Generation Challenge Programme

# Competitive and Commissioned Research Project Executive Summaries

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## 1. Identifying Genes Responsible for Failure of Grain Formation in Rice and Wheat under Drought

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**Executive Summary**
Rice and wheat provide approximately 50% of the calories consumed directly by the human population. The projected increase in this population from 6 billion in 2000 to 9 billion in 2050 requires that production of rice and wheat continues to increase as it has over the last 40 years, following the introduction of high-yielding modern varieties. Future increases will come principally from further intensification of production in the limited irrigated areas and from improved yields in the larger rainfed areas. Drought is the main cause of yield loss in rainfed rice and wheat, and losses are most severe when drought occurs at the flowering stage. Water-saving strategies for irrigated areas must also deal with the sensitivity of the flowering stage to water deficit. For these reasons, we focus here on a comparative study of drought tolerance in rice and wheat, exploiting on one hand the greater drought tolerance of wheat and, on the other hand, the recent explosion of information on the rice genome. The rice genome is approximately one-twentieth the size of the wheat genome, but these two cereals are comparatively closely related, with highly similar genes controlling growth, reproduction, and protection. Our team combines expertise on drought-stress physiology, gene expression, genome structure, biodiversity, and plant breeding. Years of research have produced detailed knowledge of which rice and wheat varieties and mutants show contrasting responses to drought during key steps of flowering such as panicle/spike emergence and pollination. Progeny derived by crossing these contrasting lines provide highly informative comparisons that help scientists to interpret the large data sets emerging from modern studies of gene expression using such techniques as microarrays and proteomics, and to identify and validate genes crucial to drought tolerance. Superior forms (alleles) of these genes can be identified in traditional varieties and other sources. Such alleles can then be efficiently transferred into popular rice and wheat varieties via DNA-assisted backcrossing to enhance drought tolerance in both cereals.

## 2. Revitalising Marginal Lands: Discovery of Genes for Tolerance of Saline and Phosphorus Deficient Soils to Enhance and Sustain Productivity

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**Executive Summary**

Soils that contain toxic levels of salts and/or are deficient in essential plant nutrients have low productivity and are commonly associated with poverty. Problems of particular importance in these soils are salinity and phosphorus deficiency. In Asia alone, more than 12 million ha are currently affected by salinity and about 50% of the rice lands are P-deficient. Salt stress often coexists with other abiotic stresses such as drought and P deficiency. Amendments and management options for these soils are too expensive for the resource-poor farmers commonly living in these areas. However, solutions through improved germplasm are affordable to farmers and are becoming more feasible with the developments in modern molecular tools that are becoming available to unravel the genetic basis of tolerance. Combining mechanisms underlying tolerance of complex traits such as salt and P-deficiency, as well as those for multiple stresses, is now feasible once the genetic components or genes for tolerance are tagged to allow them to be traced in the breeding process. We aim to identify and tag the genes for tolerance of salinity and P-deficiency. For both stresses, we have made excellent progress in understanding the biology and in identifying major chromosomal regions that are associated with tolerance. We will further fine-map these regions and use modern molecular approaches to discover the genes that are involved in tolerance using a range of molecular strategies. We will also use biological information and genes discovered from other crops to facilitate the identification of similar genes in rice. Ultimately, we will develop a marker system to allow the efficient incorporation of these genes into popular—yet intolerant—varieties, initiate a marker-assisted breeding system with NARES partners, and provide them with the training needed to carry out these activities.


## 3. Identifying the Physiological and Genetic Traits that Make Cassava One of the Most Drought Tolerant Crops

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**Executive Summary**

Cassava is usually cultivated in areas considered marginal for other crops, with soils of low fertility and long periods of droughts. Cassava's photosynthesis and growth decrease to near zero during episodes of water deficit, and it achieves most of its growth after rainfall resumes. This suggests that a key to cassava's success is its ability to regulate numerous

plant processes to rapidly change course as it navigates between episodes of favourable and unfavourable weather. The general objective of the proposed work is to determine the best traits to be used in breeding programmes for drought tolerance by elucidating the mechanisms of cassava's remarkable tolerance to drought and making full use of the expanding body of information on the physiological and molecular bases of drought tolerance in other well-studied crops. Contrasting genotypes for several traits related to drought tolerance will be selected for evaluation and segregating progenies will be developed for genetic studies. The effect of water deficit on traits which are related to the probable mechanism(s) for drought tolerance in cassava will be evaluated and compared with other well-studied crops. The selected contrasting genotypes will be crossed to generate segregating populations. In addition, drought tolerant genotypes will be selfed to provide S1 families to study recessive gene action. Evaluations will be conducted on the parental clones and the segregating progenies in semi-arid environments of Brazil, Colombia, Ghana, and Tanzania, to screen phenotypes. Segregating progenies will be analysed using a set of genome-wide molecular markers and candidate genes to identify quantitative trait loci (QTL) of component traits of drought tolerance. To assess the value of enhanced leaf retention during stress, a transgenic cassava in which a cytokinin synthesis gene is over-expressed will be field evaluated. Expected outputs of this project include an improved understanding of drought tolerance traits and their biological bases, molecular markers for key drought tolerance traits, and cassava genotypes ready to be introduced into breeding programmes.

## 4. An Eco-physiological – statistical Framework for the Analysis of GxE and QTLxE as Occurring in Abiotic Stress Trials, with Applications to the CIMMYT Drought Stress Programmes in Tropical Maize and Bread Wheat

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**Executive Summary**

When breeders try to develop adapted genotypes for abiotic stress conditions (i.e., plants with superior genetic constitution with respect to yield), they are faced with the problem that it is hard to obtain reliable estimates of genetic superiority under stress conditions. Under stress, the phenotype—that which the breeder can measure and observe—provides little information on the underlying genetics. A traditional solution uses measurements on yield or other, secondary traits in non-stress conditions to predict performance under stress. The idea is that under non-stress conditions the genetic value can be estimated more precisely, and as long as the genetic basis of the trait observed under non-stress is closely enough related to the genetic basis of yield under stress or, if the genetic correlation is high enough, then selection under non-stress is preferable. Recently, the traditional approach was challenged by an alternative approach originating from CIMMYT researchers that was built on physiological understanding of the stress response and relevant environmental characterisation of selection and stress environment. The alternative approach would facilitate a better choice of secondary traits and selection environments. Molecular marker techniques make this alternative even more attractive because of the possibility of selection at the genetic level. However, the new approach still does not live up to the expectations and we think that one of the important reasons for this partial failure is the use of a less-than-adequate statistical framework for analysing data from abiotic stress trials.

The present statistical approaches do not incorporate any explicit physiological knowledge on the part of the genotype or the environment. We propose the development of an integrated eco-physiological statistical framework, modeling yield responses on both the phenotypic and genetic level with direct dependence on physiologically relevant environmental factors. Application of this framework to existing CIMMYT data on drought stress in maize and wheat will significantly add deeper insight into the genetic and physiological mechanisms underlying drought stress in those crops. Additional features of our approach include facilities for the analysis of multiple traits and crosses. To make the methodology generally available to students and researchers in developing countries, course material and corresponding software modules will be developed. This teaching material will be presented in one-week courses in Uruguay and Kenya.

## 5. Unlocking the Genetic Diversity in Peanut's Wild Relatives with Genomic and Genetic Tools

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**Executive Summary**

Legumes, unlike other crops, fix nitrogen, need little fertilizer, and help maintain the productivity of soil. Legume seeds are among the most important sources of protein and iron for the poor. Peanut (A.hypogaea) is a legume grown throughout the tropics on about 24.8 million ha (>90% cultivated by small farmers). Peanut is particularly important in Africa, where production greatly exceeds that of any other legume, and in Asia, where production is almost as high as that of soybean. Peanut is sensitive to fungal diseases and drought stress, factors that are important reducers of yield. Improvement of peanut has been limited by an extreme genetic bottleneck at its origin, which occurred via hybridisation of two wild species followed by a rare spontaneous duplication of chromosomes. The resultant plant had hybrid vigor, but because of the difference in chromosome number, was reproductively isolated from its wild relatives. Therefore, all peanuts are probably derived from one or a few plants. This led to low diversity for important agricultural traits and very limited genetic diversity, which has constrained advances in genetics necessary for modern breeding. In contrast, wild Arachis species are very diverse and have been selected during evolution by a range of environments and diseases, providing a rich source of variation in agronomically important traits.

Recently, partners in this proposal have artificially recreated the events that gave rise to the peanut, using a wide range of diploid species. So far, four viable synthetic hybrids have been created, thus bringing the genetic diversity of the genomes of eight wild Arachis species to peanut breeding for the first time. In parallel, major breakthroughs in genetic mapping have been made using a new strategy that will allow plant breeders to work complex hybrids more efficiently. This proposal aims to build on these advances to enable the creation of peanut varieties resistant to disease and drought. In addition, we propose to include peanut in a single genetic system for legumes, allowing peanut research to benefit from the knowledge of modern "genomics."

## 6. Marker Development and Marker-assisted Selection for Striga Resistance in Cowpea

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**Executive Summary**

Cowpea is an important food grain legume grown on 9.8 million hectares of small farms in the dry savannah of tropical Africa. Current estimates place world cowpea production at 3 million tons, with 80% of its production in Africa, principally West and Central Africa where the crop productivity is low due to pests and diseases. The parasitic angiosperm Striga gesnerioides (Willd.) is one of the major limitations to cowpea productivity. Conventional breeding efforts have helped to alleviate some of the Striga problems, but pyramiding resistance to the parasite with other important agronomic and resistance traits is time-consuming and difficult. Modern technologies, such as marker-assisted selection (MAS), in combination with conventional breeding, have been successfully used for genetic enhancement of other crop species. The cooperative work proposed here, involving the International Institute of Tropical Agriculture (IITA), the Centre d'Etude Regional pour l'amelioration de l'Adaptation a la Seccheresse (CERAAS), the Institut d'Environnement et de Recherches Agricoles (INERA) of Burkina Faso, and the University of Virginia (UVA), seeks to develop a MAS strategy for cowpea that will allow the rapid, reliable identification of race-specific Striga resistance genes in breeding lines and integration of MAS for Striga resistance in their breeding programmes. The outcome of this work will be superior-performing, well-adapted cowpea varieties containing pyramided agronomic productivity, and disease and pest resistance traits available to farmers. This project will also contribute to the development of human and institutional capacity to fully integrate the use of MAS technologies in cowpea breeding. It is expected that farmers will achieve higher yields of better quality cowpea that would impact favourably on their general livelihoods.


