cowpea: Two technicians and a database manager will be trained under the cowpea project (IITA).
- Maize: A technician would be appointed at IITA to assist in collation of data and training in molecular characterization at CIMMYT.
- *Musa*: A researcher/technician from a NARS will do genotyping and analysis at CIRAD-Montpellier. A training course will be organized at IAEA on the use of microsatellite markers for 5-10 NARS participants.
- Potato: NARS training in SSR analysis and database development.
- Rice: Visiting scientist from NARS collaborator appointed for genotyping work. Workshop on application of high-throughput genomic technologies for identification of induced and natural variation in stress-related genes training in collaboration with ARBN. NARS scientists from Colombia and Brazil will be appointed to genotype rice accessions using high-throughput fluorescent SSR markers (IRRI and CIAT).
- Sorghum: Training of 3 NARS scientists (Agropolis/CAAS/ICRISAT).
- Wheat: Training of NARS scientists at INRA Clermont and Montpellier in automatic sequencer genotyping technology and data analysis.

*SP1CL3: Phenotyping Protocol Workshop.* This workshop will establish a network to ensure that ideas and knowledge flow among those partners actively involved in the evaluation of drought tolerance for different crops for the UGDCP.

*SP1CLA: IP/ABS – Policy Research.* This joint workshop will improve upon all draft reports of all projects in this cluster. The workshop will include several stakeholders within and outside the consortium.

*SP2CL1: Germplasm Evaluation.*

- Agropolis: One Senegalese MS student to participate in the project on sorghum.
- CIAT: Involvement of national scientist(s) from INTA, Nicaragua, on bean project; collaboration with EMBRAPA on cassava; and joint project on rice with EMBRAPA and CORPOICA in which scientific personnel from CORPOICA/Fedearroz will be trained.
- CIMMYT: Students from Africa will visit the Applied Biotechnology Center at CIMMYT and possibly INRA (Montpellier) during the first year. The students will be trained in maize germplasm evaluation at morphological and physiological levels. In wheat, one IAEA visiting scientist will be trained as part of a hands-on training exercise.
- ICRISAT: 2-week introductory training course in QTL mapping techniques to be led by ICRISAT biometrician. A 1-week international training course on multi-location trials for the improvement of abiotic stress tolerance in chickpea will also be held, in conjunction with IAEA.
- ICARDA: Visiting scientists and students from WANA will visit ICARDA wheat breeding program and barley improvement program to be trained on stress physiological screening techniques.
- IITA: Graduate students and visiting scientists from NARS of participating in African countries will participate on cassava project. A graduate student from one of the universities around Ibadan will be involved in the screening and genetic diversity study on cowpea.
- IRRI: Requested funding will support the training of a graduate student from a national program affiliated with IRRI's rice drought breeding effort.

*SP2CL2: Marker Development.* University students will be employed to develop thesis research in bioinformatics applied to marker development. Funding for a CAAS scholar is being requested in SP4 to backstop bioinformatics needs and help assure links between SP2CL2 and SP4. Partial funding for a scholar in bioinformatics and his/her travel in Latin America is requested in CIP budget, to collaborate with Cornell University (solanaceae/dicots) and CIAT (legumes/dicots), in communication with the scholar at CAAS and SP4. Visiting scientists from developing countries are expected to visit INIBAP and partners for a structured program of research and training in marker development for 3 months each.

*SP2CL3: Gene Expression Profiling.* Students and visiting scientists from NARS will receive training in the use of functional genomics techniques, including comprehensive data analysis, at CIMMYT. In addition, researchers from some CG centers not previously exposed to the gene expression technologies will be trained, as will postdoctorals and students from NARS.

*SP2CL4: QTL Analysis.*

- Cassava: A Thai scientist from the national cassava breeding program will be trained in QTL mapping at CIAT.
- Common bean: An undergraduate student will be trained at CIAT as part of the common bean component of this cluster.
- Musa: An MS student, working under a joint agreement with the University of Nsuuka and IITA, will perform data collection at the Nigerian sites of the University of Nsuuka, and a MS Student working under a joint agreement with the University of Makerere, Uganda, and IITA, will perform data collection in a highland field site in Uganda.
- Rice:
  - 2 MS students to work on the project at Agropolis.
  - 1 PhD student at IRRI in drought tolerance for rice.
  - Collaboration with the experts in UAS-India, RIABGR-Indonesia, IRRI, and WUR to develop an integrated concept of drought testing and mapping in rice.
- Sorghum: 1 MS student to participate in the project on sorghum at Agropolis.

*SP3CL1: MAS Workshop.* The main objective of the workshop is for capacity building among NARS in the area of MAS/B.

*SP3CL2: Marker-Assisted Selection/Breeding.*

- Rice: Pyramided introgression lines in IR64 will be genotyped by a visiting research fellow from NDUAT, Uttar Pradesh, India, who will also assist in field phenotyping. Genotyping of the IR64/Azucena fine mapping population will be completed by a student from China, who is a student at University of the Philippines, Los Baños.
- Sorghum (ICRISAT): PhD students and visiting scientists from India and Africa (Ghana or Kenya) to participate in pearl millet project and receive training in SSR-marker-assisted backcross introgressions of particular traits important to pearl millet producers in their respective regions.
- Maize (CIMMYT-INRA-IITA): Students will receive training in MAS experiments on OPVs and quantification of changes in allelic frequency across cycle of selection, a key issue for germplasm improvement through biotechnological approaches in Africa.
- Cowpea (IITA): A visiting scientist from a Nigerian institution will be involved directly with the study.
- Cassava (IITA-CIAT): Outputs of this project will be included in the workshop on MAB and GM crops (SP3CL3).
- Bean (CIAT-EMBRAPA): Bean breeders from EMBRAPA and other NARS will be invited to be involved in all stages of marker-assisted selection and development of breeding populations for drought tolerance.

- African rice (CIAT-Agropolis): Technicians at CIAT will perform crosses and conduct recurrent selection and assist/conduct molecular characterization.

*SP3CL3: Crops with Appropriate Gene Technologies.* This workshop will identify appropriate gene technologies for asexually propagated crops and will involve significant NARS participation.

*SP4CL1: Informatics Expert Network.* The Informatics Team will develop a plan and establish partnerships with institutes and networks conducting capacity-building activities in the areas of genetic resources and molecular biology. In addition to the explicit output of developing a training plan for informatics in the UGDCP, a fundamental role for all members of the network will be the identification and preparation of training materials in their own domains of expertise and the compilation of these materials into an on-line repository.

*SP4CL2: Genetic Resources, Crop, and Genomic Information and Analysis Systems.* The consultation workshop will provide capacity-building for all CP partners by presenting state-of-the-art technology in genomics database and analysis software systems. As these systems are installed locally, training will be provided for local scientists and support staff.

**ADDITIONAL YEAR ONE ACTIVITIES.** In addition to a rapid launch of the technical and capacity-building activities, the Director will launch several other important dimensions of the Challenge Program in its first year. These include:

- 1) Formulation of a Stakeholders' Committee. Discussions are underway with GFAR as to the composition, activities and budget required for this committee to be effective;
- 2) Public awareness initiatives, including development of a Web site, placement of news releases in influential scientific and development periodicals, and presentations at important scientific and policy fora, such as the Plant and Animal Genome Conference, the International Crop Science Society meetings (Brisbane 2004), and the Annual General Meeting of the CGIAR;
- 3) Identification of additional sources of financial support for the Challenge Program. Austria has expressed an interest in contributing to the Program, USAID supports a Cereals Comparative Genomics Initiative that should be merged into the overall Challenge Program agenda, the Private Sector Committee of the CGIAR has expressed keen interest in developing major support from the private sector, and philanthropic foundations such as the Bill and Melinda Gates Foundation and the Kellogg Foundation will be approached inasmuch as their agendas are consistent with the Challenge Program's scope;
- 4) Recruitment of the Subprogram Leaders (See Appendix 7)
- 5) Conduct a joint intellectual property workshop for Subprogram Leaders with their Harvest Plus CP counterparts, led by CGIAR in-house intellectual property experts.
- 6) Launch of a competitive grants program;
- 7) Conduct an annual research progress meeting;
- 8) Undertake a progress review mandated by the CGIAR Executive Council.

#### **CHALLENGE PROGRAM ADMINISTRATION**

Managerial Support (Director's office)	\$350,000
Subprogram 5: Capacity-Building	\$350,000
Annual Progress meeting and PSC/PAC meetings (at AGM)	\$100,000
First Year Review	\$25,000
Stakeholders' Committee (meeting at AGM)	\$55,000
<b>TOTAL</b>	<b>\$880,000</b>

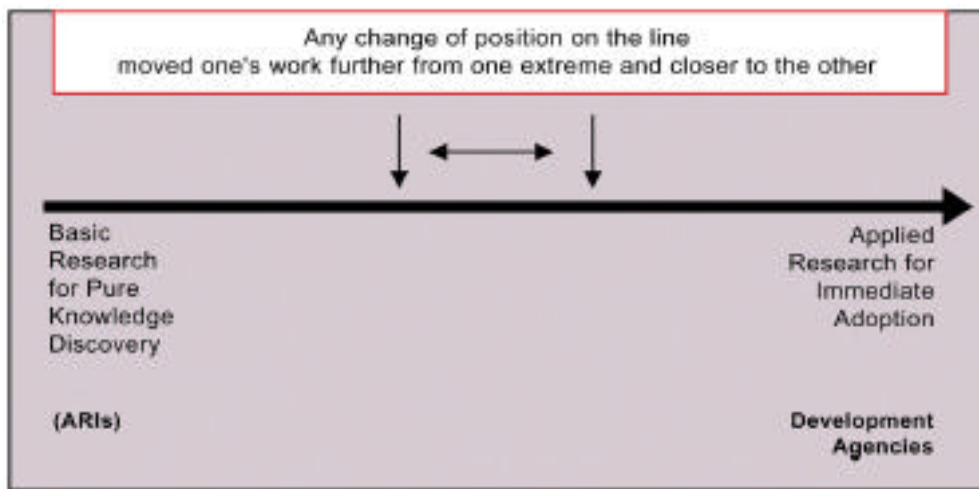


## BACKGROUND

### **BASIC SCIENCE *versus* DEVELOPMENT APPLICATIONS: A FALSE DICHOTOMY**

The modern agricultural innovation is firmly rooted in scientific discovery and the contributions made by the basic sciences. The revolution in physical chemistry and the synthesis of organic compounds in the 19<sup>th</sup> and 20<sup>th</sup> centuries allowed for the development of very inexpensive nitrogen fertilizers. The understanding of plant genetics permitted the founders of the “Green Revolution” to develop plants with an architecture, yield potential, and disease and insect resistance that allowed them to respond with high yields to the addition of nitrogen fertilizers. Yet from the period following the end of the Second World War there emerged a research paradigm that first implied, then enshrined, the idea that “basic” and “applied” research were at opposite ends of the research process—in other words, mutually exclusive. This dichotomy is illustrated in Figure 2:

**Figure 2.**

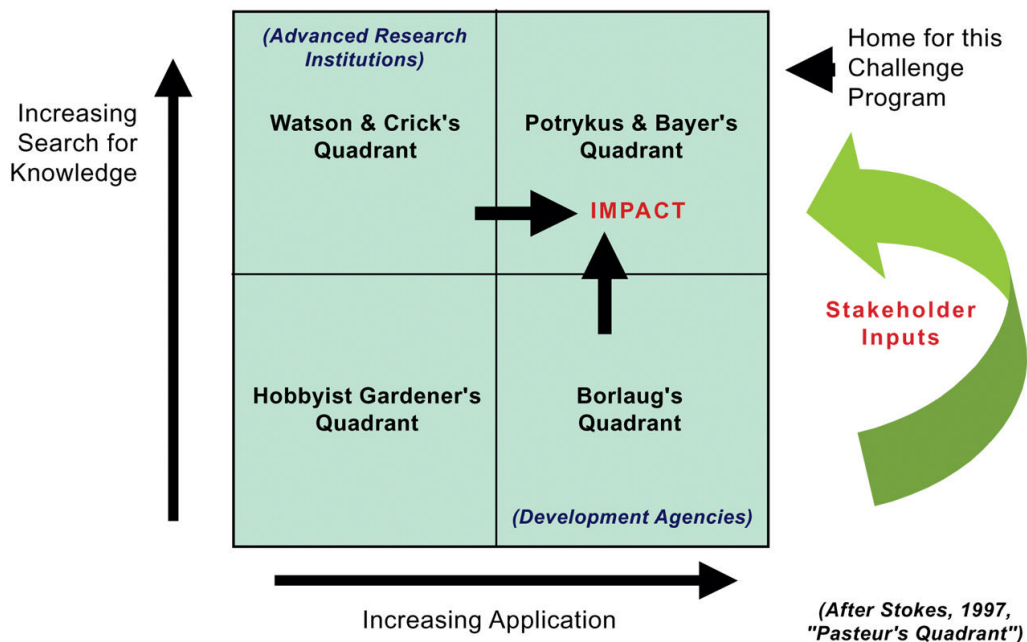


This flawed concept implies that as one moves towards basic research the work becomes decreasingly relevant to real world applications. Donald Stokes in his 1997 seminal work *Pasteur's Quadrant: Basic Science and Technological Innovation* illustrates how basic science and science directed to addressing real-world problems are independent but related processes. The Challenge Program for Unlocking Genetic Diversity in Crops for the Resource-Poor captures this insight and is illustrated in Figure 3, adapted from Stokes' work.