## 7. Measuring Linkage Disequilibrium across Three Genomic Regions in Rice

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**Executive Summary**

Rice is an important staple crop worldwide. Rice also has many advantages for genetic research, most notably the complete genome sequence and a wealth of genetic diversity. Rice therefore presents an excellent opportunity to use linkage disequilibrium (LD) mapping and association studies for allele mining to identify superior alleles that lay hidden in the vast reservoirs of global rice germplasm. Although LD mapping presents a powerful technique, little is known about the actual amount of LD across different genomic regions in rice. The main objective of this start-up grant is to measure the extent of linkage disequilibrium in three genomic regions to test the feasibility of LD mapping as the basis for allele mining in rice, through collaborative research between Cornell University and the Indonesian Centre for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD) in Bogor, Indonesia. Currently, 250 Indonesian landraces are being analysed with a set of genome-wide simple sequence repeat (SSR) markers to define the population structure across these accessions. This Generation start-up project will use the same accessions to measure the LD in three genomic regions surrounding the bacterial blight resistance genes Xa7, Xa13, and the cluster of Xa4/Xa22/Xa26. Single nucleotide polymorphism (SNP) markers will be

developed across each region by sequencing PCR products from a small subset of landraces. These SNP markers will then be genotyped across a larger subset using a high-throughput SNP assay. The SNP data will be used to measure the LD across each region and define the haplotype block structure that exists in this set of rice germplasm. This project will provide a specific measure of LD across three genomic regions that will be useful in planning the strategy for larger, more complex allele mining experiments using the global collection of rice germplasm.

## 8. Targeted Discovery of Superior Disease QTL Alleles in the Maize and Rice Genomes

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**Executive Summary**
We propose to identify, characterise, and utilise sections of the rice and maize genomes that provide superior disease resistance to cereal diseases of critical and global importance. Durable, broad-spectrum resistance would be valuable to resource-poor farmers. Although much research has been focused on qualitative (complete, race-specific) resistance, the work proposed here will focus on quantitative (incomplete, presumably race non-specific) disease resistance (QDR) because QDR is usually the more durable form or the only form available. At present, the chromosomal regions associated with QDR are defined with very low precision, and germplasm has not been systematically analysed to identify superior alleles at the loci of greatest potential utility. We propose to characterise selected maize and rice germplasm for urgently-needed disease resistance. We will initiate development of near-isogenic lines (NILs), capturing useful segments of maize and rice chromosomes in a susceptible background for detailed analysis. We will use a set of complementary strategies in the development of the NILs, including backcrossing of advanced resistant lines derived from rice varieties known for durable resistance; selection of allelic series at loci of outstanding interest based on a summary of all available disease QTL studies in maize; and selection of lines carrying alleles showing increases in frequency under recurrent selection for a maize disease. We will make use of the existing collection of rice mutants to validate the function of candidate QDR genes. The superior chromosomal segments identified in this project will be analysed in detail and utilised in the applied breeding programmes in which improving disease resistance is a high priority.

## 9. Development of Low-Cost Technologies for Pyramiding Useful Genes from Wild Relatives of Cassava into Elite Progenitors

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**Executive Summary**

Cassava (Manihot esculenta Crantz) is increasing in importance in the tropics due to its hardy nature, but suffers from a plethora of anthropod pests and diseases as well as post harvest physiological deterioration (PPD). It has been estimated that cassava farmers, typically resource-poor farmers, lose 48 million tons of fresh root to pests, diseases, and PPD every year. This makes up some 30% of total world production, valued at US$1.4 billion. Wild relatives of cassava are important sources of genes for resistance to pests and diseases and have a longer shelf life. Dramatically delayed PPD has been identified in inter-specific hybrids from Manihot walkerae. The only source of resistance to the cassava hornworm and a widely deployed source of resistance to the cassava mosaic disease (CMD) were identified in 4th backcross derivatives of M. glaziovii. Moderate to high levels of resistance to cassava green mites (CGM), white flies, and the cassava mealy bug have been found in inter-specific hybrids of M. esculenta sub spp flabellifolia. Furthermore, M.glaziovii, M. catingae, and M. carthaginensis, are adapted to semiarid lands and are potential sources of genes for tolerance to drought. But the heterozygous nature and long reproductive cycle of cassava makes introgression and pyramiding of these genes a long-term effort. For several years, molecular marker tools and a modified Advanced Back Cross QTL (ABC-QTL) scheme have been tested for cost-effective pyramiding of useful genes from cultivated and wild gene pool through the elimination of phenotypic evaluations in each breeding cycle. This proposal seeks to make marker-assisted introgression of exotic genes into elite cassava progenitors widely available through the development of low cost approaches, to expand the gene tagging effort to other traits, and to establish a systematic approach of collection, evaluation, and use of additional wild germplasm.

## 10. Exploring Natural Genetic Variation: Developing genomic resources and introgression lines for four AA genome rice relatives

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**Executive Summary**

Cereals provide the majority of calories consumed by humans. Cereal production faces growing challenges due to the increasing human population, changing nutritional requirements, and variable environmental conditions that require new approaches to crop production. Wild relatives of modern crop species have survived for millions of years using natural genetic defences to endure biotic and abiotic aggressions. These wild relatives represent a valuable source of under-utilised genetic variation that is available to plant breeders and an invaluable source of genetic information for modern genomics research initiatives. A systematic approach is required to identify and characterise genes from wild species that can be used to enhance crop productivity in a range of environments and under diverse cultural conditions. Using rice as a model, we propose to (1) develop four libraries of interspecific lines called Chromosome Segment Substitution Lines (CSSLs) targeting chromosomal introgressions from different rice relatives, (2) develop a set of 140 molecular markers (called SNPs) identified in genes associated with tolerance to abiotic stress (drought, acid soils, mineral deficiencies, or toxicities), (3) validate the utility of the SNPs by using them in the development of the CSSLs in this project and exploring

their value in breeding programmes for other cereals, and (4) analyse a set of advanced CSSLs generated from Asian x African rice crosses for their phenotypic response to drought stress.

Generating such resources and knowledge will contribute to the objectives of Subprogrammes 1 and 3 by (i) utilising natural genetic diversity to develop whole-genome libraries of CSSLs as a permanent genetic resource for both breeding and genomics-based research, (ii) producing high-throughput, cost-effective markers to facilitate access to genetic diversity in a range of different cereal species, and (iii) making the CSSLs available to breeders and geneticists so that the intersection of their efforts will continue to generate new knowledge.

## 11. Functional Genomics of Cross-species Resistance to Fungal Diseases in Rice and Wheat (CEREALIMMUNITY)

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**Executive Summary**

Resistance shown by a plant species to the majority of potentially pathogenic microbes is known as non-host resistance. The events leading to non-host resistance in plants represent one of the least understood phenomena and a remaining challenge in the field of plant-microbe interactions. Comparative genomics is a promising method to identify key genes involved in cross-species interactions and to better understand their regulation at the genetic level and their evolution. Non-host resistance also represents one promising defence mechanism in developing durable resistance against plant pathogens, namely due to its effectiveness against a broad range of pathogen species and its durability in nature. The proposed project will strengthen and extend ongoing research in rice and wheat and aims to define the signalling and effector genetic components involved in non-host resistance in cereals in order to devise novel defence strategies with the potential to yield durable resistance against host pathogens in cereals. This project aims to implement existing breeding programmes for resistance to blast and rust diseases in developing countries, taking advantage of advanced genomic platforms and technologies.

## 12. Drought Tolerant Rice Cultivars for North China and South/Southeast Asia by Highly Efficient Pyramiding of QTLs from Diverse Origins

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**Executive Summary**

Rice is the staple food for most Asian and Chinese people, but rice production uses large amounts of water. Drought has become the single largest factor limiting rice production in Northern China and the rainfed areas of South/Southeast Asia. Developing drought tolerant (DT) rice cultivars is the most efficient way to stabilise rice production and alleviate food insecurity and poverty in China and Asia. In this proposed project, we aim to develop high yielding and DT rice cultivars for Northeast/Northwest China and the rainfed areas of South/Southeast Asia by exploiting the rich genetic diversity in the primary gene pool of rice in a large backcross breeding programme integrated with efficient selection and DNA markers. Using molecular markers, linkage disequilibrium mapping, and two large sets of introgression lines (ILs) in elite Chinese japonica backgrounds, having introgressed DT from 67 diverse germplasm accessions and breeding populations derived from 7 well characterised DT IR64 lines, our goal is to discover and characterise important DT QTLs in the process of breeding for high yielding and DT cultivars for the target environments. The expected outcomes from the project will include four major aspects: (1) important DT QTLs and multiple alleles at many QTLs identified, confirmed, and characterised in the elite rice backgrounds; (2) development of superior high-yielding and DT rice cultivars for Northeast/Northwest China and the rainfed areas of South/Southeast Asia; (3) knowledge, theory, and strategy generated for genetic improvement of complex phenotypes; and (4) training of 10 young scientists from China and South/Southeast Asia in molecular breeding. More importantly, information and knowledge generated from the proposed project will allow CAAS to establish modern breeding systems that fully integrate the molecular tools with the current breeding programmes for genetic improvement of major crops in China.

## 13. Development of Informative DNA Markers through Association Mapping in Maize to Improve Drought Tolerance in Cereals

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**Executive Summary**

Drought and low soil fertility are the major limiting factors for cereal-crop production in developing countries. The objective of this project is to use the natural variation inherent in the maize genome for the dissection of drought tolerance and for the identification of superior alleles. While maize grows in a wide range of environments and is the most diverse crop in the world, we do not know the genes that are responsible for these adaptations. For phenotypic selection, crops need to be fully evaluated in every environment, which is costly and time consuming, although it does allow genetic progress. Association studies, as proposed in this project, are based on correlation between a gene sequence and plant performance for target traits, and represent a powerful approach to evaluating candidate genes regulating plant phenotype. This project will focus on evaluating the genes in two major pathways that are involved in drought tolerance. We will build upon previous mapping approaches that have identified genomic regions containing a few hundred genes, and use high resolution approaches that can evaluate individual genes. This high resolution mapping

will require combining rapid molecular approaches with careful evaluation of diverse germplasm for drought tolerance and physiological response. Additionally, by screening several hundred diverse lines, this project maximises its potential to identify the best alleles in the maize gene pool. The discovery of superior alleles at the gene level will permit the development of molecular markers that can facilitate breeding drought tolerance in a wide range of germplasm. One important benefit of working with the natural variation is that any discovery can be rapidly converted to improved breeding materials without the societal and regulatory obstacles of transgenic materials. Because of the genetic and physiological commonalities among cereal crops, this knowledge gathered in maize can be applied to all other cereal crops.