Only by directing cutting-edge plant biology, molecular genetics, and physiology towards the most complex and intractable problems confronting agriculture in developing countries can we expect to make progress. The upper right hand quadrant illustrates this convergence of application-driven research with research directed towards understanding basic biology. Stokes named this quadrant after Louis Pasteur, a practically oriented scientist who discovered numerous basic principles of biology that continue to shape the discipline more than a century after his death. For the purposes of this Challenge Program and for adopting a plant biology perspective, we can place the development of “golden rice” by Dr. Ingo Potrykus and Dr. Peter Bayer in this quadrant. Clearly they drew heavily on the basic scientific work exemplified by Watson and Crick, co-discoverers of the structure of DNA. Likewise Bayer and Potrykus draw upon the focus and the broadly

improved plant varieties—Borlaug’s Quadrant—to carry their “golden rice” traits to farmers’ fields, from where they will ultimately benefit hundreds of millions of the world’s poorest people.

**Figure 3.**



This model of scientific discovery and impact is at the heart of this Challenge Program. It reflects a truly revolutionary departure from the “business as usual” model of research both within CGIAR Centers and among the Advanced Research Institutions. The Challenge Programs were formed to create a new model for research that will allow the investments in the system to address the most serious problems facing mankind today by creating solutions that effectively combine high-quality, cutting-edge science with vehicles for delivering the products of that science to the people who need them most.

### **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 CGIAR Centers 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, and the development of this Challenge Program was motivated by these concerns:

- The rate of increase in potential and realized productivity of key crops under favorable 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.
- 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.
- Productivity gains for dryland cereals and grain legumes appear to be increasing and new technologies offer scope for further increases in genetic gain.

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.

The Challenge Program for 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—and with technology that remains in the public domain. Through this Challenge Program, 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 Challenge Program takes advantage of a timely opportunity: the genomics revolution is contributing very large quantities of information about biological systems, while the information revolution is providing unprecedented abilities to store, access, and process data. Together, they offer the ability to uncover new biological phenomena at the gene level and make that information 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.

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:

- 1) 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.
- 2) 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.

- 3) 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 key crops in marginal environments.

### **THE MISSION**

The Challenge Program for 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.

### **THE RATIONALE**

The publication in 2001 of two drafts of the human genome, the complete DNA sequence that encodes the instructions to build and operate a human 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 food crops in the service of agriculture for impoverished people.

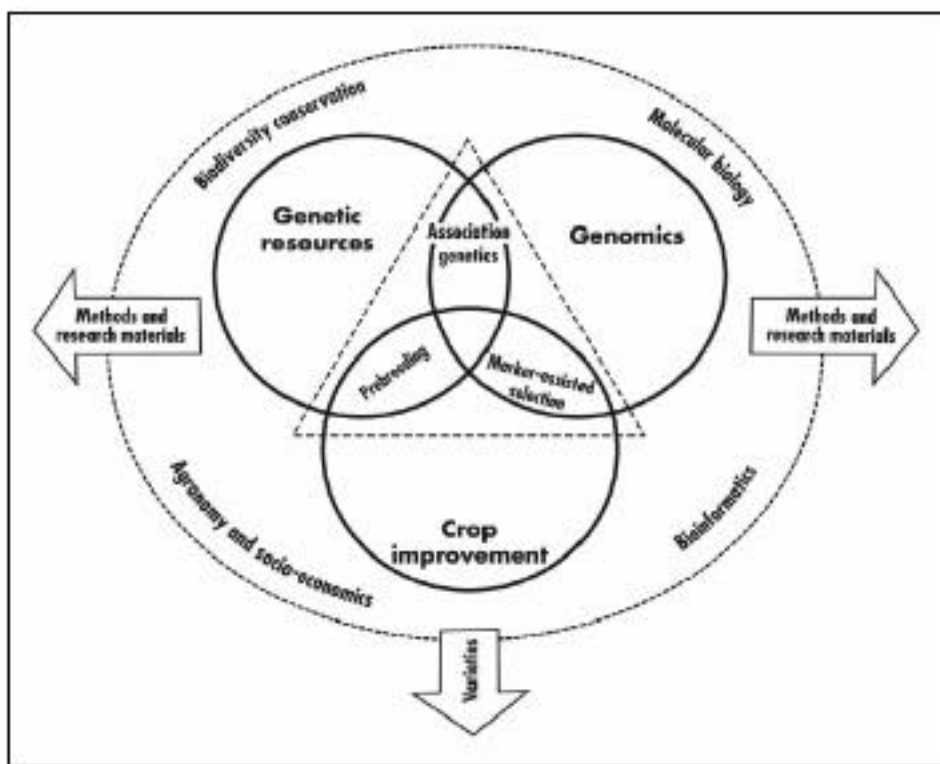
In some respects, agricultural scientists are in a better position than their biomedical colleagues to achieve their goals. Whereas medical scientists painstakingly have to acquire informative pedigrees that can be used to track the inheritance of genes of interest, the CGIAR Centers and NARS already 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 that is held in trust. The Centers alone currently conserve over 650,000 samples of landraces, traditional varieties, wild species, old cultivars, new cultivars under development, and breeding lines. 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 4).

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) 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.

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.

**Figure 4. Conceptual basis for the Challenge Program for Unlocking Genetic Diversity in Crops for the Resource-Poor.**



The three components of this 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.

## **PARTNERS**

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](http://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.

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.

# WORKPLAN DEVELOPMENT PROCESS

## PROGRAM ADJUSTMENTS

*Initial Program Design.* The concept note for the Challenge Program for Unlocking Genetic Diversity in Crops for the Resource-Poor was first presented to the AGM in October 2001. This Challenge Program was then selected as a Pilot Challenge Program along with the Water for Food and Biofortification Challenge Programs. The full program proposal was developed over the course of several meetings in 2002 and was submitted to the Interim Science Council (iSC) in July 2002. The iSC raised some questions about the business section of the proposal but gave a strong endorsement on the proposal's science and technical aspects. The Challenge Program proposal then went to ExCo and AGM (September and October 2002, respectively), at which concern on several issues in the document were raised, primarily related to adequate stakeholder participation in the program development. The ExCo wisely counseled more stakeholder consultation (described below). Though these consultations delayed the implementation of the Challenge Program, it was time well spent and will reap large rewards as the program develops.

*Stakeholders Meeting in Alexandria.* In January 2003, a UGDPCP stakeholders meeting was convened in Alexandria, Egypt, to address the concerns raised by ExCo and AGM. At that meeting, stakeholders discussed whether the scope and focus of the Challenge Program were appropriate; how to establish better partnerships with NARS, ARIs, and the private sector; how to incorporate better mechanisms for capacity-building; strategies for handling IP issues; competitive grants systems; and the governance structure of the Challenge Program. The resulting new draft proposal now incorporated all the mandate crops of the CGIAR system, added Capacity-Building as a separate but cross-cutting sub-program, expanded the Program Steering Committee to include GFAR and *ex officio* ExCo representation, and laid out numerous management recommendations (including parameters for a competitive grants program). The Challenge Program drafting team submitted a revised proposal to ExCo in February 2003 that reflected the outcomes of the Alexandria meeting and addressed ExCo's comments on the earlier draft. After another round of review, ExCo gave final endorsement of the Challenge Program proposal in late May 2003, and the CGIAR approved it in July. As of the CGIAR's approval, the World Bank had pledged US \$3M and the European Union had pledged 4M Euro per annum to the Challenge Program for Unlocking Genetic Diversity in Crops for the Resource-Poor.

## WORKPLAN DEVELOPMENT

*Technical Planning Workshop.* The Challenge Program held its Technical Planning Workshop in Wageningen, the Netherlands, from 25-29 August 2003. More than 40 scientists from 15 participating institutes, ARIs, and NARS attended the workshop (Appendix 5), as well as representatives from GFAR and the Private Sector Committee. Through a collegial and collaborative process, the workshop participants developed a five-year agenda for the Challenge Program, objectives for the first year of work and an outline for the detailed first year workplans, guidelines for commissioned research, and comprehensive expectations of the Challenge Program Director and the Program Steering Committee. The Program Steering Committee met 1-2 September in Wageningen, where they endorsed the outputs of the Technical Planning Workshop and established several committees to facilitate workplan development and oversee research once it gets underway.

At the Technical Planning Workshop, the five Subprograms of the Challenge Program were further segmented into "research clusters." Fourteen total, each research cluster was assigned a cluster lead (one of the workshop participants) to head up the discussion and development of a detailed first



year workplan over email in the coming months. First drafts of the workplans were due 7 October. The cluster leads dedicated immense amounts of time and energy to maintaining the collegial spirit of the Technical Planning Workshop and developing comprehensive, collaborative workplans with all of the Challenge Program partners.

### **WORKPLAN REFINEMENT**

An external review panel reviewed the workplans from 13-17 October and sent them back to the cluster leads with comments and suggestions. The cluster leads incorporated the external review panel's comments where possible (while adhering to principles agreed upon at the Technical Planning Workshop) and submitted their final workplans on 24 October. Once the Subprogram Leaders (SPLs) are in place—we aim to have them on board by mid-January 2004—there will be further opportunity for review and adjustments to the first year workplans. In the future, the Challenge Program's research and development will be directed by the four SPLs under the management of the Challenge Program Director (who will also serve as the leader for the fifth sub-program, Capacity Building).

The Challenge Program for Unlocking Genetic Diversity in Crops for the Resource-Poor got a later start—nine months later, in fact—than the other two pilot Challenge Programs, but the Challenge Program participants are enthusiastic about and dedicated to a strong first year for this Challenge Program. Although there was limited time to develop the first year workplans, the participating institutes have been receptive to external review of the workplans and flexible about redistributing funds and rearranging research activities when necessary to accommodate important scientific or application considerations.

### **DIRECTOR RECRUITMENT**

The process for the CP Program Director selection and terms of reference were agreed upon at the Stakeholders Meeting in Alexandria. Immediately after the final Challenge Program approval from the ExCo an international search was initiated and a search committee formed. The search committee consisted of Masa Iwanaga of CIMMYT; Desiree Hautea of the Institute for Plant Breeding at the University of the Philippines; Zhihua Ye of CAAS; Yves Savidan of Agropolis; and Hubert Zandstra of CIP. The search process included notification of institutions in the broader CGIAR stakeholder community, publication of the announcement in prestigious journals (*Nature* and *The Economist*), and newsletters of professional societies. Three top candidates were invited for interview at IPGRI, immediately following the PSC meeting in early September. The top candidate, Robert Zeigler, was offered and accepted the position and will formally assume the position on 15 December 2003. He will be hosted by CIMMYT.

### **SUB-PROGRAM LEADER RECRUITMENT**

The management team of the Challenge Program will be made up of the Director and four Sub-Program Leaders. The Sub-Program Leaders are currently under recruitment (see Appendix 7 for the terms of reference for their responsibilities and the process by which they will be selected).

### **LESSONS LEARNED**

Among the many lessons learned in the development of this Challenge Program, four categories stand out: process, science, governance and management, and resources.

*Process.* At the earliest stages of proposal development, there were negative feelings among some key stakeholders about the process. Some felt excluded from the process, and some felt that key resources were migrating or being directed away from what they felt were integral aspects of this Challenge Program. Some worried that the heavy focus on a science framework came at the expense of due process among Challenge Program partners and stakeholders. Also, the sheer size and scope of this Challenge Program is uncharted territory for molecular biologists and geneticists,

which presented challenges as well. Wide participation in the development of the proposal was clearly essential, but a common vision (for instance, drought tolerance as proof-of-concept) was not easily achieved among such a diverse group of partners and stakeholders. In addition, this Challenge Program was delayed nine months, but the delay afforded the CP team ample time to engage disgruntled or previously uninvolved stakeholders.

*Science.* In the arena of science, the UGDCP encountered several challenges. Many CGIAR centers count their gene collections as sources of intense pride, so where to locate the Challenge Program leadership was a difficult decision. Navigating the perceptions among scientists and stakeholders—and the general public—of genomics, genetic modification, and the concept of a “science-driven” agricultural development program was also a difficult task. The UGDCP encompasses some of the most contentious scientific issues of our era: GMOs, public-private sector interactions, and IPR management, among others. The mission to develop a public platform for the products of the UGDCP has also proved easier said than done. But the excitement among partner scientists has been palpable throughout the development of the UGDCP. The power of comparative biology and enhanced utilization of genetic potential are compelling arguments to move a program such as the UGDCP forward.

*Governance and Management.* The UGDCP has three lead centers—IPGRI, IRRI, and CIMMYT—which has helped ensure its success so far. As the Host Center, CIMMYT is responsible for the UGDCP’s finances, as well as IP management. The Program Steering Committee includes not only representatives from the various CG centers, ARIs, and NARS partners, but also from GFAR. The Program Director’s role has taken on increasing importance as the UGDCP has developed, as has the involvement of other stakeholders, such as the private sector and small NARS. Concerns over transaction costs have arisen as well.

*Resources.* The quest for new non-traditional resources versus redirection of traditional funds translated into a slow start for the UGDCP, and meant that the Challenge Program had to confront early on the perceptions of biotechnology as well as issues related to adopting a program that was so close to the “heartland” of the CGIAR system. That is, there is possible inherent conflict between maintaining adequate funding for ongoing essential activities related to genetic resources and crop improvement and generating new financial support for this Challenge Program. The private sector will be a key provider of proprietary technologies and other in-kind support (e.g., capacity building). An important lesson learned is that it is imperative that the UGDCP be specific in its requests of the private sector. The other Challenge Programs will also be an important resource for the UGDCP, in terms of sharing of experiences, ideas, results, and strategies for handling IPR, public relations and communications, and resource mobilization.

## SUBPROGRAM BUDGET SUMMARIES

This section breaks down in more detail the budgets by Subprogram as they relate to deliverables, activities, institutions, and crops, as appropriate. The overall budget will be reviewed by the Program Director and the Subprogram Leaders in the first quarter of the year. This informal assessment will identify potential cost-saving measures, such as combined workshops and meetings. Only modest adjustments, if any, to the technical aspects of the work plan should occur. Detailed cluster work plans have been compiled into a final document, which is available upon request.



## **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. 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.

An important 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. Thus, this Subprogram will make a major contribution to the main objective of the Challenge Program: 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.

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 analyzed 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 consistent with overall CGIAR policies will be developed that ensures NARS have ready access to technologies and products arising from the Challenge Program (Cluster 4).

*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).

## Sub-Program 1: Genetic Diversity of Global Genetic Resources

Cluster 1: Composite Genotype Sets																				
Year 1 Deliverables	Activities	Budget	Agropolis	CAAS	CIAT	CIMMYT	CIP	Cornell	EMBRAPA	ICARDA	ICRISAT	IITA	IPGRI	IRRI	JIC	NIAS	WUR	WARDA	CAS	INIBAP
1) 11 Composite Collection data sets, delivered to SP4 for integration with experimental data and publication through CGIAR websites; 2) 11 primary Composite Collections maintained as seed (wheat, barley, sorghum, maize, rice, cowpea, common bean, chickpea) or plants or tissue (cassava, potato, and Musa) ready for use to DNA extraction for main studies; and 3) 3 mini-composite collections maintained as seed (cowpea) or plants or tissue (potato and Musa) ready for use for DNA extraction for pilot studies.	1) Assemble data on global collections.	\$135,110	X	X	X	X	X		X	X	X	X	X	X				X		X
	2) Identify germplasm selection criteria and methodology.	\$51,083	X	X	X	X	X		X	X	X	X	X	X						X
	3) Analyze data.	\$125,337	X	X	X	X	X		X	X	X	X	X	X						X
	4) Select germplasm for inclusion in composite collection.	\$88,470	X	X	X	X	X		X	X	X	X	X	X				X		X
TOTAL		\$400,000																		
Cluster 2: Collection of Marker Sets/Genotyping/Data Analysis																				
Year 1 Deliverables	Activities	Budget	Agropolis	CAAS	CIAT	CIMMYT	CIP	Cornell	EMBRAPA	ICARDA	ICRISAT	IITA	IPGRI	IRRI	JIC	NIAS	WUR	WARDA	CAS	INIBAP
1) Marker technologies and reliable marker sets selected for barley, cassava, chickpea, common bean, cowpea, maize, Musa, potato, rice, sorghum and wheat; 2) 19,462 accessions genotyped; 3) At least 822,600 marker data available as follows; 4) Diversity analyses accomplished on the collected crop datasets; 5) At least 25 NARS scientists trained in genotyping and data analysis at consortium members' laboratories; 6) 10-12 NARS centers of excellence selected to serve as hubs for training and capacity building activities to address the needs identified in all regions; 7) At least twenty NARS (users) invited for a needs assessment exercise in the relevant areas of the different subprogrammes (genetic diversity analysis with molecular data, comparative genetics and genomics, gene transfer and crop improvement, and crop information systems); and 8) Effective collaboration established between CGIAR centers, ARIs and NARS both inside and outside the CP consortium.	1) Collection of marker sets	\$95,343	X	X	X	X	X				X	X	X							X
	2) Genotyping	\$1,336,331	X	X	X	X	X			X	X	X	X	X						X
	3) Data analysis	\$568,322	X	X	X	X	X				X	X	X	X	X					
TOTAL		\$2,000,000																		
Cluster 3: Phenotyping Protocol Workshop																				
Year 1 Deliverables	Activities	Budget	Agropolis	CAAS	CIAT	CIMMYT	CIP	Cornell	EMBRAPA	ICARDA	ICRISAT	IITA	IPGRI	IRRI	JIC	NIAS	WUR	WARDA	CAS	INIBAP
Present and discuss phenotypic screening protocols to evaluate plant phenotype under drought conditions.	1) One week workshop	\$100,000	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X		

Cluster 4: IP/ABS -- Policy Research																				
Year 1 Deliverables	Activities	Budget	Agropolis	CAAS	CIAT	CIMMYT	CIP	Cornell	EMBRAPA	ICARDA	ICRISAT	IITA	IPGRI	IRRI	JIC	NIAS	WUR	WARDA	CAS	INIBAP
1) Develop various policy briefs from research and workshop reports for use by the CP in working to establish institutional policies; 2) Lay the foundation for a wider policy discussion with stakeholders outside the CP consortium, including the private sector, national policy makers, and NGOs; and 3) Work toward establishing a "gold standard" for biotechnology policy issues to ensure that the resource-poor gain and retain access to genetic resources and biological products relevant to them.	1) Define "resource-poor" for CP context.	\$13,000	X										X						X	
	2) Analyze opportunities for humanitarian licenses.	\$16,000				X								X					X	
	3) Analyze liability and stewardship issues in client/partner countries.	\$25,000				X											X		X	
	4) Analyze other IP mechanisms and concepts as they relate to the CP.	\$24,000											X				X		X	
	5) Develop a framework for addressing benefit-sharing issues at a global and case-specific level.	\$25,000											X					X		X
	6) Analyze national access legislation and international guidelines in regards to their implications for the CP.	\$28,000								X		X		X						X
	7) Analyze the impact of IPR on institutions, the seed sector, and smallholder farmers in developing countries.	\$0*																X		
	8) Analyze the implications of access and benefit sharing regulations for the conservation and use of genetic resources.	\$0*												X						
	9) Genetic Resources Policy Initiative -- analyze options for genetic resources policies by/in developing countries.	\$0*												X						
	10) Joint policy workshop to improve on draft reports.	\$53,000		X		X	X			X		X		X	X	X		X		X
	Not yet allocated	\$16,000																		
	TOTAL	\$200,000																		

\* in-kind contribution

Budget by crop, where applicable:

CROP	SP1CL1	SP1CL2
Barley	\$ 37,151	\$ 41,000
Wheat	\$ 26,298	\$ 207,944
Maize	\$ 14,717	\$ 238,000
Sorghum	\$ 38,617	\$ 100,997
Rice	\$ 47,819	\$ 206,000
Millet		
Common bean	\$ 42,189	\$ 201,000
Chickpea	\$ 38,589	\$ 34,724
Cowpea	\$ 37,148	\$ 212,000
Cassava	\$ 40,505	\$ 206,000
Potato	\$ 39,848	\$ 122,000
Musa	\$ 37,117	\$ 130,000



## **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. 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.

**Sub-Program 2: Comparative Genomics for Gene Discovery**

<b>Cluster 1: Germplasm Evaluation</b>																			
<b>Year 1 Deliverables</b>	<b>Activities</b>	<b>Budget</b>	<b>Agropolis</b>	<b>CAAS</b>	<b>CIAT</b>	<b>CIMMYT</b>	<b>CIP</b>	<b>Cornell</b>	<b>EMBRAPA</b>	<b>ICARDA</b>	<b>ICRISAT</b>	<b>IITA</b>	<b>IPGRI</b>	<b>IRRI</b>	<b>JIC</b>	<b>NIAS</b>	<b>WUR</b>	<b>WARDA</b>	<b>INIBAP</b>
1) A broad set of well-characterized germplasm under water-limited conditions. 2) The selection of suitable genotypes for genetic studies. 3) An updated list of target traits (within and across genomes) plus related protocols involved in the drought tolerance process. 4) The selection of recipient or donor lines for marker-assisted selection. 5) A methodology for the design of field and greenhouse experiments.	1) Phenotypic characterization of core collections conserved ex situ in genebanks or in situ in breeding programs.	\$172,900	X	X	X	X			X	X		X		X					
	2) Detailed phenotypic characterisation of selected lines and populations that will serve as the base for genetic studies.	\$95,800	X		X	X	X			X	X			X					
	3) Adoption and evaluation of screening protocols.	\$31,300	X		X			X		X					X				
<b>TOTAL</b>		<b>\$300,000</b>																	
<b>Cluster 2: Marker Development</b>																			
<b>Year 1 Deliverables</b>	<b>Activities</b>	<b>Budget</b>	<b>Agropolis</b>	<b>CAAS</b>	<b>CIAT</b>	<b>CIMMYT</b>	<b>CIP</b>	<b>Cornell</b>	<b>EMBRAPA</b>	<b>ICARDA</b>	<b>ICRISAT</b>	<b>IITA</b>	<b>IPGRI</b>	<b>IRRI</b>	<b>JIC</b>	<b>NIAS</b>	<b>WUR</b>	<b>WARDA</b>	<b>INIBAP</b>
1) Concise recommendations on two promising strategies for the development of universal anchor markers for conserved orthologous sets of genes for use across monocots, across dicots, and if possible between monocots and dicots; 2) Algorithms for extraction of candidate sequences for conserved genes from EST databases tested and shared (with SP2C3 and SP4); 3) probes, primers, and sequence data corresponding to sets of universal markers for use in monocots and dicots; 4) comparative maps of selected dicots and monocots enhanced with 20 COS or conserved EST/SSR markers each; 5) comparative maps of banana enhanced with orthologues from rice/sorghum; and 6) together with other SP2 work clusters, SP2C2 will contribute to the assembly and documentation of candidate gene collections for drought resistance-related pathways.	1) Test and validate COS and other consensus markers as tools to develop and enhance comparative maps within and across crop families.	\$170,141		X	X		X		X	X		X		X					X
	2) Extract and assemble sets of putative orthologous candidate genes for drought resistance from existing genome resources to enhance gene discovery		\$119,859		X	X		X			X		X		X				
<b>TOTAL</b>		<b>\$291,225</b>																	
<b>Cluster 3: Gene Expression Profiling</b>																			
<b>Year 1 Deliverables</b>	<b>Activities</b>	<b>Budget</b>	<b>Agropolis</b>	<b>CAAS</b>	<b>CIAT</b>	<b>CIMMYT</b>	<b>CIP</b>	<b>Cornell</b>	<b>EMBRAPA</b>	<b>ICARDA</b>	<b>ICRISAT</b>	<b>IITA</b>	<b>IPGRI</b>	<b>IRRI</b>	<b>JIC</b>	<b>NIAS</b>	<b>WUR</b>	<b>WARDA</b>	<b>INIBAP</b>
1) Sets of genes involved in plant response to water-limited conditions, with special emphasis on few target pathways; 2) Sets of genes representing changes in expression within and across genomes identified from profiling experiments conducted on a panel of appropriate genotypes; 3) Candidate stress-related genes provided for mapping (in silico mapping or binning in QTL regions); 4) Feasibility of a common gene expression platform for monocot or dicot evaluated; 5) In conjunction with "Marker Development" cluster in SP2, a set of conserved candidate genes for stress response established as diagnostic markers--providing a source of conserved anchor markers for germplasm characterization in SP1; 6) EST libraries produced for several species under stress conditions; and 7) Researchers at different participating labs trained in gene expression technologies.	1) Consolidate available gene/sequence data for stress-response pathways.	\$24,000												X		X	X		
	2) Compare expression profiles of selected genetic stocks under stress.	\$196,000		X		X	X			X				X		X	X		
	3) Resource development (millet, cassava, bean, and cowpea).	\$60,000				X							X	X					
<b>TOTAL</b>		<b>\$280,000</b>																	