## 14. Characterisation of Genetic Diversity of Maize Populations: Documenting global maize migration from the centre of origin

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**Executive Summary**

Although maize hybrids represent the most economically important portion of the species, maize breeding populations, open pollinated varieties (OPVs), landraces, and wild relatives contain the majority of the diversity found in maize, much of which has never been incorporated into improved varieties. Following a complicated pattern of introductions, populations originally from the centre of origin in Central America have been introduced into other countries, becoming adapted to many new growing conditions and local stresses, including drought. Past studies of maize population diversity have revealed useful clues as to relationships and patterns of diversity; however, a complete, global picture of maize diversity is lacking because analysis of heterogenous populations has been until recently very expensive and time-consuming. Phenotypic characterisation of cultivated maize and wild teosinte populations for traits important to breeders and farmers has been done only in a very limited manner, and at the molecular level, essentially not at all.

Drought tolerance is a trait of extreme importance to farmers who have access to limited resources, but is difficult to phenotype (especially in wild species) and sufficient diversity is lacking in current breeding germplasm, so a great need for new diversity exists. This study aims to complete the global picture of maize diversity and spread by collecting and analysing maize populations from geographic regions that have been underrepresented in previous studies as well as representatives of the wild ancestor of maize (teosinte). Structural characterisation will occur at the molecular level using SSR markers. The populations containing the most unique alleles at the SSR loci will then be characterised for markers associated with drought tolerance, as these are the populations most likely to contain new alleles i potentially for drought related loci. The genetic characterisation data will provide useful information for utilising these populations in genomic studies and breeding efforts to create drought tolerant maize.

## 15. Determination of a Common Genetic Basis for Tissue Growth Rate under Water-limited Conditions across Plant Organs and Genomes

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**Executive Summary**

The effort to minimise the impact of drought on yield needs new approaches for bridging traditional breeding to molecular genetics. Recent advances in comparative genomics allow information to be moved from one genome into another for identifying key genes controlling drought tolerance. However, comparison between species remains difficult because compared processes, organs, and conditions differ between species in most published studies. We will undertake a multiple-species, multiple-organ study on a key process: growth maintenance under water deficit. The project combines new approaches of phenotyping (controlled conditions and field), modeling, quantitative genetics, comparative genomics, and first steps towards association genetics. It also combines the strengths of research in "advanced" countries, CGIAR centres, and developing countries. It is applied to three cereals (wheat, maize, and rice) for growth maintenance of leaves and to three organs (leaves, roots, and reproductive organs) in maize. The project will adopt the approach of characterising environmental conditions in all experiments (including those for genomics), and analysing germplasm under controlled environment and field conditions using a modeling approach. Common genomic regions and genes important for growth will be identified through existing and new QTL data across the three cereals. Comparison of gene expression in common tissue across and within species will be used to identify candidates for detailed analysis. Questions to be addressed will include: How do identified genes contribute to growth maintenance in different climates around the world and how does that correlate with yields? And, what combinations of alleles optimise the growth of key tissues in droughted rice, wheat, and maize under different environments? A comparative study of the three species will generate results that feed into modeling work, thereby interpreting and using (for breeding) the genotype x environment interaction of key traits involved in drought tolerance such as early vigour, high light interception, or maintenance of reproductive development.

## 16. Isolation and Characterisation of Aluminium Tolerance Genes in the Cereals: An Integrated Functional Genomic, Molecular Genetic and Physiological Analysis

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Newton Carneiro, EMBRAPA
Robert Schaffert, EMBRAPA
Sandra Brammer, EMBRAPA
Pericles Neves, EMBRAPA
Rosangela Bevitori, EMBRAPA
Samuel Gudu, Moi University, Kenya

**Executive Summary**

One of the most important soil-related factors limiting agriculture in developing countries is acid soil pH (pH < 5). Acid soils occur for both natural and human-derived reasons. On acid soils, regardless of their source, toxic levels of aluminium (Al) ions are released into soil solution, where they damage roots and impair their growth and function. This damage results in reduced nutrient and water uptake, with concomitant reductions in crop yield. There is considerable natural variation in Al tolerance both within and between plant species, and we have assembled an interdisciplinary group of scientists to take advantage of this variation to improve crop tolerance to Al toxicity on acid soils. This proposal details an interdisciplinary project that will characterise recently isolated cereal Al tolerance genes as well as identify novel Al tolerance genes and physiological mechanisms in a range of cereal species (sorghum, maize, rice, and the Triticeae). The research group we have assembled has considerable expertise in the genetics, molecular biology, and physiology of aluminium tolerance in these crops, and has available the necessary genetic resources to ensure the success of this project. We will use information from candidate genes identified in wheat and sorghum, as well as ongoing progress from our genetic mapping and cloning programme in maize, to identify and verify candidate Al tolerance genes in several cereals species. The long-term goals of this research are to generate cereal genotypes expressing improved Al tolerance that ultimately can be distributed to farmers who till acid soils in Africa and other developing regions, thus exploiting a wide range of still hidden genetic variation for Al tolerance. Increasing the Al tolerance of staple crops, such as maize and sorghum, will help increase yields and, thus, food security.

## 17. Allele Mining Based on Non-Coding Regulatory SNPs in Barley Germplasm

**Principal Investigator:**

Michael Baum, ICARDA

**Collaborating Scientists:**

W. Powell, University of Adelaide, Australia
P. Langridge, Australian Centre for Plant Functional Genomics Pty Ltd
Mark Tester, Australian Centre for Plant Functional Genomics Pty Ltd
J. K. Eglinton, University of Adelaide, Australia
M. Morgante, Universita' di Udine Via delle Scienze, Italy
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Stefania Grando, ICARDA
Sripada Udupa, ICARDA
Maria van Korff, ICARDA
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**Executive Summary**

In recent years, analysis of genetic variation has focused on the study of changes in DNA coding for proteins. It is now becoming increasingly clear that this only accounts for one aspect of heritable variation and for many traits, notably tolerance to environment stresses, the level of gene expression is also likely to be of great importance. If changes in gene expression underlie many evolutionary changes in phenotype, then identifying the genetic variants that regulate gene expression is a significant and important endeavour. One of the key problems in genetics is how to identify this type of variation. We propose a robust, quantitative approach to efficiently identify plant genes that harbour such regulatory variants. The approach is novel and particularly amenable to plants since it is based on monitoring gene expression in experimentally created hybrids. A successful outcome will provide a new mechanism to connect genotype to phenotype based on changes in gene expression rather than changes in the structure of an encoded protein. This approach will be used to characterise a series of genes identified and to reveal potential candidates for tolerance to drought, frost, cold, and salinity stresses. The approach is generic and widely applicable. The project will also involve training researchers in developing countries and will create a high quality, collaborative network of researchers delivering new knowledge on genetic diversity and translatable outputs for the developing world.

# SP1 COMMISSIONED GRANTS

## 2005-06: Supporting Emergence of Reference Drought Tolerance Phenotyping Centres

**Principal Investigator:**
Frederico Ozanan Machado Durães, EMBRAPA
**Co-Principal Investigators and Collaborating Scientists (EMBRAPA):**
Antonio Carlos de Oliveira
Antonio Marcos Coelho
Camilo de Lélis Teixeira Andrade
Elto Eugenio Gomes e Gama
Fredolino Giacomini dos Santos
Paulo Emílio P. de Albuquerque
Manoel Xavier dos Santos
Reinaldo Lúcio Comide
Beatriz da Silveira Pinheiro
Cleber Morais Guimarães
Orlando Peixoto de Morais
Natoniel Franklin de Melo
Luiz Balbino Morgado
Hélio Wilson Lemos de Carvalho
Luciana Marques de Carvalho
Milton José Cardoso
Edson Alves Bastos
Francisco Rodrigues Freire Filho
Maria da Glória Trindade
Walter Quadros Ribeiro Jr.

**Executive Summary**
The development of drought tolerant varieties for crops of economical importance presents a major challenge for the 21st century, considering that agriculture growth will be limited by world water availability. A first step is to select germplasm adapted to water stress conditions through appropriated screening techniques and defined protocols. Thus, the great challenge is the identification and characterisation of drought tolerant genitors to provide material to be used in genetic breeding programmes focused on regions historically known as prone to water deficit during crop growing season. The improvement of drought tolerance relies on the manipulation of the traits that limit yield and their accurate phenotyping under the prevailing field conditions being targeted. This issue is particularly crucial for the breeding programme and identification of QTLs for traits categorised as adaptive as compared to constitutive traits per each species. For this purpose it is necessary to amplify an infrastructure to allow plant exposure to water deficit pressure to be used for the evaluation of genotypes and characterisation of plant physiological responses to these stress conditions.

The objectives of this project are to develop useful phenotypic evaluation protocols for cereals (maize, sorghum, rice, and wheat) and legume crops (common bean and cowpea), as well as to establish the amplification of the three Phenotyping Centre of Excellence for Drought Tolerance Studies composed of phenotyping central laboratories. These laboratories include a controlled environment field and greenhouse as well as a training unit for researchers and research assistants, in addition to six-eight experimental stations located in regions with well

defined dry season periods to assure total soil moisture control during the drought phenotyping field experiments. In fact, the project seeks to establish a scientific and service net, like a model to drought tolerance phenotyping of cereals and legumes, including national and international genotypes.

Embrapa-National Maize and Sorghum Research Centre, as the main coordinating institution, has over 30 years of experience working with the application of phenotyping methodologies, conducting maize and sorghum breeding programmes, and releasing drought tolerant germplasm. All partners have extensive experience with other crops such as rice, bean, wheat, etc. The innovative character of the present proposal consists of having different crop expertise aggregated in one single project, stimulating the exchange of personal experiences, providing simultaneous experiment conduction and data integration, establishing news and future partnerships for simulation models, and promoting knowledge diffusion by planning and organising training courses.