Cluster 4: QTL Analysis																				
Year 1 Deliverables	Activities	Budget	Agropolis	CAAS	CIAT	CIMMYT	CIP	Cornell	EMBRAPA	ICARDA	ICRISAT	IITA	IPGRI	IRRI	JIC	NIAS	WUR	WARDA	INIBAP	
1) QTL locations and importance for DT-related traits on various genetic maps, with comparison with existing or in-CO generated data; 2) Molecular markers for the selection of DT identified for marker-assisted selection programs; 3) DT-related phenotypic data on segregating populations; 4) DT-interesting segregating population made available to the scientific community; 5) Molecular marker-based genetic maps completed for DT-segregating populations (wet lab or <i>in silico</i> ); 6) Delivering of an exhaustive inventory of the information publicly available about DT-QTL locations on crop genetic maps; 7) Meta-analyses of QTL positions; 8) Geographical genotyping of interspecific population and localization of chromosomal fragments linked to DT; 9) Comparative mapping with reference genomes; 10) Co-localization of DT-QTLs and candidate genes for DT; and 11) Screening techniques validated for DT in segregating populations.	1) Acquisition of DT-relative phenotypic data on segregating populations useful for gene/QTL mapping.	\$77,164	X		X	X			X			X		X			X	X		
	2) Completion of genetic maps based populations segregating for DT.	\$62,658	X		X															X
	3) Comparative analysis of genotypic/phenotypic data to infer gene/QTL for DT positions on crop genetic maps.	\$																		
	4) Initiate an exhaustive data mining of the information publicly available about DT-QTL locations on different crop genetic maps.	\$20,178	X			X														
TOTAL		\$160,000																		

Budget by crop, where applicable:

CROP	SP2CL1	SP2CL2	SP2CL3
Barley	\$ 9,300	\$10,816.67	\$ 31666.67**
Wheat	\$ 34,300	\$76,424.66	\$ 31666.67**
Maize	\$ 28,000		\$ 40,000.00
Sorghum	\$ 27,400		
Rice	\$ 54,700	\$32,037.00	\$ 31666.67**
Millet			
Common bean	\$ 25,400	\$16,284.00	\$ 25,000.00
Chickpea	\$ 22,800	\$10,816.67	
Cowpea	\$ 21,000	\$16,284.00	
Cassava	\$ 43,500	\$32,568.00	\$ 20,000.00
Potato	\$ 23,600	\$64,900.00	\$ 41,000.00
Musa	\$ 10,000	\$31,093.00	

\*\*Comparative expression analysis of drought response in rice-wheat-barley using rice gene chip as a common platform.

**NOTE: SP2CL3 also includes cross-genome experiments and *Arabidopsis* analysis not accounted for under the crops listed in this table.**

### **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 utilizing 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.

### Sub-Program 3: Gene Transfer and Crop Improvement

#### Cluster 1: Training Workshop on Marker-Assisted Selection/Breeding

Year 1 Deliverables	Activities	Budget	Agropolis	CAAS	CIAT	CIMMYT	CIP	Cornell	EMBRAPA	ICARDA	ICRISAT	IITA	IPGRI	IRRI	JIC	NIAS	WUR	WARDA	INIBAP
1) NARS capacity strengthened by training 40 NARS staff in MAS/B approaches; 2) 10 proposals developed, based on case studies involving different crops, such as rice, sorghum, millet, chickpeas, maize, cassava, beans, cowpea, Musa, potato and yams; and 3) The proposals will further form the basis for competitive grants.	1) Coordination of training workshop.	\$10,000										X							
	2) Participation in training workshops.	\$187,000	X	X	X	X	X	X	X	X	X	X	X		X	X	X		
TOTAL		\$197,000																	

\*\$50,000 from available Challenge Program funds; additional funds to cover costs of workshop are being sought from donors.

#### Cluster 2: Marker-Assisted Selection

Year 1 Deliverables	Activities	Budget	Agropolis	CAAS	CIAT	CIMMYT	CIP	Cornell	EMBRAPA	ICARDA	ICRISAT	IITA	IPGRI	IRRI	JIC	NIAS	WUR	WARDA	INIBAP
1) Advanced species (maize, pearl millet, sorghum, and rice): additional existing markers identified and tested. Protocols established and documented for testing available markers; 2) Intermediate species (bean, chickpea, and cowpea): markers identified; and 3) Latecomers (cassava): mapping population development initiated.	1) Millet: Marker-assisted backcrossing of putative QTLs for terminal drought tolerance	\$46,800			X						X	X							
	2) Maize: Quantification of changes in allelic frequency in 5 maize OPVs and MAS at the 22 loci based on a selection index and development of improved populations.	\$70,000	X			X						X							
	3) Sorghum: Marker-assisted backcrossing of stay-green component of terminal drought tolerance in sorghum.	\$46,800				X						X	X						
	4) Rice: Combine drought tolerance and blast resistance.	\$46,480	X												X				
	5) African rice: Characterization of <i>O. glaberrima</i> genetic resources and utilization in marker assisted composite population breeding	\$19,470	X			X													
	6) Bean: Marker-assisted selection with available populations.	\$35,400				X				X									



Cluster 4: Recurrent Parents																			
Year 1 Deliverables	Activities	Budget	Agropolis	CAAS	CIAT	CIMMYT	CIP	Cornell	EMBRAPA	ICARDA	ICRISAT	IITA	IPGRI	IRRI	JIC	NIAS	WUR	WARDA	INIBAP
List of selected candidate recurrent parent cultivars from the three crop clusters, according to information available from consortium partners; e.g. multilocation evaluation trials, pedigrees, descriptor data and any other information from experiments (both on-station and on-farm).	Compile list of recurrent parents	\$50,000			X	X	X				X	X	X		X				
	TOTAL	\$50,000																	

Budget by crop, where applicable:

CROP	SP3CL2	SP3CL4
Barley		\$4,000
Wheat		\$4,000
Maize	\$70,000	\$4,000
Sorghum	\$46,800	\$4,000
Rice	\$86,480	\$4,000
Millet	\$46,800	
Common bean	\$35,400	\$4,000
Chickpea	\$20,300	\$4,000
Cowpea	\$49,056	\$4,000
Cassava	\$15,694	\$4,000
Potato		\$4,000
<i>Musa</i>		\$4,000



**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.

Sub-Program 4: Genetic Resources, Genomic, and Crop Information Resources																	
Cluster 1: Expert Network																	
Year 1 Deliverables	Activities	Budget	Agropolis	CAAS	CIAT	CIMMYT	CIP	Cornell	EMBRAPA	ICARDA	ICRISAT	IITA	IPGRI	IRRI	JIC	NIAS	WUR
1) Link informatics specialists at all UGDCP partner sites with adequate time commitment to UGDCP; 2) Develop policy and guidelines on how informatics activities of the UGDCP should be conducted, including guidelines for the implementation of data standards, quality control, and software development and sharing; 3) Develop an operational framework and commission project to coordinate infrastructure and collaboration tools; 4) Integrate informatics specialists into a team of experts to manage informatics projects and provide technical expertise; 5) Define technical parameters for practical implementation of UGDCP policies on data ownership, access, and security; 6) Provide support for the deployment of enhanced IT infrastructure at appropriate sites; 7) Provide support for the commissioning or harmonization of LIMS at genetic resources characterization sites of the UGDCP; and 8) Develop a plan for informatics training for CP partners and external collaborators.	1) Identify informatics staff.	\$400,020			X	X	X			X	X	X	X	X			
	2) Develop informatics policies & guidelines.	\$4,720	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	3) Host virtual environment.	\$35,400											X				
	4) Network liaison, management & technical consultation.	\$58,360	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	5) Bioinformatics research.	\$94,400				X	X	X						X	X	X	X
	6) Local informatics support.	\$76,400			X	X	X			X	X	X	X	X			
	7) Design and develop informatics platform.	\$ -	X	X	X	X	X	X	X	X	X	X	X	X	X	X	X
	8) Specify and deploy shared high capacity computing.	\$141,600						X				X			X		
	9) Specify and deploy LIMS.	\$136,000				X	X	X			X	X	X	X	X		
	10) Review, develop, and deliver training.	\$53,100						X				X		X	X		
TOTAL	\$1,000,000																

Cluster 2: Genetic Resources, Crop, and Genomic Information and Analysis Systems																	
Year 1 Deliverables	Activities	Budget	Agropolis	CAAS	CIAT	CIMMYT	CIP	Cornell	EMBRAPA	ICARDA	ICRISAT	IITA	IPGRI	IRRI	JIC	NIAS	WUR
1) White papers produced in collaboration with ICT-KM project on data standards; 2) Workshop to review white papers and reach consensus on information systems issues; 3) Standards developed in the areas of germplasm documentation, fingerprinting/allele data, mapping data, functional genomics data, and data exchange and interoperability; 4) a decentralized information network linking germplasm and molecular information designed and prototyped for initial CP data; 5) ensure linkages between the CP information network and SINGER and other systems where relevant; 6) 3 CP partners' germplasm information networks integrated into a prototype CP network; and 7) 7 CP partners' information systems upgraded to meet the standards criteria needed for later integration into CP information network.	1) Evaluation of needs and options for genomics information and analysis systems.	\$60,180	X	X	X	X	X	X		X	X	X	X	X	X		X
	2) Consultation: evaluation of needs and options.	\$192,300	X		X	X	X	X	X	X	X	X	X	X	X	X	X
	3) Design of germplasm information systems and interoperability according to agreed specifications.	\$67,250	X	X	X	X	X			X	X	X	X	X	X		
	4) Implementation of agreed strategy for CP partners germplasm information systems.	\$680,270	X	X	X	X	X	X		X	X	X	X	X	X		
	TOTAL	\$1,000,000															

### **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.

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. The specific capacity building activities that have been built into the first 4 Subprograms are summarized as follows:

*SPICLI: Composite Genotype Sets.* The process of constructing the composite collections will significantly enhance expertise and understanding of methodologies for the formation of targeted core collections. NARS involved in compilation of composite collections include: National Bureau

of Plant Genetic Resources of India (in collaboration with ICRISAT); National Plant Genetic Resources of Syria and Jordan (in collaboration with ICARDA); NARS scientists and students from Peru (in collaboration with CIP); and 2-3 NARS scientists will be trained (through CIAT).