### 2005-07: Whole Plant Physiology Modeling of Drought Tolerance in Cereals

**Principal Investigator:**
Marcel de Raïssac, Cirad

**Collaborating Scientists:**
Delphine Luquet, Cirad-Agropolis
François Tardieu, Cirad-INRA
Renée Lafitte, IRRI
M Dingkuhn, Cirad-Agropolis
JC Combres, Cirad-Agropolis
C Welker, Cirad-INRA
Scott Chapman, CSIRO. Australia
Graeme Hammer, University of Queensland
B. Bouman, IRRI
M Bänzinger, CIMMYT
M Reynolds, CIMMYT
R Trethowan, CIMMYT
Eva Weltzien, ICRISAT
Frederico Duraes, EMBRAPA
Mark Cooper, Pioneer

**Executive Summary**
The present project is a continuation of the GCP phenotyping workshop organised in July in Montpellier, where more than 40 breeders and physiologists from inside and outside the consortium met for a week. Conclusions of the workshop (available on GCP website (www.generationcp.org) stressed the importance modeling in supporting phenotyping processes for drought tolerance by: (i) a quantification of traits and integration of their impact on yield, (ii) a genetic analysis of adaptive traits, and (iii) a characterisation of target population of environments.

The need for better interactions between physiologists, modelers, and breeders to develop a comprehensive approach and improve phenotyping methods and outputs was also stressed during the meeting and must be kept in mind as a main issue of this project.

This project is the only GCP project to develop modeling approaches and deliver new tools. Consequently, it proposes interactions or complements with other initiatives:

- Competitive Project 4 "An ecophysiological-statistical framework for the analysis of G X E and QTL X E," focusing on more statistical concepts, in which some environmental characterisations will be carried out using the same models for wheat and maize as in this project.

- The commissioned project on "Simulation on marker-assisted selection strategies." An attempt will be made to link these two projects on the basis of component 3 activities.
- The commissioned project on "Reference drought tolerance phenotyping centres." A first interaction is planned on environment characterisation of these centres by model use.
- Interaction will be sought with the project on "Modeling alternate drought tolerance strategies on globally important crops" lead by IFPRI on the impact of improved drought tolerance characterisation.

## 2006-01: Developing Strategies for Allele Mining within Large Collections

**Principal Investigator:**

N.R. Sackville Hamilton, IRRI

**Collaborating Scientists:**

M. Lorieux, CIAT
C. Brondani, EMBRAPA
H. Upadhyaya, ICRISAT
R. Varshney, ICRISAT
B.J. Furman, ICARDA
S. Udupa, ICARDA
M. Baum, ICARDA


**Executive Summary**

The GCP SP1 has undertaken new steps towards rationalising the utilisation of germplasm collections. It has assembled a large percentage of the diversity of crop genepools into progressively refined subsets as composite, core, and reference collections. These will enable improved understanding of the structure of genetic diversity and its ecogeographic distribution, and discovery of new functional genes and the range of alleles of each gene included in the composite collections.

However, they represent only a small percentage of the larger collections: in the case of rice, the composite collection contains only around 2% of the germplasm held in the genebank at IRRI, and probably less than 0.5% of global holdings in all rice genebanks. Many distinctive alleles, haplotypes, and genotypes have not been captured in the composite collections. The next big challenge is to explore this additional diversity.

This project seeks to establish a strategy for efficiently exploring diversity held within the large collections outside the composite collections. The strategy constitutes true "allele mining": "tunnelling" through the collections, sampling and testing accessions as we go, and using the results to determine where to tunnel next.

SP1 results to date will be analysed to identify genetic gaps and boundaries in the composite collection, and to establish relationships between the rich new molecular data and the sparse passport and phenotypic data previously available. Objective functions will be developed to predict which additional accessions are most likely to lie in specified locations of the hyperspace of molecular data. Those accessions will be fingerprinted to test the predictions and thence to refine the objective functions. The efficiency of the approach will be analysed. The output will be a generic strategy for discovering novel diversity without systematically fingerprinting every accession and will be more efficient than using random subsets.


## 2006-02: A Dataset on Allele Diversity at Orthologous Candidate Genes in GCP Crops

**Principal Investigator:**

Dominique This, Agro-Montpellier, Agropolis-France

**Executive Summary**

Many candidate genes have been proposed during the last years that could explain some aspects of tolerance to drought stress, for a specific crop and in a specific environment. However, the relationship between gene structural polymorphism and functional diversity is seldom clear. Moreover, whether this information may be valuable for different species is poorly investigated. The Generation Challenge Programme is the only initiative that can coordinate a global approach with parallel components in a wide range of crops. Within the SP1 and SP2 subprogrammes, this project proposes to produce and deliver a public dataset of allelic diversity at orthologous candidate genes across seven important GCP crops. A set of 10 to 12 genes corresponding to enzymes involved in sugar metabolism, or regulatory components of drought tolerance/water use efficiency, will be investigated for their orthologous relationships among crops, and their sequence polymorphism will be assessed in a sample of 300 reference accessions for each crop. This reference germplasm, derived from selection after SSR genotyping and meant to be submitted to drought related phenotyping in complementary projects, will allow testing association between observed polymorphism and trait variability. We will thus establish a GCP resource that will be useful to quickly capture the value of results obtained in the most advanced genetic studies with regards to drought tolerance. It will enable production of scientifically coherent sets of (ortho)allelic diversity data with high information content and scope for application and impact. As such, it will facilitate establishment of collaborations with partners who run high-throughput genomics facilities. It is also meant to attract partnerships with advanced research groups interested in particular biological processes, metabolic pathways, and gene families. This resource may, then, allow plant breeders to identify specific progenitors in their crops based on gene haplotypes to further improve adaptation to environmental stresses.

## 2006-03: SNP Analysis of the Genetic Diversity along the Rice Genome (HAPLORYZA)

**Principal Investigator:**

Kenneth L. McNally, IRRI

**Collaborating Scientists:**

Claire Billot, Agropolis-CIRAD
Brigitte Courtois, Agropolis-CIRAD
Gérard Second, Agropolis-IRD
Dominique Brunel, INRA-CNG
Mark Lathrop, CNG

**Executive Summary**

Asian cultivated rice occurs as two major types, indica and japonica, that appear to have arisen from independent domestication events. Even though rice is a predominantly self-pollinated crop, both types can frequently be found within the same region allowing the prospect for genetic exchange between them.

Since whole genome sequences are available for each type, we now have the opportunity to identify single nucleotide polymorphisms (SNP) suitable for determining the extent of linkage disequilibrium and haplotype structure that is indicative of their differentiation. In this project, the high quality japonica Nipponbare sequence (IRGSP) will be compared to the whole genome shotgun indica 93-11 (Beijing Genomics Institute) sequence to identify a set of 1536 SNPs suitable for undertaking genome scans. These SNPs will be genotyped across 900 types predicted to cover the range of indica/japonica diversification and prospective natural hybrids between them. The genotyping platform will consist of single base extension SNP assays implemented on the Illumina BeadArray platform at the National Genotyping Centre at Evry.

The outcome of this effort will be a fine scale LD map for common SNP variation among the indica and japonica types of rice. This will also help to clarify the origin of the peculiar rice varietal groups, such as the aus or basmati types, in relation to indica and japonica. Analysis of this SNP data with phenotypic data on a range of traits will

allow the identification of loci governing the differentiation between the two major types, opening the way for effective manipulation of subtle variation that has hindered the full exploitation of this diversity in hybridisation programmes.

More generally, the indica-japonica pattern represents a typical case of diversity derived from admixture. This may reveal patterns of relationships whose existence enables LD-based mapping of genes of agricultural interest and may inspire applications in other inbreeding species.

## 2006-04: Phenotyping in the Field: Global capacity accessible to the GCP – Inventory of phenotyping resources and capacity for the CGP

**Principal Investigator:**

Jane Toll, IPGRI

**Collaborating Scientists and Institutions:**

A.Blum, Plantstress.com, Israel
Mahalakshmi Viswanathan
GCP consortium and collaborating institutions
Challenge Programme on Water for Food

**Executive Summary**

Plant genetic resources and the knowledge about their resistance to biotic and abiotic stresses are critical for ensuring their usefulness in germplasm enhancement. Marker-assisted selection (MAS) in crop breeding programmes is aimed at improving the efficiency and effectiveness of breeding for those traits that are influenced by the environment and therefore have low heritability. Therefore accurate phenotyping is key to the success of the development of MAS breeding programmes. As the GCP is currently placing emphasis on drought – this study will initially limit its area to drought but experience gained can be extended to other traits as required. As the emphasis of GCP moves towards other abiotic (salinity, aluminium toxicity, etc) stress and biotic stress phenotyping network resources creation will be undertaken.

Drought, or improved productivity under limited water conditions, is a trait that has often found limited success in breeding programmes. Opportunity for the use of linked markers in breeding for performance under drought lies in their use for selection of difficult, low heritability, or expensive-to-measure traits such as root growth or water soluble carbohydrate content. Many traits are reported to confer drought tolerance in crops e.g., matching phenology to water supply, through photoperiod sensitivity, developmental plasticity, mobilisation of pre-anthesis dry matter, rooting depth and density, low root hydraulic conductance, narrow xylem vessel, early vigour (canopy), leaf area maintenance (´stay-green´), osmotic adjustment, low lethal water status, reduced stomatal conductance, leaf movements, leaf reflectance, heat tolerance, low epidermal conductance, and transpiration efficiency. All this is compounded by the different crops which may have specific drought responses beyond those mentioned above. It is easier to select for traits conferring drought tolerance (which can be related to gene actions) than to breed for yield under stress conditions, which may be due to many traits pyramiding together to confer the tolerance. Reliable and repeatable phenotyping protocols are therefore central to the development of MAS for drought.

The phenotyping of drought resistance traits employs field or laboratory/screen-house facilities with precision irrigation methods. The traits measured also need special equipments and methods to measure. Breeders have developed their own modifications of physiological testing, which were not always documented. Such facilities and methodologies exist among the consortium members and some have developed well-coordinated drought networks. Some of these facilities and techniques require trained and skilled manpower to operate. This study will collate all the available resources and capacities that are available among the consortium members, and suggest ways to optimally use these facilities for crops and regions.

## 2006-05: Development and Genotyping of a Faba Bean Composite Collection

**Principal Investigators:**
B.J. Furman, ICARDA
M. Baum, ICARDA
**Collaborating Scientists:**
G. Duc, INRA
M.J. Suso, IAS

**Executive Summary**

The Generation Challenge Programme Subprogramme 1 has the main goal of exploring genetic diversity of global germplasm collections of the Consultative Group of International Agricultural Research (CGIAR). An integral goal of the Generation Challenge Programme is to develop composite collections representing the genetic variation present in the entire collection for the rational use of genetic resources in crop improvement programmes. Such composite collections will then be characterised with anonymous molecular markers. This molecular characterisation will allow for a study of the diversity across a given genus and will potentially identify candidate genes involved in resistance to biotic and abiotic stresses.