*SP1CL2: Collection of Marker Sets/Genotyping/Data Analysis.*

- Cassava: Two NARS scientists from developing countries will genotype accessions using Dart markers at CAMBIA (CIAT/IPGRI). At IITA, a laboratory technician and database manager will be trained in data capture and automated fragment analysis at IITA's Plant Biodiversity Genomic Facility in Kenya.
- Chickpea: Two NARS scientist (India and Syria) will be trained in genotyping as well as data analysis.
- Common bean: NARS scientists from Bolivia, Colombia, and Mexico (and likely Kenya) will be trained in fluorescent microsatellite technology with lab exchanges between these institutions to standardize technology (CIAT/EMBRAPA).
- Cowpea: Two technicians and a database manager will be trained under the cowpea project (IITA).
- Maize: A technician would be appointed at IITA to assist in collation of data and training in molecular characterization at CIMMYT.
- *Musa*: A researcher/technician from a NARS will do genotyping and analysis at CIRAD-Montpellier. A training course will be organized at IAEA on the use of microsatellite markers for 5-10 NARS participants.
- Potato: NARS training in SSR analysis and database development.
- Rice: Visiting scientist from NARS collaborator appointed for genotyping work. Workshop on application of high-throughput genomic technologies for identification of induced and natural variation in stress-related genes training in collaboration with ARBN. NARS scientists from Colombia and Brazil will be appointed to genotype rice accessions using high-throughput fluorescent SSR markers (IRRI and CIAT).
- Sorghum: Training of 3 NARS scientists (Agropolis/CAAS/ICRISAT).
- Wheat: Training of NARS scientists at INRA Clermont and Montpellier in automatic sequencer genotyping technology and data analysis.

*SP1CL3: Phenotyping Protocol Workshop.* This workshop will establish a network to ensure that ideas and knowledge flow among those partners actively involved in the evaluation of drought tolerance for different crops for the UGDCP.

*SP1CL4: IP/ABS – Policy Research.* This joint workshop will improve upon all draft reports of all projects in this cluster. The workshop will include several stakeholders within and outside the consortium.

*SP2CL1: Germplasm Evaluation.*

- Agropolis: One Senegalese MS student to participate in the project on sorghum.
- CIAT: Involvement of national scientist(s) from INTA, Nicaragua, on bean project; collaboration with EMBRAPA on cassava; and joint project on rice with EMBRAPA and CORPOICA in which scientific personnel from CORPOICA/Fedearroz will be trained.
- CIMMYT: Students from Africa will visit the Applied Biotechnology Center at CIMMYT and possibly INRA (Montpellier) during the first year. The students will be trained in maize germplasm evaluation at morphological and physiological levels. In wheat, one IAEA visiting scientist will be trained as part of a hands-on training exercise.
- ICRISAT: 2-week introductory training course in QTL mapping techniques to be led by ICRISAT biometrician. A 1-week international training course on multi-location trials for the improvement of abiotic stress tolerance in chickpea will also be held, in conjunction with IAEA.

- ICARDA: Visiting scientists and students from WANA will visit ICARDA wheat breeding program and barley improvement program to be trained on stress physiological screening techniques.
- IITA: Graduate students and visiting scientists from NARS of participating in African countries will participate on cassava project. A graduate student from one of the universities around Ibadan will be involved in the screening and genetic diversity study on cowpea.
- IRRI: Requested funding will support the training of a graduate student from a national program affiliated with IRRI's rice drought breeding effort.

*SP2CL2: Marker Development.* University students will be employed to develop thesis research in bioinformatics applied to marker development. Funding for a CAAS scholar is being requested in SP4 to backstop bioinformatics needs and help assure links between SP2CL2 and SP4. Partial funding for a scholar in bioinformatics and his/her travel in Latin America is requested in CIP budget, to collaborate with Cornell University (solanaceae/dicots) and CIAT (legumes/dicots), in communication with the scholar at CAAS and SP4. Visiting scientists from developing countries are expected to visit INIBAP and partners for a structured program of research and training in marker development for 3 months each.

*SP2CL3: Gene Expression Profiling.* Students and visiting scientists from NARS will receive training in the use of functional genomics techniques, including comprehensive data analysis, at CIMMYT. In addition, researchers from some CG centers not previously exposed to the gene expression technologies will be trained, as will postdoctorals and students from NARS.

*SP2CLA: QTL Analysis.*

- Cassava: A Thai scientist from the national cassava breeding program will be trained in QTL mapping at CIAT.
- Common bean: An undergraduate student will be trained at CIAT as part of the common bean component of this cluster.
- Musa: An MS student, working under a joint agreement with the University of Nsuuka and IITA, will perform data collection at the Nigerian sites of the University of Nsuuka, and a MS Student working under a joint agreement with the University of Makerere, Uganda, and IITA, will perform data collection in a highland field site in Uganda.
- Rice:
  - 2 MS students to work on the project at Agropolis.
  - 1 PhD student at IRRI in drought tolerance for rice.
  - Collaboration with the experts in UAS-India, RIABGR-Indonesia, IRRI, and WUR to develop an integrated concept of drought testing and mapping in rice.
- Sorghum: 1 MS student to participate in the project on sorghum at Agropolis.

*SP3CL1: MAS Workshop.* The main objective of the workshop is for capacity building among NARS in the area of MAS/B.

*SP3CL2: Marker-Assisted Selection/Breeding.*

- Rice: Pyramided introgression lines in IR64 will be genotyped by a visiting research fellow from NDUAT, Uttar Pradesh, India, who will also assist in field phenotyping. Genotyping of the IR64/Azucena fine mapping population will be completed by a student from China, who is a student at University of the Philippines, Los Baños.
- Sorghum (ICRISAT): PhD students and visiting scientists from India and Africa (Ghana or Kenya) to participate in pearl millet project and receive training in SSR-marker-assisted backcross introgressions of particular traits important to pearl millet producers in their respective regions.

- Maize (CIMMYT-INRA-IITA): Students will receive training in MAS experiments on OPVs and quantification of changes in allelic frequency across cycle of selection, a key issue for germplasm improvement through biotechnological approaches in Africa.
- Cowpea (IITA): A visiting scientist from a Nigerian institution will be involved directly with the study.
- Cassava (IITA-CIAT): Outputs of this project will be included in the workshop on MAB and GM crops (SP3CL3).
- Bean (CIAT-EMBRAPA): Bean breeders from EMBRAPA and other NARS will be invited to be involved in all stages of marker-assisted selection and development of breeding populations for drought tolerance.
- African rice (CIAT-Agropolis): Technicians at CIAT will perform crosses and conduct recurrent selection and assist/conduct molecular characterization.

*SP3CL3: Crops with Appropriate Gene Technologies.* This workshop will identify appropriate gene technologies for asexually propagated crops and will involve significant NARS participation.

*SP4CL1: Informatics Expert Network.* The Informatics Team will develop a plan and establish partnerships with institutes and networks conducting capacity-building activities in the areas of genetic resources and molecular biology. In addition to the explicit output of developing a training plan for informatics in the UGDCP, a fundamental role for all members of the network will be the identification and preparation of training materials in their own domains of expertise and the compilation of these materials into an on-line repository.

*SP4CL2: Genetic Resources, Crop, and Genomic Information and Analysis Systems.* The consultation workshop will provide capacity-building for all CP partners by presenting state-of-the-art technology in genomics database and analysis software systems. As these systems are installed locally, training will be provided for local scientists and support staff.

## **NEXT STEPS**

In addition to a rapid launch of the technical and capacity building activities, the Director and Subprogram Leaders will launch several other important dimensions of the Challenge Program. These will include:

- 1) Formulation of a Stakeholders' Committee. Discussions are underway with GFAR as to the composition, activities and budget required for this committee to be effective;
- 2) Public awareness initiatives, including development of a Web site, placement of news releases in influential scientific and development periodicals, and presentations at important scientific and policy fora, such as the Plant and Animal Genome Conference, the International Crop Science Society meetings (Brisbane 2004) and the Annual General Meeting of the CGIAR;
- 3) Identification of additional sources of financial support for the Challenge Program. Austria has expressed an interest in contributing to the Program, USAID supports a Cereals Comparative Genomics Initiative that should be merged into the overall Challenge Program agenda, the Private Sector Committee of the CGIAR has expressed keen interest in developing major support from the private sector, and philanthropic foundations such as the Bill and Melinda Gates Foundation and the Kellogg Foundation will be approached inasmuch as their agendas are consistent with the Challenge Program's scope;
- 4) Recruitment of the Subprogram Leaders (See Appendix )
- 5) Conduct a joint intellectual property workshop for Subprogram Leaders with their Harvest Plus CP counterparts, led by CGIAR in-house intellectual property experts.
- 6) Launch of a competitive grants program;
- 7) Conduct an annual research progress meeting;
- 8) Undertake a progress review mandated by the CGIAR Executive Council.

# APPENDIX 1

## Program Steering Committee Members

#	LAST NAME	FIRST NAME	ORGANIZATION	COUNTRY
1	Serageldin	Ismail	PSC Chair	Egypt
2	Savidan	Yves	Agropolis	France
3	Ye	Zhihua	CAAS	China
4	Pachico	Douglas	CIAT	Colombia
5	Iwanaga	Masa	CIMMYT	Mexico
6	Kresovich	Stephen	Cornell	U.S.
7	Zandstra	Hubert	CIP	Peru
8	Vialatte*	Phillipe	ExCo	France
9	Eugenio de França	José Geraldo	EMBRAPA	Brazil
10	Erskine	William	ICARDA	Turkey
11	Keatinge	Dyno	ICRISAT	India
12	Ortiz	Rodomiro	IITA	Nigeria
13	Frison	Emile	IPGRI	Italy
14	Cantrell	Ron	IRRI	Philippines
15	Hirochika	Hirohiko	NIAS	Japan
16	Louwaars	Niels	Wageningen	Netherlands
17	Smith	Olanrewaju	GFAR	Italy
18	Snape	John	John Innes Centre	UK
19	Zeigler*	Robert	UGDCP	Mexico

\**Ex officio* member



## APPENDIX 2

### UGDCP Meeting in Mexico 14-15 May 2002

**Marianne Banziger**  
Physiologist, Maize Program  
CIMMYT  
*Zimbabwe*

**John Bennett**  
Senior Molecular Biologist, Div. of Plant Breeding, Genetics and Biochemistry  
IRRI  
*Philippines*

**Richard Bruskiewich**  
IRRI  
*Philippines*

**Maria del Carmen de Vicente**  
Plant Molecular Geneticist  
CIAT  
*Colombia*

**Emile Frison**  
Director General (as of Aug. 1, 2003)  
SGRP Programme Leader  
IPGRI  
*Italy*

**Samy Gaiji**  
SINGER Project Leader  
IPGRI  
*Italy*

**Michael D. Gale**  
Director, John Innes Centre  
*United Kingdom*

**Emmanuel Guiderdoni**  
Group Leader, Functional Analysis of the Rice Genome  
Cirad-Amis  
*France*

**David Hoisington**

Director, Applied Biotechnology Center  
CIMMYT  
*Mexico*

**Michael T. Jackson**

Director, Program Planning and Coordination  
IRRI  
*Philippines*

**Stephen Kresovich**

Cornell University  
*United States*

**Hei Leung**

IRRI  
*Philippines*

**Thomas Metz**

Scientist, Genetic Resources Information Systems Management  
IPGRI  
*Italy*

**Calvin O. Qualset**

Director, Genetic Resources Conservation Program  
Division of Agriculture and Natural Resources  
University of California Davis  
*United States*

**Bent Skovmand**

Director, Nordic Gene Bank  
*Mexico*

**Jane Toll**

Coordinator, CGIAR System-Wide Genetic Resources Programme Secretariat (SGRP)  
IPGRI  
*Italy*

**Richard Trethowan**

Wheat Breeder, Wheat Program  
CIMMYT  
*Mexico*

**GENETIC RESOURCES CHALLENGE PROGRAM  
TASK FORCE MEETING  
27-28 MAY 2002**

**IPGRI HQ  
Rome, Italy**

**Monday 27 May**

Bus will collect participants from Santa Prisca at 08.30

<b>Morning session - Chair: Tim Reeves, CIMMYT</b>		
09.30 - 10.00	Introduction ➤ Individual/organization ➤ Role of Task Force (TF)	All  Tim Reeves
10.00 - 10.15	Brief comments on issues to be addressed by TF	All
10.15 - 10.45	<i>Coffee (with IPGRI staff) in Staff Room</i>	
10.45 - 11.15	Progress to date and tasks ahead	Cal Qualset
11.15 - 11.45	Science/Technical Focus	Cal Qualset
11.45 - 13.00	Business Plan	
13.00 - 14.00	<i>Lunch on terrace</i>	
<b>Afternoon session - Chair: Ron Cantrell, IRRI</b>		
14.00 - 17.30	Key decisions ➤ Core parties ➤ Structure ➤ Oversight ➤ Management ➤ 'Core'/Commissioned/Competitive	
15.15 - 15.45	<i>Coffee</i>	
17.30	Bus will collect from IPGRI to return to hotel	
19.30	Bus will collect from hotel to go to Restaurant	
10.30	Bus will collect from restaurant and return to the hotel	

**Tuesday 28 May**

Bus will collect participants from Santa Prisca at 08.15

<b>Morning session - Chair: Coosje Hoogendoorn, IPGRI</b>		
09.00 - 10.00	Funding	
10.00 - 10.30	<i>Coffee</i>	
10.30 - 12.30	Future tasks for proposal development	
12.30 - 13.30	<i>Lunch - terrace</i>	
<b>Afternoon session - Chair: Tim Reeves, CIMMYT</b>		
13.30 - 15.00	Working groups (Board room and ground floor meeting room)	
15.15 - 15.45	<i>Coffee</i>	
15.00 - 17.00	Summary ➤ Redrafting ➤ Deadlines ➤ Actions ➤ Next meeting	
17.00	Close	
17.30	Arrangements for participants to be taken to hotel/airport	

## Participant List

Santa Prisca Hotel, Largo Gelsomini 25, Rome. Tel. 065750009

	<b>Arrival</b>	<b>Departure</b>
Tim Reeves	Arrived	29 May
Ron Cantrell	Arrived	Wednesday 29 May at 1540
C. Tini Colijn-Hooymans	Sunday 26 May 18:55	Tuesday 28 May 19:45
Luis Antonio Barreto	Sunday 26 May 1930	Saturday 1 June 1845
Cal Qualset	Monday 27 May 0855	Thursday 30 May 1010 a.m.
Mike Gale	Sunday 26 May 2215	Tuesday 28 May 1715
Dr. Ye Zhihua	Sunday 26 May 1625	Wednesday 29 May 1805
Peter Nannes 24 May: Lancelot Hotel 0670450615 25 May: Delta Hotel 06770021 26 May: Santa Prisca	Friday 24 May 1810	Thursday 30 May 1010 a.m.