The International Centre for Agricultural Research in the Dry Areas (ICARDA) has a global mandate for Faba Bean improvement and as such houses one of the largest collections globally with 10,809 accessions from 69 countries. This collection is maintained in two types of germplasm collections (Robertson 1985). Original germplasm accessions are maintained as heterogeneous composite bulks known as the International Legume Faba Bean (ILB) collection. This collection contains 5749 accessions. A Faba Bean Pure Line (BPL) collection has been derived from the ILB collection by the creation of single plant progeny rows. This collection contains 5,060 accessions. Most of these germplasm accessions have been characterised for various morphological and agronomic traits. In addition, INRA in Dijon, France and INIA in Cordoba, Spain house large collections of European Faba Bean with 1,500 and 1,150 accessions, respectively. From these collections, we propose here to identify a composite germplasm set of approximately 1,000 accessions to be characterised utilising molecular markers to determine the genetic structure of this composite collection.

## 2006-06: Genotyping of Composite Collection of Finger Millet

**Principal Investigator:**
HD Upadhyaya, ICRISAT
**Collaborating Scientists:**
R.K. Varshney, ICRISAT
D. Hoisington, ICRISAT
C.L.L. Gowda, ICRISAT
C.T. Hash, ICRISAT
S. Chandra, ICRISAT

**Executive Summary**

Finger millet, Eleusine corcana (L.) Gaertn., is an important coarse grain food crop in Africa and South Asia. It's a hardy crop that can be grown in very diverse environments from almost at sea level to about 2,000 meter above sea level. Globally, millets are grown in 3.5 million ha, with a total production of 4.5 million tons annually. China, India, Myanmar, Nepal, and Srilanka in Asia and Uganda, Rwanda, Zaire, and Kenya in Africa are the major producers of finger millet. Finger millet seeds are rich in calcium and iron, and contain 7-14% seed protein that has higher tryptophan, cystine, and methionine contents than many cereals. There have been very limited crop improvement efforts to boost the production and productivity of this crop in spite of the fact that it is the hardiest crop and the seeds have high biological food value.

An important goal of the Generation Challenge Programme is to facilitate the extensive genetic characterisation, using molecular markers, of vast genetic resources to identify diverse accessions with beneficial traits for use in molecular genetics and crop improvement programmes. The genebank at ICRISAT holds 5,940 accessions of finger millet from 24 countries. Since the entire collection cannot be used for molecular characterisation, it is important to develop a composite collection representing finger millet germplasm. Using morphological descriptors and characterisation and evaluation data on 5,940 accessions, ICRISAT scientists developed a composite collection of 1,000 accessions in 2005 that were further grown, and a single panicle selfed from each accession that was harvested at maturity, processed, and whose seed samples kept in gene bank. We propose to determine the genetic structure of this composite collection using 20 DNA markers.

## 2006-29: Preparing IITA-Cassava Reference Germplasm for Distribution and Association Mapping

**Principal Investigator:**
Dominique Dumet, IITA
**Collaborating Scientists:**
Morag Ferguson, IITA
A. Bode, IITA
Martin Fregene, CIAT

**Executive Summary**
IITA, CIAT, and EMBRAPA have completed the genotyping of 3,000 cassava clones, using 36 primers. A reference set is being selected from this data. It is important that this reference set is made readily accessible to anyone who would like it. The movement of cassava between Africa and South America has been hindered by quarantine restrictions for many years. This is due to Frog Skin Disease in South America and Cassava Mosaic Disease (CMD) in Africa. Within Africa the movement of cassava germplasm has recently been exacerbated by the emergence of different strains of CMD and cassava brown streak virus (CBSV). Cassava plantlets must be in-vitro and certified disease free to be distributed. This project aims at putting the IITA reference cassava germplasm collection, and selected known drought tolerant varieties in-vitro, certifying it disease-free, and multiplying it for multi-locational drought tolerance evaluations leading to association mapping studies. In addition, the IITA reference set will be exchanged with that from CIAT.

## 2006-30: Development and Genotyping of a Foxtail Millet Composite Collection

**Principal Investigator:**
HD Upadhyaya, ICRISAT
**Collaborating Scientists:**
R.K. Varshney, ICRISAT
C.T. Hash, ICRISAT
D. Hoisington, ICRISAT
C.L.L. Gowda, ICRISAT
S. Chandra, ICRISAT

**Executive Summary**
The genus Setaria is widely distributed in warm and temperate areas, and foxtail millet (Setaria italica (L.) Beauv.) is the most economically valuable coarse grain food crop, largely grown in China, India, Russia, and the United States. Globally, the millets are grown on 3.5 million ha, with a total production of 2.9 million tons and productivity of 0.83 t ha-1. Millet grains, including foxtail millet, are rich in calcium, iron, phosphorous, vitamins, sulphur-containing amino acids, and soluble fibre content. Because of these properties, minor millets have been recently designated as "nutritious millets" for the poor man's diet. There have been very limited crop improvement efforts to boost the production and productivity of this crop in spite of the fact that it is a very hardy crop and its seeds have high biological food value.

The Rajendra S. Prasad gene bank at ICRISAT holds 1,481 cultivated and 54 wild relative accessions of foxtail millet from 26 countries. These germplasm accessions have been characterised for various morphological and agronomic traits. To facilitate the use of germplasm in breeding, it is important to develop a composite collection capturing most of the genetic variation present in the entire collection. An important goal of the Generation Challenge Programme is to help genebank curators to develop composite collection, representing most of the genetic variation present in the entire collection, for the rational use of genetic resources in crop improvement programmes. We propose to develop a composite collection of 500 accessions that will be genotyped using 20 SSR markers to determine the genetic structure of this composite collection.

## 2006-31: Development and Genotyping of a Pearl Millet Composite Collection

**Principal Investigator:**

HD Upadhyaya, ICRISAT

**Collaborating Scientists:**

C.T. Hash, ICRISAT
S. Senthilvel, ICRISAT
R.K. Varshney, ICRISAT
D. Hoisington, ICRISAT
K.N. Rai, ICRISAT
R.P. Thakur, ICRISAT
S. Chandra, ICRISAT

**Executive Summary**

Pearl millet [Pennisetum glaucum (L.) R. Br.] is an important coarse grain food, feed, and fuel crop in Africa and South Asia. This hardy C4 cereal can be grown in very diverse environments—from sea level to about 1,800 meters above sea level. Pearl millet is grown in over 40 countries, predominantly in Asia and Africa. It is cultivated in 29 m ha, supporting >100 million people. China, India, Pakistan, and Yemen in Asia and Nigeria, Niger, Mali, Senegal, Burkina Faso, Sudan, and Tanzania in Africa are the major countries producing pearl millet. In addition, the crop is expanding rapidly in the acid soil savannahs of Latin America, where it finds use as the mulch component in conservation tillage systems of soybean production, and as an annual green fodder crop. The grains of pearl millet are rich in minerals that are high in fat (3.5-7.0%), and contain 10-14% protein that has high tryptophan, cystine, and methionine contents compared to other major cereal crops such a rice, wheat, and maize. Efforts to boost the production and productivity of this crop have been reasonably successful in India, where average grain yields have more than doubled over the past 40 years due to a combination of genetic improvement and improved crop management. Elsewhere there have been very limited crop improvement efforts to boost the production and productivity of this crop in spite of the fact that it is the hardiest tropical cereal crop, grown in the hottest, driest regions where dryland agriculture is practiced, and its grains have high food and feed value.

The Rajendra S. Prasad gene bank at ICRISAT holds 20,844 cultivated and 750 wild relative accessions of pearl millet from 50 countries. To make use of germplasm in applied plant breeding, it is important to develop a composite collection capturing most of the genetic variation present in the entire collection. An important goal of the Generation Challenge Programme is to help CGIAR's genebank curators to develop such composite collections, representing most of the genetic variation present in the entire collection for each crop, for the better management of genetic resources, and facilitate their wider use in crop improvement programmes. We propose to develop a composite collection of 1,000 pearl millet breeding lines and germplasm accessions that will be genotyped using 20 DNA markers to determine the genetic structure of this composite collection.

## 2006-32: Molecular Characterisation of a Representative Pigeonpea Germplasm Sample

**Principal Investigator:**

HD Upadhyaya, ICRISAT

**Collaborating Scientists:**

Legume Molecular Scientist, ICRISAT
Subhash Chandra, ICRISAT
KB Saxena, ICRISAT

Executive Summary

Pigeonpea is a major grain legume crop of the tropics and subtropics, grown as a field and/or a backyard crop in about 87 countries between 300 N and 300 S latitudes. Of the 25 countries in Asia where pigeonpea is grown, India, Myanmar, and Nepal are the major producers. Kenya, Malawi, Uganda, Mozambique, and Tanzania in southern and eastern Africa, and the Dominican Republic, Venezuela, Haiti, and Puerto Rico in Latin America are the other important pigeonpea growing countries. In India, which accounts for more than 80% of the world's pigeonpea production, the seed is primarily consumed as dhal (decorticated dry split peas) and in Latin America immature seeds are used as vegetable and canned peas. Various parts of the pigeonpea plant are used as feed, fodder, fuel wood, and green manure. It also arrests soil erosion especially in sloping lands, and enriches the soil with organic content and provides nitrogen through symbiotic rhizobia. Therefore, due to these multiple uses, pigeonpea plays an important role in subsistence agriculture.

The genebank at ICRISAT, Patancheru, India, has conserved 13,077 accessions of cultivated pigeonpea and 555 accessions of 41 wild species from 74 countries. However, the use of germplasm in pigeonpea improvement programmes is limited.

## 2006-33: Development and Genotyping of a Composite Germplasm Sample of Potato

**Principal Investigator:**

Marc Ghislain, CIP

**Executive Summary**

This project aims at completing the work plan established for the "Marker Analysis-Data Analysis-Potato" activity funded by the Generation Challenge Programme (GCP) in 2004. The actual cost of the experiments in our conditions is such that we mobilised in-kind contribution from CIP core budget in 2005, which is now drying out. The earlier experiments achieved very exciting results. Hence, we request an additional US$18,500 from the GCP.

The production of the SSR marker data set for potato was initiated after the high throughput genotyping (HTG) facility was established at the end of the first semester of 2004. This facility has been entirely assigned to the GCP activity on a tier 1 crop: Potato. To date we have concluded the identification of 31 new SSR markers to complement the 22 already in use at CIP before the initiation of the GCP activity. Using these 53 SSR markers, 716 landraces of cultivated potato were genotyped on the LI-COR 4300 using the M13 tailing protocol. This large data set was completed at the end of the first semester of 2005. Genetic analysis has revealed significant structure among and probably within the cultivated potato groups. Samples of two genetic mapping populations have also been included in order to map the new SSR markers. The germplasm analysed to date makes up just under 80% of the 1,083 clonal accessions proposed for CIP's Composite Genotype Set.

A number of landraces were omitted from the 2004-2005 analysis due to delays in obtaining leaf tissue from in vitro plants or acquisition status which is now being clarified. Since phenotyping data are available for these, their genotyping would allow them to be included with germplasm that will be used for association mapping and other activities of the GCP. In addition, no advanced hybrids or improved varieties have been analysed yet, beyond a small start made for identification purposes in our breeding programme. CIP and NARS breeders have their preferred gene pool that has not been genetically characterised. This germplasm was identified by potato breeders in 2004 and to a large extent included in the composite genotyping set. However, due to limited experience with

genotyping large collection and with the new HTG facility, we did not reach our target of genotyping 1,083 genotypes with 50 SSR markers. We decided to leave out breeder's material in order to produce a valuable data set which has intrinsic interest. We have now gained significant experience and see that it is essential to genotype the germplasm used by breeders. The objective is to understand what germplasm has been exploited by breeders as well as engage this community in a common research strategy, making better use of the tools derived from molecular genetics.

# SP2 COMMISSIONED GRANTS

## 2005-09: Systematic Evaluation of Rice Mutant Collections for Conditional Phenotypes with Emphasis on Stress Tolerance

**Principal Investigator:**
Andy Pereira, WUR
**Co-Principal Investigators:**
Hirohiko Hirochika, NIAS
Hei Leung, IRRI
Emmanuel Guiderdoni, AGROPOLIS
Mathias Lorieux, IRD/CIAT
Manabu Ishitani, CIAT
Tiegang Lu, CAAS
Qifa Zhang / Deming Jin, HAU, China
**Collaborating Scientists:**
Gyn An Pohang, Univ. Science and Technology, Korea. Srinivasan Ramachandran Temasek Lifesciences Laboratory, Singapore
Narayana Upadhyaya, CSIRO
Venkatesan Sundaresan, UC Davis

**Executive Summary**
The rice genome sequence provides the basic framework for the functional analysis of monocot genomes. International efforts have produced rice mutant resources that are a powerful functional genomics tool to identify the function of the sequenced genes. This consortium proposes to create a platform to identify genes that can contribute to a phenotype of resistance/tolerance to abiotic/biotic stresses. Expression analysis of various plant genomes has revealed genes that respond to environmental stresses. In addition, the ongoing functional analysis of Arabidopsis and other model plants identifies genes and associated mechanisms involved in stress tolerance. This comparative genomics information will be integrated to identify a set of candidate rice genes predicted to be associated with drought and other stress responses.

In a reverse genetic strategy, we will use sequence-indexed knockout mutant resources developed by the international rice community to identify insertions in the target stress-associated genes. These insertions include rice Tos17 transposons, heterologous Ac-Ds transposons, and T-DNA inserts that are identified by available flanking sequences (FSTs), supplemented by PCR-based screens for inserts. In addition, TILLING will be used to supplement the mutant coverage, and also provide non-transgenic stocks for field testing. To resolve gene redundancy, gain-of-function overexpression lines will be generated by transformation of appropriate constructs, and available activation tag populations will also be accessed for overexpression mutants.

To facilitate novel gene discovery, a forward genetics mutant screen will be carried out with random genotypes that have been sequence indexed, thus aiding their further analysis. The mutant genotypes will be phenotyped for drought and disease stress parameters at appropriate growth stages in greenhouse and field-based screens. Genotypes with altered stress tolerance phenotypes will be tested for other abiotic/biotic stresses. Whole genome microarray analysis will be conducted to identify the downstream genes and characterise the stress response mechanism involved. The genes can be utilised directly by transformation to provide stress tolerance, or for cereal comparative genomics studies and allele mining for breeding.

## 2005-10: Collection, Distribution, Phenotyping and Genotyping Directed towards Utilisation of Existing Wheat Genetic Stocks to Enhance Tolerance/Resistance of Wheat Cultivars to Abiotic and Biotic Stresses with Emphasis on Drought

**Principal Investigators:**
Tom Payne, CIMMYT
**Collaborating Scientists:**
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Tetsuo Sasakuma, Kihara Institute for Biological Research, Japan
Hitashi Tsujimoto, Tottori University, Japan
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John Snape, John Innes Centre
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Bikram Gill and Bernd Friebe, Kansas State University
Perry Gustafson, USDA-ARS, University of Missouri
Adam Lukaszewski, University California Riverside
Mark Sorrells, Cornell University

**Executive Summary**
Since 1936, a wealth of genetic stocks has been developed in tetraploid (Triticum turgidum L.) and hexaploid (T. aestivum L.). These genetic stocks include material containing intervarietal and interspecific translocations, chromosome and chromosome arm additions and deletions, chromosome and alien substitution addition lines, mono- and polysomic series, recombinant doubled haploid populations, mapping populations, NILs, point and other mutations, and synthetics. Hexaploid wheat is allopolyploid in origin, and the homoeology existing between its three component genomes allows for a range of aneuploidy (i.e. additions, substitutions, deletions, etc.) to be tolerated.

These genetic stocks were often developed for specific purposes, e.g., as new source of disease resistance genes, but have seldom been systematically screened for other value-added traits of interest. A few genes introduced from other species, e.g., rye (Secale cereale L.), have had a tremendous impact on wheat improvement. It can be assumed that a systematic screening of available genetic stocks will reveal useful genetic variation for many value-added traits of immediate interest to breeders. An important advantage is that any gene characterised in any of the existing or newly created wheat genetic stocks can be transferred to improved wheat cultivars without requiring the utilisation of any biolistic or Agrobacterium transformation techniques. And finally, it is anticipated that the distribution of these genetic stocks worldwide will result in many research projects, in particular in the area of gene identification (including across species/genera), marker development, and association mapping, which will greatly increase our knowledge of wheat genetics and breeding efficiency in the future.

It is intended that, to the fullest extent feasible, all genetic stocks within this project will be placed within the Multilateral System of Access and Benefit Sharing to be established under the International Treaty of Plant Genetic Resources for Food and Agriculture (ITPGRFA), and that they may be freely distributed under the standard ITPGRFA material transfer agreement (MTA). (FAO has an explanatory page about the Treaty at http://www.fao.org/ag/cgrfa/itpgr.htm, and a video at http://www.fao.org/videocatalogue/index.jsp?lang=EN).

It is also intended that, to the fullest extent feasible, results obtained from using these genetic stocks will be considered to be public goods which can be used without restrictions by others. Due to a number of ambiguities in the ITPGRFA that have not yet been resolved, it is not feasible to anticipate all potential implications of the ITPGRFA at this time. Accordingly, to the extent that any germplasm used in this project is protected by

intellectual property rights, and to the extent that placing such germplasm within the Multilateral System would be inconsistent with such rights, the parties will endeavour to devise a system for working with and distributing such germplasm that both respects those intellectual property rights and achieves the public goods aims of this project as outlined above.

The preference of this programme, however, shall be for using germplasm that is free of intellectual property rights. Stocks that are initially requested through the proposed central database-facilitated CIMMYT website or by normal email to CIMMYT representing the consortium of key genetic research groups listed in our full proposal, may later actually be sent out from the originator's programme. This may be especially the case for cytogenetic stocks requiring the resident expertise to guarantee quality maintenance of the stocks. CIMMYT would function in that case as a clearing house for routing the requests. The latter routing would allow the material to be shared under the originator's MTA.

## 2005-11: Legume Mutant Resource Development

**Principal Investigator:**

Matthew Blair, CIAT


**Executive Summary**

Grain legumes have a paucity of mutant resources compared to Arabidopsis and the cereals. Between the two broad branches of grain legumes, the tropical legumes have fewer mutant stocks compared to the temperate legumes. A well-developed mutant stock, particularly in genotypes of common bean (Phaseolus vulgaris), a simple diploid species with a small genome (650 Mb), will serve the broad community involved in tropical legume improvement, aiding gene-discovery both in common bean, the most widely consumed grain legume for human consumption and a major protein and mineral source in East Africa and Latin America, as well as in two tropical legume relatives: cowpea (Vigna unguiculata), a food crop important in West African agriculture, and soybean (Glycine max), a major industrial and feedstock crop around the world. Mutant stocks in common bean will allow researchers to conduct both forward (systematic phenotypic screening) and reverse genetics (TILLING or Targeting Induced Local Lesions In Genomes) experiments aimed at understanding the genes involved in abiotic and biotic stress tolerance as well as those genes involved in biological nitrogen fixation in the tropical legumes. Mutations will be sought in common bean genes that have been isolated at CIAT and shown to be associated with drought tolerance. The phenotypic effect of these mutations will be analysed as a proof of concept for the value of the mutant stocks generated by this project.


## 2005-12: A Saturated Potato Mutant Population for Functional Genomics among Solanaceae and Tuber Crops

**Principal Investigator:**

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**Collaborating Scientists:**

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Matilde Orillo, CIP
Glenn Bryan, Scottish Crop Research Institute
Robbie Waugh, Scottish Crop Research Institute
John Bradshaw, Scottish Crop Research Institute
Gavin Ramsay, Scottish Crop Research Institute

Dani Zamir, Hebrew University of Jerusalem
Naama Menda, Hebrew University of Jerusalem
Yaniv Semel, Hebrew University of Jerusalem

**Executive Summary**
Complete sequencing of genomes and transcriptomes provides baseline genetic information, which is increasingly being exploited between related species by comparative genomics. However, the identification of gene function remains one of the most challenging tasks of plant functional genomics. The virtually unlimited number of alleles and allele combinations possible for a single organism makes necessary the development of special tools and genetic stocks designed for functional analyses. Tuber crops, including the potato, generally have limited or poorly accessible genetic stocks. A saturated mutant population of a wild potato species is proposed here as a genetic resource useful for forward and reverse genetics in Solanaceae and other tuber crops. Ethyl methane sulphonate (EMS) mutagenesis will be performed on botanical seed of a diploid self-compatible and near-homozygous accession of the tuber-bearing species Solanum verrucosum to produce approximately 400,000 mutant chromosomes in 20,000 M2 seeds. Validation of the mutant population will be conducted for target genes already characterised in tomato and the data will be presented in the Solanaceae Genome Network (SGN).