### Dinner 27 May 2002

**Restaurant: L'Archeologia, via Appia Antica 139. Roma. Tel. 06788 0494**

*Bus collecting from Santa Prisca at 1930*

*Bus returning to hotel at 2230*

Tim Reeves  
 Ron Cantrell and wife  
 Coosje Hoogendoorn  
 C. Tini Colijn-Hooymans  
 Luis Antonio Barreto and wife  
 Cal Qualset  
 Ye Zhihua  
 Mike Gale  
 Peter Nannes  
 Jane Toll  
 Patti Sands  
 Jan Engels and wife  
*Total 15 persons*

## APPENDIX 3

### **STAKEHOLDER MEETING - CGIAR CHALLENGE PROGRAM:**

Unlocking genetic diversity in crops for the resource-poor  
(CIMMYT, IPGRI and IRRI)

14-15-16 January, 2003

Alexandria Library, Egypt

### **AUSTRALIA**

**Australian Centre for International Agricultural Research (ACIAR)**

Tony Fischer, Research Program Manager, Land and Water Program

### **BELGIUM**

**Bayer BioScience**

Ed Roumen, Development Manager Rice

### **BRUSSELS**

**European Initiative on Agricultural Research for Development (EIARD)**

Paul E Harding, Executive Secretary, European Initiative on Agricultural Research for Development (EIARD)

### **CHINA**

**Chinese Academy of Agricultural Sciences**

Zhihua Ye, Director General and Professor, Science & Technology Management Department

### **COLOMBIA**

**International Center for Tropical Agriculture (CIAT)**

Douglas Pachico, Director of Research

Matthew W. Blair, Germplasm Specialist/Bean Breeder - Biotechnology Unit

### **FRANCE**

**AGROPOLIS**

Yves Savidan, Chief Executive Officer

**Centre de cooperation internationale en recherche agronomique pour le developpement (CIRAD)**

Anne-Yvonne Le Dain, Director of Cirad-Amis

Christian Hoste, Senior Adviser, Director for External Relations

Jacques Meunier, Deputy Director for Research

### **EGYPT**

**Agricultural Research Center**

Magdy A. Madkour, Vice President

**Alexandria Library**

Ismail Serageldin, Director

**International Center for Agricultural Research in Dry Areas (ICARDA)**  
Habib Halila, Regional Coordinator, Nile Valley & Red Sea Regional Program

**INDIA**

**International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)**  
Rolf Folkertsma, Patancheru

**ITALY**

**European Forum on Agricultural Research for Development (EFARD)**  
Enrico Porceddu, EFARD Vice president

**Food and Agricultural Organization of the United Nations (FAO)**  
Elcio Guimarães, Senior Officer (Cereals/Crops)

**GFAR**

Oliver L. Oliveros, GFAR Secretariat

**International Plant Genetic Resources Institute (IPGRI)**

Coosje Hoogendoorn, Deputy Director General, Programmes  
Samy Gaiji, Scientist, SINGER Project Leader  
Susan Bragdon, Senior Scientist, Law and Policy  
Patti Sands, Programme Assistant to Deputy Director General, Programmes

**JAPAN**

**National Institute of Agrobiological Sciences**  
Kosuke Nakajima, Vice President

**JORDAN**

**National Center for Agricultural Research and Technology Transfer (NCARTT)**  
Al Fayad Mousa, Director of Biodiversity, Genetic Resource program

**KENYA**

**International Livestock Research Institute**  
Ralph Richard von Kaufmann, International Livestock Research Institute

**MEXICO**

**International Maize and Wheat Improvement Center (CIMMYT)**  
Masa Iwanaga, Director General  
Peter Ninnes, Executive Officer for Research  
David Hoisington, International Maize and Wheat Improvement Center (CIMMYT)

**MOROCCO**

**Institut National de la recherche Agronomique (INRA)**  
Nsarellah Nasserlehaq, Plant breeder/geneticist/wheat

**NETHERLANDS**

**International Service for National Agricultural Research (ISNAR)**  
Victoria Henson-Apollonio, Manager, CGIAR Central Advisory Service on IP

**Plant Research International**

Niels P. Louwaars, Manager International Cooperation

**NIGERIA**

**Research for Development Council**

Robert Asiedu, Member, Research for Development Council, International Institute of Tropical Agriculture

**PERU**

**Research International Potato Center (CIP)**

Pamela K. Anderson, Deputy Director General for Research  
Merideth Bonierbale, Head, Crop Improvement and Genetic Resources Department

**PHILLIPINES**

**International Rice Research Institute (IRRI)**

Ronald Cantrell, Director General

**SYRIA**

**International Center for Agricultural Research in Dry Areas (ICARDA)**

Adel El-Beltagy, Director General

**U.K.**

**John Innes Centre**

Mary Anderson, Contracts Manager

**Syngenta**

Simon Bright, Head, Technology Interaction

**U.S.A.**

**Cooperative State Research Education and Extension Service**

Philip Schwab, Science Policy and Legislative Affairs

**Cornell University**

Ronnie Coffman, Chair, Department of Plant Breeding and Director, International Programs

**Kansas State University, Plant Biotechnology Center**

Robert S. Zeigler, Professor and Head Department of Plant Pathology &  
Director, Plant Biotechnology Center

## APPENDIX 4

### STAKEHOLDER MEETING

*Challenge Program:* Unlocking Genetic Diversity in Crops for the Resource-Poor

*Where:* Alexandria Library, Egypt

*When:* 14-15-16 January, 2003

**Monday 13 January:** Arrivals – Cairo or fly direct to Alexandria

**Tuesday 14 January:**

9:00 – 9:15 am	Welcome (I. Serageldin, Chair-Designate, Challenge Program Steering Committee)
9:15 – 9:30 am	Introduction (M. Iwanaga, Director General, CIMMYT)
9:30 – 9:45 am	Introduction of participants (self introductions)
9:45 – 10:30 am	An overview of the Challenge Program: Proposed activities (C. Hoogendoorn, M. Gale, D. Hoisington)
10:30 – 10:45 am	Questions of clarification
10:45 – 11:15 am	Break
11:15 – 12:30 am	Discussion of the Challenge Program proposal, including its focus
12:30 – 14:00 am	Lunch
14:00 – 16:00 am	Presentation of regional research and other interests in genetic resources, genomics, information systems and capacity building (ASARECA, SADC, CORAF, APAARI, FORAGRO, AARINENA, FARA, EIARD, GFAR, private sector, NGOC)
16:00 – 16:30 am	Break
16:30 – 18:00 am	Discussion of regional priorities and the work of the CGIAR centres that relates to this Challenge Program

**Wednesday 15 January:**

9:00 – 9.30	An overview of the business plan (P. Ninnes)
9:30 – 10:30	Discussion of the business plan including governance and management, partnerships, competitive grants process, involvement of NARS, ARIs.
10:30 – 11:00	Break
11:00 – 12:30	Small working groups to discuss: Role of Program Advisory Committee; Partnerships with ARIs (public, private), NARS; IP Management; Competitive grants process.
12:30 – 14:00	Lunch
14:00 – 16:00	Summary of working group discussions



16:00 – 16:30	Break
16:30 – 17:30	Next steps (R. Cantrell, M Iwanaga, G. Hawtin/C. Hoogendoorn)
17:30 – 17:45	Summary of discussions (I. Serageldin)

**Issues to be discussed**

1. Is the focus of the Challenge Program appropriate?
2. How can the Challenge Program expand/enhance its partnerships with NARS; with advance research institutes in the private and public sectors?
3. What mechanisms should be put in place to enhance capacity building efforts?
4. How will IP issues be addressed?
5. How should the competitive grants process operate?
6. How is the Challenge Program different from the core mandates of some centres?

## APPENDIX 5

### Technical Planning Workshop Participants

#	LAST NAME	FIRST NAME	ORGANIZATION	COUNTRY
1	Game	Alf	BBSRC	UK
2	Jia	Jizeng	CAAS	China
3	Ye	Zhihua	CAAS	China
4	Lu	Tiegang	CAAS	China
5	Ziegler	Robert	CCGI-Comparative Cereal Genomics Initiative	U.S.
6	Blair	Matt	CIAT	Colombia
7	Ishitani	Manabu	CIAT	Colombia
8	Lorieux	Mathias	CIAT	France
9	Iwanaga	Masa	CIMMYT	Mexico
10	Ninnes	Peter	CIMMYT	Mexico
11	Hoisington	Dave	CIMMYT	Mexico
12	Ribaut	Jean Marcel	CIMMYT	Mexico
13	Bonierbale	Merideth	CIP	Peru
14	Ghislain	Marc	CIP	Peru
15	Glaszmann	Jean-Christophe	Agropolis	France
16	TBA		Agropolis	France
17	Gregory	Peter	Cornell	U.S.
18	Arraes Pereira	Pedro Antonio	EMBRAPA	Brazil
19	Lopes	Mauricio	EMBRAPA and GFAR	Brazil
20	Brasileiro	Ana Maria	EMBRAPA	France
21	Blake	Tom	ICARDA	Turkey
22	Crouch	Jonathan	ICRISAT	India
23	Hash	Tom	ICRISAT	India
24	Ortiz	Rodomiro	IITA	Nigeria
25	Ingelbrecht	Ivan	IITA	Nigeria
26	Roux	Nicholas	IPGRI	Italy
27	Hoogendoorn	Coosje	IPGRI	Italy
28	de Vicente	Carmen	IPGRI	Italy
29	Metz	Thomas	IPGRI	Italy
30	Gaiji	Samy	IPGRI/SGRP	Italy
31	Leung	Hei	IRRI	Philippines
32	McLaren	Graham	IRRI	Philippines
33	Ellis	Noel	John Innes Centre	UK
34	Hirochika	Hirohiko	NIAS-Japan	Japan
35	Char	Bharat	Private Sector Committee-Mahyco Research Centre	India
36	Bjarnason	Magni	Private Sector Committee-Pioneer	Germany
37	Levine	Taya	Training Resources Group (facilitator)	U.S.
38	Herman	Joni	Training Resources Group (facilitator)	U.S.
39	Louwaars	Niels	Wageningen	Netherlands
40	Pereira	Andy	Wageningen	Netherlands
41	Hautea	Desiree	UP Institute of Plant Breeding	the Philippines
42	Prsic	Vesna	GFAR	Netherlands
43	Oliveros	Oliver	GFAR	Italy

# APPENDIX 6

'Unlocking Genetic Diversity in Crops for the Resource-Poor'  
 Technical Planning Meeting, 25-29 August 2003, Wageningen, The Netherlands