## 2005-13: Crop Gene Expression Profiles and Stress-gene Arrays

**Principal Investigator:**
Tiegang Lu, CAAS
**Co-Principal Investigators:**
Guozhen Liu, Beijing Genomics Institute, China
Shoshi Kikuchi, NIAS
Manabu Ishitani, CIAT
**Collaborating Institutions:**
IRRI
CIMMYT

**Executive Summary**
cDNA/oligo microarrays currently provide a robust and accessible platform for genome-wide expression analysis. Whole-genome arrays have been developed for rice, barley, maize, and possibly wheat. The maize and rice chips are being used in Year 1 commissioned research in the Generation Challenge Programme (GCP). The identification of stress-tolerance genes by a combination of genome-wide expression and protein-protein interaction analyses has proven promising. While gene expression analyses are being pursued in multiple crops, relatively few attempts have been made to integrate experiments to enable cross-species comparison, which will provide opportunities to study the evolution of biological systems. The GCP has a unique opportunity to generate pan-crop gene expression data for comparative analysis and data mining which allows us to draw evolutionary inferences concerning specific trait(s) and to elucidate the global properties of expression networks in crops.

Drought tolerance is a complex trait in plants. Our challenge is to link molecular phenotype to physiological or morphological trait(s) that have been observed in drought tolerant plants/crops. It will be difficult to comprehend gene expression patterns across crops without knowing the physiological phenotype of drought resistance even if existing or developed ortholog arrays are feasible for cross-species comparisons. To address this problem we plan to focus on a common physiological trait found across crops under drought. This will allow us to identify underlying molecular components for a common physiological trait across crops.

We propose to apply single or multiple microarray platforms to identify candidate genes that are associated with a phenotype of drought resistance across selected crops. The proposed workplan will apply existing rice microarray

technology created by NIAS and BGI and test the feasibility of developing ortholog arrays for use in multiple crops. The proposed project will enhance synergy with other projects involved in gene expression studies (maize, millet, wheat) in the GCP toward elucidation of gene function.

### 2005-15: Musa Genome Frame-map Construction and Connection with the Rice Sequence

**Principal Investigator:**
Takuji Sasaki, NIAS
**Co-Principal Investigators:**
Nicolas Roux, INIBAP-IPGRI
Isabelle Hippolyte, Agropolis-Cirad
Manoel Souza, EMBRAPA
**Collaborating Scientists:**
Pat Heslop-Harrison, University of Leicester, UK
Jaroslav Dolezel, Institute of Experimental Botany, Czech Republic

**Executive Summary**
Developing basic genomic tools to assist germplasm exploitation is important for Musa (banana), especially in the context of the use of Musa genomic diversity. Currently, BAC libraries and germplasm resource collections are available, but EST collections are not publicly available and there are no characterised mapping populations available. The development and assembly of publicly accessible EST collections and framework maps anchored with genetic markers are top priorities for this species, along with initiation of genomic sequencing to identify genes and regulatory genome regions in this important staple crop of developing countries that involves two different genomes and many triploid cultivars.

The GCP is interested in promoting the development of such genomic resources and integrating them with ongoing trait-based research in Musa. The GCP also awaits assessment of the utility of rice-based information for application in Musa and other mandate crops. The GCP is thus requested to support the development of genomic resources for the anchoring of chromosomal regions harbouring valuable traits as well as targeted comparative genomic sequencing relating the A and B Musa genomes and the rice genome. The approach suggested will utilise existing resources of Musa germplasm, maps, and genomic resources, and the outputs will be publicly available resources and markers for exploiting breeding-relevant genetic variation within Musa.

### 2005-17: Comparative QTL Mapping for Drought Tolerance

**Principal Investigator:**
Mathias Lorieux, IRD/CIAT
**Co-Principal Investigators:**
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Stephen Beebe, CIAT
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**Executive Summary**
The first sub-project (led by CIAT) aims at 1) pursuing the identification of QTLs for drought that were mapped on the common bean genome. The target trait will be the capacity of common beans to maintain the transport of

photosynthetically-fixed carbon into grain under drought stress. 2) Using candidate genes to define optimal genetic markers for the transfer of these QTLs. 3) Aligning drought QTLs between legume species and determining the most important regions for saturated mapping.

The second sub-project (led by Agropolis) will focus on 1) refining rice QTLs for root development, 2) providing a rice genetic framework for comparative mapping of drought related QTLs and candidate genes, and 3) providing QTL data for in silico determination of candidate genes.

The genetically determined QTL from these sets of experiments conducted in different crop species will contribute to the convergent evidence for pinpointing common or unique candidate genes important for drought tolerance.

# SP3 COMMISSIONED GRANTS

## 2005-18: Development of Low-Cost Gene-Based Trait Assay Technologies in Cereals

**Principal Investigator:**
Casiana M. Vera Cruz, IRRI
**Co-Principal Investigator:**
Manilal Williams, CIMMYT
**Collaborating Scientists and Institutions:**
Jianli Wu, China National Rice Research Institute
Eduardo Redoña, Philippine Rice Research Institute
Masdiar Bustamam, Indonesian Agricultural Biotechnology and Genetic Resources Research Institute
Usha Barwale-Zehr, Mahyco Research Foundation, India
Valerie Verdier, IRD-Agropolis
E. Raman Babu, VPKAS, India
Chughtaisajjad Ur Rehman, National Agricultural Research Centre, Pakistan
K.M. Karunaratne, Field Crops Research & Development Institute, Sri Lanka
Bhuiyan Safiful Alam, BARI, Bangladesh
Dil Prasad Sherchan, NARC, Nepal
SME breeding companies
Instituto de Ciencia y technologia Agricolas (ICTA), Guatemala
Instituto Nacional de Investigación Agropecuaria (INIA), Venezuela
Kenya Agriculture Research Institute (KARI), Kenya

**Executive Summary**
The Generation Challenge Programme (GCP) has a primary focus on the development of gene-based markers for drought tolerance using comparative genomics and comparative biology. These efforts aim to drive rapid progress across three main crop groups (cereals, legumes, and clonal crops) through comparative analysis with model systems. The development of effective gene-based molecular breeding systems for drought tolerance is clearly a long-term goal in most crops. However, it is fundamentally important that the GCP works with end-users from an early stage to foster the integration of successful, low cost applications of gene-based MAS technologies. Most importantly, we must build champions for these new technologies among breeding programmes of national agricultural research systems (NARS) and small-to-medium-sized enterprise (SME) breeding companies across the major regions of the developing world. Clearly, gene-based technologies for abiotic stress tolerances are only just emerging. Thus, other target traits must be focused upon for this initial pilot project concerning the proof-of-concept for technology product delivery pathways associated with gene-based marker-assisted selection tools. This also offers the added advantage for this preliminary project of being able to target traits with a somewhat simpler genetic basis than drought tolerance. In this context, we envisage two very different models for helping NARS and SME breeders establish their own molecular breeding success stories:
(i) low cost (both in terms of capital investment and assay unit costs), low tech (to save time and offer scalable options) assay technologies that can be used by anyone anywhere;
(ii) low cost (most critically with respect to assay unit costs), high throughput (in terms of millions of samples per year) assay technologies that can be used in shuttle genotyping/MAS service labs.

## 2005-19: Evaluation and Deployment of Transgenic Drought-Tolerant Varieties

**Principal Investigator:**
John Bennett, IRRI

**Collaborating Scientists:**
Idupulapati Rao, CIAT
Matthew Reynolds, CIMMYT
Vincent Vadez, ICRISAT
Enrique Chujoy, CIP
Kazuko Yamaguchi-Shinozaki, JIRCAS
Kazuo Watanabe, University of Tsukuba

**Executive Summary**
Drought is an important limitation on productivity for all of the mandated crops of the CGIAR system. While land and water resource management improves water harvesting and water use efficiency at the field, community, and regional levels, progress in breeding for enhanced drought tolerance is essential for achieving improved crop water productivity and greater food security for hundreds of millions of the rural poor who depend on rainfed agriculture. Water savings in irrigated agroecosystems will also require breeding for tolerance of water deficit.

Although lines of several mandated crops are now available with shorter duration (drought escape) and DNA markers are being identified for deeper and more penetrating roots (drought avoidance), there is also a considerable potential for deploying drought tolerance genes that enable plants to survive and recover from unavoidable periods of low plant water status, especially at the sensitive reproductive stage.

## 2005-20: Optimising Marker-assisted Breeding Systems for Drought Tolerance in Cereals through Linkage of Physiological and Genetic Models

**Principal Investigator:**
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**Collaborating Scientists:**
Mark Dieters, University of Queensland
Graeme Hammer, Agricultural Production Systems Research Unit (APSRU)
Jiankang Wang, CIMMYT
Maarten van Ginkel, CIMMYT
Richard Trethowan, CIMMYT
Eva Weltzien, ICRISAT
Tom Hash, ICRISAT
Gary Atlin, IRRI
Marianne Banziger, CIMMYT
Mark Cooper, Pioneer

**Executive Summary**
The dynamic linkage of crop modeling and genetic/breeding simulation allows us to simulate such things as the introgression or marker-assisted selection of traits as affected by population genetic structures, selection criteria (e.g. direct or indirect selection for yield), and trait by environment interactions. The aim of this project is to build up the gene to trait information using data from QTL and physiological experiments and to further improve the ability of our crop simulation models to capture the effects of traits and their integration to yield. It will aim to combine these 'gene-to-phenotype' physiological models with existing genetic models for other traits such as disease and quality. Simulating molecular breeding programmes will enable optimisation of MAS strategies and provide a platform for integrating a range of knowledge-based outputs from the GCP into breeding programmes.

## 2005-21: Planning for Effective Product Development, Delivery, and Use

**Principal Investigator:**
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**Collaborating Scientists:**

Silvia Salazar, Consultant (Lawyer), Costa Rica
Maria Ines Mendosa, Consultant (Lawyer), Columbia
Shawn Sullivan, Consultant (Lawyer), USA
Zenete Franca, IFPRI-ISNAR
Rosemary Wolson, University of Capetown
Jocelyn Webster, AfricaBio


**Executive Summary**

Through competitive and commissioned research projects, the Generation Challenge Programme (GCP) is building an extensive number and range of research outputs targeted at the identification of useful germplasm, traits, genes, and alleles for use in enhancing drought tolerance in cereal, legume, and clonal crops. The GCP is also generating knowledge and tools to help plant breeders manipulate those genetic factors. It is well accepted that these resources, tools, and knowledge can be used to improve the food, nutritional, and economic security of small-holder farmers and their families in drought-prone areas. However, uptake of research outputs and seed-based technologies has been patchy and often disappointing. It is, therefore, essential for biotechnologists to consider the entire innovation-to-impact pathway whilst designing and carrying out their research programmes. This type of holistic approach is a highly complex multidisciplinary and multisector endeavour. Yet this is the way to increase the rate of uptake of GCP research outputs by ensuring the development of products that provide end-users with practical, user-friendly, appropriate technology packages that meet their needs, capabilities, and capacities.