## PROGRAM

	Monday	Tuesday	Wednesday	Thursday	Friday
7:00	Breakfast				
9:00	<u>Opening Session</u> Welcome - Masa Iwanaga Martin Kropff Introductions & Getting Started  CP Overview History of the CP (M. Iwanaga) Proposed Research Agenda (C. Hoogendoorn) Management Structure and Collaboration Expectations (P. Ninnes)	<ul style="list-style-type: none"> <li>Discussion of Small Group Outputs</li> </ul> <b>First Year Work Plan Development</b> <ul style="list-style-type: none"> <li>Small Group Work</li> </ul>	<ul style="list-style-type: none"> <li><b>Discussion of First Year Work Plans</b> (continued)</li> </ul>	<b>First Year Priority Activities and Budget allocation estimates</b>  <b>Small Group Work and Discussion</b>	<b>Input into CP management process – operationalizing collaboration</b>  PSC Program Director Planning Leads Consortium Members
	Break				
	CP Overview (continued) Reactions and Q & A  <b>Overview of Workshop Objectives and Agenda</b> <ul style="list-style-type: none"> <li>Establishing Workshop Guidelines</li> </ul>	Small Group Work (continued)	Discussion (continued)	Reports on small group work	Management Issues Discussion (continued)
12:30	Lunch				
13:30	<b>CP Resources</b> Surfacing the scientific and other resources available to the CP <ul style="list-style-type: none"> <li>Small Group Work by Institutions</li> <li>Reports and Discussion</li> </ul>	<ul style="list-style-type: none"> <li>Small Group Work (continued)</li> </ul>	<b>Competitive Grant Systems</b> - Alf Game Why commissioned research (CR) and competitive research grants (CRG)? <ul style="list-style-type: none"> <li>How to best implement CR &amp; CRGs?</li> </ul>	<b>Visits to Wageningen science centers</b>	Wrap-up Summary of discussions and decisions <b>Next steps</b>
	Break				
	<b>Reality Testing the CP Five Year Agenda:</b> Review and Update of Subprogram Long and Short Term Goals <ul style="list-style-type: none"> <li>Small Group work</li> </ul>	<b>Presentations of First Year Work Plans</b>	<ul style="list-style-type: none"> <li>Small Group Work</li> </ul>		
17:00	End of Day's Session				
19:00	Dinner				

# APPENDIX 7

## **Challenge Program: Unlocking Genetic Diversity in Crops for the Resource-Poor Program Steering Committee Meeting Agenda**

1-2 September 2003

Wageningen, The Netherlands

### Objectives:

- Clarify role of PSC in support of Challenge Program success
- Agree on an operating approach
- Consider and endorse
  - Research Plan and Approach
  - Program Director Search Committee Short List

### AGENDA

**Chair:** I. Serageldin

1. Call to Order, Introductions, and Review of Revised Agenda *Monday 09:00 – 09:30*
2. Challenge Program Status Overview *Monday 09:30 – 10:30*
  - Progress to Date (M. Iwanaga)
  - Governance/Management Framework (P. Ninnes)
  - Technical Workshop Summary (R. Ortiz)

Questions and Answers

### BREAK

3. Clarifying PSC Role and Function *Monday 10:45 – 12:30*
  - Consortium Member Perspective
  - Role/Function of PSC and proposed Executive CommitteeQuestions and Answers  
Vote/ratification of suggested approach

### LUNCH

4. Program Director Search *Monday 13:30 – 15:00*
  - Presentation of Program Director TOR/Role
  - Expectations of the PD generated at the Technical WorkshopQuestions and Answers
  - Search Committee Report on status of search
  - Endorsement of short list of candidates

### BREAK

5. Research Plan *Monday 15:12 – 17:00*
  - Presentation of CP Research Programme and First Year Resource Realities (C. Hoogendoorn)

- Overview of Workshop Output: 5-Year Plan and First Year Research Program and Allocation of Resources (C. Hoogendoorn)

Questions and Answers

- Endorsement of Research Plan

CLOSE

6. Open/Review of Agenda *Tuesday 9:00 – 9:15*

7. Fundraising, Partnership Development, and Communications *Tuesday 9:15 – 10:30*

- Group discussions: a key element of the PSC role is the active pursuit of additional resources, a commitment to ensuring broad partnerships, and establishing an effective mode of communication between partners.

BREAK

8. Election of Executive Committee *Tuesday 10: 45 – 11:30*

9. Summary and Next Steps *Tuesday 11:30 – 12:00*

CLOSE

## APPENDIX 8

### Director Recruitment Process

The job announcement was advertised in *Nature* and *The Economist* and was circulated widely via e-mail. A total of 39 applications were received. One-half of the applications were from developing countries. Many highly qualified candidates applied.

The Search Committee was established from a sub-set of the Program Steering Committee (PSC). Additionally, the interim Science Council Chair nominated one person for the Search Committee. The Search Committee comprised:

- (1) Dr. Masa Iwanaga, Chair.
- (2) Dr. Desiree Hautea, Director, UP Institute of Plant Breeding, Philippines (nominee from iSC).
- (3) Dr. Zhihua, Ye, Chinese Academy of Agricultural Sciences, Beijing, China.
- (4) Dr. Hubert Zanstra, Director General, CIP (nominee of the CDC Chair)
- (5) Dr. Yves Savidan, Agropolis, France.

The Search Committee met on August 31 to develop a shortlist using a set of agreed criteria. A progress report was presented to the Program Steering Committee (PSC) on September 1<sup>st</sup> in Wageningen. The PSC endorsed the search process, including plans for interviews of the shortlisted candidates at IPGRI in Rome.

The Search Committee interviewed three candidates at IPGRI during September 11-12. Interviews for each candidate consisted of 2 hours discussion with the Search Committee and a one-hour seminar, which was open to IPGRI staff.

### Position Announcement



Director, Challenge Program:  
"Unlocking Genetic Diversity in Crops for the  
Resource-Poor"

FUTURE™  
HARVEST

**An exciting opportunity for a prominent scientist and research manager to lead a new consortium to create a unique public platform for accessing and developing genetic resources for developing countries**

The Consultative Group on International Agricultural Research (CGIAR) ([www.cgiar.org](http://www.cgiar.org)) supports 16 Future Harvest Centers working in more than 100 countries to mobilize cutting-edge science to reduce hunger and poverty, improve human nutrition and health, and protect the environment. The CGIAR is funding three new Challenge Programs ([http://www.cgiar.org/research/res\\_cp.html](http://www.cgiar.org/research/res_cp.html)) focusing on complex research issues of overwhelming global significance. Under the **Challenge Program for Unlocking Genetic Diversity in Crops for the Resource-Poor**, a new consortium will establish research partnerships in genetic diversity, comparative genomics, gene transfer and crop improvement, information

systems, and capacity building for developing country national agricultural research systems (details at <http://www.cgiar.org/pdf/cpunlocking.pdf>).

The CGIAR seeks a Director to provide leadership to the Challenge Program by coordinating and liaising with a large number of scientists located in institutions around the world. S/he will ensure that the Program delivers outputs and outcomes consistent with its objectives and that research milestones and other performance indicators are fulfilled. The Director will achieve this objective by building effective alliances across institutions in developing and industrialized countries, as well as coordinating a small team of lead scientists who will manage the five subprograms. The Program has an indicative budget of about US\$ 12 m pa. Funding for approximately half of the budget has been identified, and the Director will take the lead in identifying and pursuing the additional funding. S/he will report to the Challenge Program Steering Committee, participate in meetings of this Committee, and convene meetings of the research program management team.

The Director will be employed through one of the CGIAR Centers: CIMMYT ([www.cimmyt.org](http://www.cimmyt.org); to be based in Mexico); IPGRI ([www.ipgri.cgiar.org](http://www.ipgri.cgiar.org); to be based in Italy); and IRRI ([www.irri.org](http://www.irri.org); to be based in the Philippines). The Center where the director is based will provide administrative and other logistical support for the Challenge Program.

**We seek candidates with the following skills:**

- A PhD in biological sciences with at least 10 years of relevant post-PhD experience;
- Demonstrated experience in leading multidisciplinary research teams;
- Demonstrated experience in research and project management;
- A proven track record of fundraising;
- Strong experience with developing country agricultural research; and,
- Willingness to travel extensively.

The ideal candidate will possess excellent communication skills in written and spoken English. S/he will lead and manage with sensitivity to diverse cultures and nationalities. An ability to monitor and report on research progress to tight deadlines is essential, as is an ability to represent the Program at the international level. The ability to operate in a major language other than English is an advantage.

An internationally competitive and attractive salary and benefits package will be negotiated with the successful candidate, who will be appointed for five years initially. Further details about the position may be obtained from Dr. Masa Iwanaga ([m.iwanaga@cgiar.org](mailto:m.iwanaga@cgiar.org)) Director General, CIMMYT. Applicants from CIMMYT, IPGRI, and IRRI are advised that, if appointed to this post, they will not be hosted by the Center where they are currently based.

To apply, send a letter of application with your recent curriculum vitae, including address and fax number, and have letters of recommendation sent from three referees to the address below, by **8 August 2003** or until the position is filled (Reference 2003/03).

**Human Resources Manager**

**(Reference 2003/ 03)**

CIMMYT, Int.

Apdo. Postal 6-641 06600 Mexico, D.F. MEXICO

Phone: (+52) 55-5804-2004 Fax: (+52) 55-5804-7558

Email: [jobs-cimmyt@cgiar.org](mailto:jobs-cimmyt@cgiar.org) or [jobs@cimmyt.exch.cgiar.org](mailto:jobs@cimmyt.exch.cgiar.org)

# APPENDIX 9

## **SPL Recruitment Process**

### **Challenge Program: Unlocking Crop Genetic Resources for the Poor Sub-Program Leaders Responsibilities, Recruitment and Remuneration**

The Challenge Program: Unlocking Crop Genetic Resources for the Poor (hereafter referred to simply as the UGDCP) is composed of five sub-programs (SP), four of which will have Sub-Program Leaders (SPLs). The fifth (Capacity Building) will be led by the CP- Director. The SPLs and the UGDCP Director will form the management team of the Challenge Program. Thus, effective leadership by the SPLs will be critical to the success of the CP. This leadership will be achieved by selecting and empowering the most creative, committed, and skilled scientists from within the UGDCP Consortium.

This paper puts forth a three stage process by which we will select and reward SPLs:

#### **1) SPL Responsibilities, as derived from the approved UGDCP document.**

- a. Provide intellectual leadership within the SP.
- b. Assemble research teams within their respective SPs that will be composed of CG Center, NARS, and ARI scientists.
- c. Harmonize the outputs and workplans derived from the Technical Planning Workshop in Wageningen with a longer term vision for their respective SPs.
- d. Lead the development of annual and multi-year work plans within the SP.
- e. Develop technical terms of reference for his/her SP within the CP competitive grants program.
- f. Coordinate activities and interactions within the SP such that competitively awarded projects and commissioned projects complement one another to achieve the SP objectives.
- g. Serve as the contact for establishing private sector and other stakeholders relationships with the activities of the SP.
- h. Monitor the scientific quality, quantity, and timeliness of SP outputs.
- i. Propose adjustments to the structure of the SP as events dictate.
- j. Work with the CP Director and the other SPLs to ensure that the combined information and outputs from each SP meet the expectations of the CP.
- k. Provide semi-annual progress reports to the CP Director. The purpose of these reports is not simply to monitor progress but also to allow the CP Director to communicate CP progress to donors and other stakeholders in a timely manner.

#### **2) SPL Support Policy**

All SPLs must come from an institution that is a member of UGDCP consortium. The purpose of the SPL support policy is to enhance the careers of UGDCP scientists who assume the significant leadership responsibilities outlined above. Likewise, we seek to insure that institutions that offer their scientists' time to the UGDCP as SPLs are not deprived of resources. There are three independent components of the support package: 1) institutional compensation; 2) additional research support for the SPL; and, 3) a modest salary bonus.



*Institutional Compensation:* The SPLs will devote approximately 50% of their time to CP-related issues. While most of their commitment will be research-related and not management-related, a significant amount could be additional to current institutional activities. The SPLs' home institution would commit in-kind support of \$400,000 annually. If an institution can demonstrate that its in-kind support will already meet the \$400,000 level without charging the SPL costs against its contribution, then 50% of SPL salary and benefits, plus 18% indirect costs may be reimbursed to the institution by the Challenge Program.

*SPL Compensation:* The SPL compensation is two-fold: maintenance of the research program and a personal salary adjustment.

*Research Program Maintenance:* Scientists selected as SPLs (see below) will have demonstrated superior scientific skills and achievements in the area covered by the Sub-Program, expressed a desire to assume the responsibilities associated with the position, and possess management experience in interacting across disciplines and institutions. Despite this commitment and history of superior performance, the UGDCP recognizes that the demands on the SPL could negatively impact the scientists' careers unless there are means to provide additional research support. The UGDCP will provide each SPL (1 – 4) with \$100K operational support per year, from which the institution may charge up to 18% indirect cost recovery. These resources will be used by the SPL in research directly applicable to the objectives of the relevant SP, and the outputs of this work will be accountable as specific outputs of the UGDCP. The SPLs will be eligible to serve as PIs on up to two funded competitive grants at any one time.

*Personal compensation:* Each SPL will receive a salary adjustment in recognition of the additional time the SPL will invest in the CP. This adjustment will be determined by, and conform to, the salary/benefits structure and policies of the SPL's home institution. However, approximately 10% should be considered as an upper limit.

### **3) SPL Selection Process**

*Recruitment:* A call for applications will be sent to each UGDCP Consortium member and to the lists of attendees at the August 2003 Technical Planning Workshop Wageningen. The announcement will include the responsibilities and compensation.

*Application Process:* More than one scientist may apply from each Consortium member, but only one SPL can be appointed from a given institution. Nominations are encouraged. Each applicant/nominee should submit:

*Cover letter:* The letter (not to exceed 2 pages) should include a statement of why the SPL position is of interest, a vision of the operations and outcomes of the SP, and the candidate's proposal for how this can be achieved. The letter should *not* address why the candidate is qualified for the position, as that should be evident from the CV.

*Curriculum vitae:* A brief (2 pp.) summary CV that includes personal data, education, languages, and a career chronology. The chronology should briefly summarize the responsibilities and achievements at each position.

*Publications and other evidence of relevant scientific achievement:* Provide a complete list of publications from the past five years and all publications prior to the last five years that are of relevance to the Sub-Program. Publications should be grouped into peer-reviewed and non peer-reviewed sections.

*Non-published relevant products.* Since different institutions place different weights on the value of publication in peer-reviewed journals, the applicants should include a description of non-published verifiable significant accomplishments or products relevant to the UGDCP.

*Evidence of research management /coordination experience and achievement:* Applicants should provide a listing and short description of relevant projects and research teams in which they have had a leadership role (1 p max.).

*Description of current and projected work at their respective institution:* The SPL's overall research program during the lifetime of the project will be expected to add value to the Challenge Program. Thus the candidate should show how his or her research activities will support and complement the objectives of the particular SP and of the UGDCP as a whole (1/2 p max).

*References:* Provide three references. Contact information must include e-mail address and telephone number.

*Director concurrence:* A letter from the relevant director-level supervisor from the applicant's home institution that s/he accepts that the scientist will work with the UGDCP, agrees with the compensation and incentive packages presented above, and acknowledges that it will be additional to the applicant's current operational budget. This additionality to the SPL operating budget will be respected in future institutional upward or downward budgetary adjustments. The director should also state that the responsibilities of the SPL will be considered as part of his or her normal responsibilities and that this will be recognized in annual performance evaluations.

#### **4) Evaluation and Appointment Process**

Applications should be submitted by e-mail to the interim CP Communications Assistant, Ms. Jennifer Nelson ([j.nelson@cgiar.org](mailto:j.nelson@cgiar.org)), no later than 14 December, 2003. The CP Director-Designate will review the applications, contact referees, and develop an annotated ranking for the applicants, including strengths and weaknesses, along with pertinent information obtained from the referees. The CP Director-Designate will recommend a SPL for each and forward a complete list of applicants and the packages of the top two or three (depending on the total number of applicants) to a PSC sub-committee. This sub-committee will consist of one CGIAR center, and the PSC representative from JIC and EMBRAPA. The ARI and NARS members were selected based on prior participation of other NARS and ARIs in the Director Search Committee and Workplan Oversight Committee. Upon their endorsement, the Director Designate will submit SPL assignments to the full PSC for a "no objection" approval, allowing 5 days for a response. Appointments of the SPLs are targeted for 10 January 2004.

## APPENDIX 10

### **In-Kind Contributions**

#### **Agropolis**

**SP2CL1:** One year of experiments on the same material (sorghum), salaries and benefits of researchers involved: 0.3 full time scientist (FTS).

**SP3CL2:** RICE: \$5,000. MAIZE: (INRA) 30 % scientist time, 50% technician time. AFRICAN RICE: \$24,000.

#### **CAAS**

**SP2CL2:** 50% of two senior scientists' and 90% of one Ph.D. student's time. High throughput robotics and genotyping. Bioinformatics platform. Dataset of EST-SSR derived from wheat known to be orthologous across wheat, maize, and rice.

**SP3CL3:** \$1,170

#### **CIAT**

**SP1CL1:** \$28,000

**SP2CL1:** BEAN: 10% of salaries and benefits of 3 scientists and support staff involved, and field, greenhouse and laboratory facilities. CASSAVA: 10% of the time of 2 senior scientists at CIAT scientists, salaries of 2 support staff, and green house and field operation facilities. RICE: Salaries and benefits of scientists and support staff involved, and laboratory and field facilities.

**SP2CL2:** CIAT-BMZ: Bean genomics (20K counterpart); bean ESTs; cassava ESTs.

**SP2CL3:** 10% of three senior scientists time. Laboratory space and equipment including DNA sequencers, microarray spotter and reader, thermocyclers, electrophoresis units, etc. Experience with cDNA and microarray construction. Computer hardware and software for data analysis

**SP3CL2:** CASSAVA: 5% time of a scientist, field space facilities for molecular marker analysis, and computer hardware for data entry and analysis => \$5,000. BEAN: Salaries and benefits of scientists and support staff involved from CIAT and EMBRAPA; laboratory, greenhouse and field facilities at CIAT and at CNPAF – EMBRAPA; collaborative and on-going projects related to drought tolerance funded by other donor (BMZ/GTZ) to CIAT for years 2003-2005. AFRICAN RICE: \$17,000.

**SP3CL3:** \$5,310

**SP3CL4:** \$1,000

#### **CIMMYT**

**SP1CL1:** \$6,000

**SP2CL1:** MAIZE: CIMMYT will contribute research time of J-M Ribaut (10%) and P. Monneveux (5%) and will cover some field expenses WHEAT: CIMMYT will contribute researcher time of M. Reynolds (5%) and of R Trethowan (5%)

**SP2CL3:** 20% of a scientist's time, 30% technician time. Applied Biotechnology Center laboratory at CIMMYT equipped with thermocyclers (both PCR and quantitative RT-PCR), electrophoresis units etc. Computing hardware and software for data analysis arising from the microarray experiments and mapping

**SP3CL2:** 15% of a scientist time, 30% technician time and 50% of expenses related to the field experiment.

**SP3CL3:** \$1,170

**SP4CL4:** \$1,100

**CIP**

**SP1CL1:** \$5,000

**SP2CL2:** CIP-USAID: Comparative mapping project in potato; BMZ: Potato genomics (40K counterpart)

**SP2CL3:** CIP-INIA Spain: characterization of native potato genetic diversity (\$1.1 M/yr, 2003-2006). CIP-Austrian Min. of Finances: gene expression analysis for potato disease resistance (\$.6 M/yr, 2003-2006).

**SP3CL3:** \$5,310

**SP3CL4:** \$1,000

**EMBRAPA**

**SP1CL1:** \$1,000

**SP2CL1:** CASSAVA: 10% of a senior scientist's time at EMBRAPA

**SP3CL2:** BEAN: Salaries and benefits of scientists and support staff involved from CIAT and EMBRAPA; laboratory, greenhouse and field facilities at CIAT and at CNPAF – EMBRAPA; collaborative and on-going projects related to drought tolerance funded by other donor (BMZ/GTZ) to CIAT for years 2003-2005.

**SP3CL3:** \$1,170

**ICARDA**

**SP1CL1:** \$32,000

**SP2CL1:** WHEAT: 10% of the time of 2 senior scientists and salaries of 2 support staff. BARLEY: 10% of the time of 2 senior scientists and salaries of 2 support staff. CHICKPEA: 10% time of one senior scientist and 40% time of one support staff. Green house and field facilities.

**SP2CL2:** Mapping of 50 COS markers on the durum mapping populations project -- phenotyping and genotyping Arta/H. spontaneum 41-1 BC2F2 population, 20K available

**SP3CL3:** \$1,170

**SP3CL4:** \$2,000

## **ICRISAT**

**SP1CL1:** \$6,500

**SP2CL1:** CHICKPEA: ICRISAT's chickpea marker-assisted breeding project for root traits supported by various restricted projects will provide salary support for scientists, PhD thesis researchers, and technical support staff involved in this activity. Details to be provided. SORGHUM: Field, laboratory and computer facilities for the conduct of the experiment, and 20% of the time of first PI (FRB) to manage the experiment and data analysis

**SP3CL2:** SORGHUM: in-kind contribution in terms of salary and operational funds = US\$20,000 matching funds from DFID PSP pearl millet markers project, and access to laboratory facilities for high throughput DNA isolation and SSR marker genotyping (2% of capital cost of recently purchased equipment) = US\$13,000. MILLET: in-kind contribution in terms of salary = US\$4,000, and access to laboratory facilities for high throughput DNA isolation and SSR marker genotyping (2% of capital cost of recently purchased equipment) = US\$13,000. CHICKPEA: \$4,000

**SP3CL4:** \$2,000

## **IITA**

**SP1CL1:** \$20,000

**SP2CL1:** CASSAVA: 10% time of a principal scientist time, 20% of visiting scientist time and research technicians. Field space, facilities for molecular marker analysis, and computer hardware for data entry and analysis. IITA scientists time (10%) will be committed to the study while laboratory, screen-house and field facilities will also be available for carrying out the studies.

**SP2CL2:** IITA-USAID: Euphorbiacea genomics (\$20K counterpart)

**SP2CL3:** 10% of three senior scientists time. Laboratory space and equipment including DNA sequencers, microarray reader, thermocyclers, electrophoresis units, etc. Experience with cDNA construction. Computer hardware and software for data analysis

**SP3CL1:** 1) venue for the Workshop meetings and seminars will be provided by IITA as in-kind contribution, 2) accommodation, transport from and to the airport for the participants and resource people not based at IITA Headquarters will be provided by IITA at its Headquarters at discounted subsidized rate, 3) access to the e-mail and photocopying facilities will be provided for the participants and resource personnel, 4) IITA will be hosting the welcoming banquet at the beginning of the Workshop for the participants and resource people => \$30K

**SP3CL2:** MAIZE: 10% time of scientist time and 30% time of a technician. COWPEA: \$10,000. CASSAVA: 5% time of a scientist, field space, facilities for molecular marker analysis, and computer hardware for data entry and analysis => \$5,000.

**SP3CL3:** \$5,310

**SP3CL4:** \$4,000

## **IPGRI**

**SP1CL1:** \$22,000

**SP1CL4:** Project 8: Access and Benefit Sharing; Project 9: Genetic Resources Policy Initiative -- share results with cluster and CP.

**SP3CL3:** \$1,170

**IRRI**

**SP1CL1:** \$19,000

**SP2CL1:** IRRI will contribute researcher time (10% for R. Lafitte, 5% for J. Bennett and K. McNally), additional support from two nationally recruited staff, and partial overhead costs.

**SP2CL2:** IRRI-BMZ: Rice drought tolerance project (\$20K counterpart) -- stress gene EST libraries, rice; bioinformatics group.

**SP2CL3:** SDC Mutant Bank, (\$970,000, 2002-2004) and BMZ Drought tolerance (\$1.4 M, 2001-2003).

**SP3CL2:** \$44,000

**SP3CL3:** \$1,170

**SP3CL4:** \$1,000

**Wageningen**

**SP1CL4:** Project 7: Impact of IPRs on the breeding industry and smallholder farmers in developing countries – share results with CP.

**SP2CL3:** WUR Bioinformatics contribution under projects from the genomics initiative CBSG and EU funded project PLANET towards integrated plant functional genomics databases. 1 fte/year PhD and supplies, funded by Dutch Science foundation for ‘Identification of drought responsive pathways in Arabidopsis.’

**INIBAP**

**SP2CL2:** BAC libraries of 3 *Musa* genotypes and *Musa acuminata* mapping population; additional external funds for visiting scientists.