Emphasis on using an explicit end-user orientated mapping and planning process to improve product development and delivery is a new approach for many of the scientists involved in GCP research projects. Current strategic biotechnology research projects often define indicators for their outputs in terms such as "publication of the results in…". However, the GCP Subprogramme 3 is committed to populating the intellectual space between conventional academic research outputs and the deployment of research-based products that can have tangible impacts on primary agricultural development parameters. Historically, this is a hugely neglected research domain in the public sector and is surely a major reason for the sub-optimum uptake of research outputs. For this reason, the GCP wishes to move far beyond traditional technology hand-over and training models. Instead, tangible product development and deployment plans must include information on how outputs will serve the end-users, why those end-users would favour transfer/adoption of these new technologies, where the critical linkages for product testing, refinement, and delivery are embedded in the plans, and who or what may be the rate limiting steps for product development and deployment. It is fundamentally important that these issues are considered at the project design phase by adequate representation and decision-making influence by stakeholders from across the entire innovation-to-impact pathway.

Adoption of a more holistic and product-driven approach requires substantial changes in institutional policies and processes, in the perspectives of individual scientists. Many consortium member institutions are already advancing towards these general goals. To complement this, the GCP is committed to fostering targeted progress by creating resources, tools, and case studies for assisting current and future projects. It is envisaged that ultimately the GCP will establish a framework of criteria and guidelines in support of mandatory inclusion of product development and deployment activities in all competitive and commissioned projects. Initially we propose to pilot this approach in a facilitated mode during 2006 and autonomously from 2007 (with assistance from GCP Helpdesk support services). Thus, this project proposes to collaborate with project scientists to develop a number of diverse case studies from fundamentally important areas of the current competitive and commissioned programmes. These case studies will be used to develop specific product development and delivery pathways, generic process templates, resources and guidelines for pathway analysis, and defining policy statements. In this way, not only will the most immediate concerns be dealt with but resources and patterns of behaviour will also be established for use in the development of future project proposals.

## 2006-07: Molecular Breeding Communities of Practice

*Proposal pending*

# SP4 COMMISSIONED GRANTS

## 2005-22: Development of GenerationCP Domain Models

**Principal Investigator:**
Richard Bruskiewich, IRRI
**Collaborating Scientists:**
Reinhard Simon, CIP
Manuel Ruiz, CIRAD
Tom Hazekamp, IPGRI
Masaru Takeya, NIAS
Jane Morris, ACGT
Guy Davenport, CIMMYT

**Executive Summary**
The Generation Challenge Programme (GCP) domain modeling task, funded in 2005, evolved a general object model specified across several crop-relevant data types using Unified Modeling Language (UML), now published in Cropforge. Up to now, this model has largely been developed by a small dedicated team of GCP subdomain editors. As part of the process of developing these models, the editors informally surveyed and assessed published models and ontology in their respective fields for possible integration into the Generation CP domain model. Each team has also consulted with some domain experts to verify the content of their models but a general review by a larger community of stakeholders remains to be done. The Generation CP platform and web service tasks also took initial steps toward domain model implementation. Although providing for further refinement of the domain modeling, the task work plan for 2006 emphasises broader community involvement in the form of a public review workshop of the current Generation CP domain models and emphasises validation of the model by further implementation of the model in the GCP platform.

## 2005-23: Implementation of Web Services Technology in the GCP Consortium

**Principal Investigator:**
Milko A. Skofic, IPGRI
**Collaborating Scientists:**
Samy Gaiji, IPGRI
Rajesh Sood, IPGRI
Tom Hazekamp, IPGRI
Reinhard Simon, CIP
Richard Bruskiewich, IRRI
Mathieu Rouard, IPGRI
Dag Terje Endresen, IPGRI
Graham McLaren, IRRI
Martin Senger, IRRI

**Executive Summary**
The Generation Challenge Programme's success relies on the availability and exchange of scientific data. Such data is available in different formats and media, making its sharing a difficult task. The deployment of web services aims at providing a standard mechanism for publishing and accessing scientific data, enabling consortium members to access all resources regardless of format and platform.

### 2005-24: Application and Development of Web Services Technology

**Principal Investigator:**
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**Collaborating Scientists:**
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Mathias Lorieux, CIAT
Manuel Ruiz, CIRAD
Masaru Takeya, NIAS
Andy Pereira, WUR
Milko Skofic, IPGRI/INIBAP
Mathieu Rouard, IPGRI/INIBAP

**Executive Summary**
2004/5 saw the introduction of web services technology into the Generation CP (GCP). The 2006 work plan focuses on further refinement of MOBY technology developments initiated in 2005, including collaboration with the BioCASE, GDPC, SoapLab, and NCGR/VPIN project development communities to cross-integrate their respective data transfer protocols with MOBY. This evolving technology will be embedded into the GCP software platform in a systematic manner. Concurrently, a pilot project will be established to highlight MOBY and related web services applications in the GCP by commissioning a crop-specific MOBY network, focusing initially on the exchange of functional genomics information for rice. By tackling the important design issues inherent in the development of such a specific data exchange network, this pilot project will provide a model for the commissioning of information networks in future years (2007 and beyond) for other GCP crops, and for the eventual development of a comparative crop (plant) information network.

### 2005-25: Creation and Maintenance of Data Templates

**Principal Investigator:**
Guy Davenport, CIMMYT
**Collaborating Scientists:**
Richard Bruskiewich, IRRI
Jaap Buntjer, KeyGene
Andrew Farmer, NCGR
Tom Hazekamp, IPGRI
Thomas Metz, IRRI
Jane Morris, ACGT

**Executive Summary**
The development of GCP templates and file formats is essential for storage and cross analysis of data produced by different GCP partners. We propose to continue the improvement of existing GCP templates and file formats, and the development of new ones. Data templates and formats will be consistent with domain models being developed under the Domain Modeling task.

We will develop stand-alone tools to aid users in manually populating templates and generating correctly formatted data from high throughput technologies and analytical tools. A project database for the curation of GCP metadata is essential for the maintenance and development of GCP templates. This metadata database is to be used to guide revision of current templates and development of future templates. It will be developed jointly with the Central Registry task. All software developed in this project will be interoperable as much as possible with software developed in GCP projects and will reuse open source components where possible.

## 2005-26: Management of the Generation CP Central Registry

**Principal Investigator:**
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Subhash Chandra, ICRISAT
Guy Davenport, CIMMYT
Samy Gaiji, IPGRI
Reinhard Simon, CIP
Milko Skofic, IPGRI
Rajesh Sood, IPGRI
Dag Terje Endresen, IPGRI/NGB

**Executive Summary**
A large amount of data is being generated within the Generation Challenge Programme. These data are stored and maintained at different locations, using different formats and standards. Organising and publishing information on the Web through a Central Registry provides an overview of available data resources ('yellow pages' directory) from a single point. This is critical for the successful completion of the tasks that require data from various sources. The GCP Central Registry was established in 2005. In 2006 the aim of this project is to increase the depth and range of the resources it manages. The approach is to strengthen and further develop components of the Central Registry and to actively approach and assist GCP Partners to register new resources. The project focuses on components such as:

- The technical maintenance and management of the Central Registry
- Building up the Central Registry's resource collection through a pro-active approach of potential providers
- The further development of the Central Registry with indexing systems, data visualisation tools, and links to data analysis tools
- Content management resulting in more extensive controlled vocabularies and enhanced data validation rules
- Help desk to support providers and users

To obtain an insight in how users perceive the Central Registry, a selected group of users will be asked to provide feedback on the Central Registry's impact and the measure in which it meets their needs.

## 2005-27: Integration of the High Performance Computing (HPC)-Facilities in the GenerationCP Toolbox

**Principal Investigator:**
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Roland Schlafeitner, CIP
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Jayashree Balaji, ICRISAT
David Hoisington, ICRISAT
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Richard Bruskiewich, IRRI
Manuel Ruiz, CIRAD
Guy Davenport, CIMMYT
Marcos Costa, EMBRAPA

Guy Davenport, CIMMYT
Jorge Franco, CIMMYT
Marilyn Warburton, CIMMYT
Jiankang Wang, CIMMYT
Etienne de Villiers, ILRI

**Executive Summary**
The third year of the task "Integration of the High Performance Computing (HPC)-facilities in the GenerationCP toolbox" is totally dedicated to the development of Use Cases and the promotion of effective use of the HPC facilities both within SP4, and for the service of the SP1-3 & SP5 projects. The goal is to achieve the maximum use of the HPCs by a wide cross-section of GCP collaborators and partners.

The critical milestone is for several GCP scientists at the next ARM to present their most successful cases using GCP tools on the HPCs: scientists both in and outside the HPC hosting institutes, analysing their workflow and demonstrating significant benefits derived from the HPCs. We aim to clearly demonstrate a growing set of user-friendly tools at the service of an expanding user community.

The aim is to demonstrate the cost/benefit derived from the substantial investment in HPC facilities and support teams. Given that the time window of effective lifetime for advanced IT equipment is 3 to 5 years, depending on depreciation criteria, this third year is critical to establish the ongoing viability of the HPC systems.

## 2005-31: Development of Ortholog-Function Display Tools

**Principal Investigator:**
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Brigitte Courtois, CIRAD
Manuel Ruiz, CIRAD
Christophe Perin, CIRAD
Mathieu Conte, CIRAD
Masaru Takeya, NIAS
B. Jayashree, ICRISAT
Natalia Martins, EMBRAPA

**Executive Summary**
Comparative biology across multiple crop species is a key strategy in the GCP for the identification of stress-responsive gene loci and their corresponding alleles of high agronomic value for application in breeding for stress tolerance.

Critical to the task of comparative biology is the elucidation of evolutionarily conserved gene orthology relationships across species and related paralogy relationships within a gene family. Such orthologous and paralogous gene loci almost invariably share common gene functions, thus important inferences of comparative biology may be possible once such relationships are clearly defined.

This GCP Subprogramme 4 commissioned research project therefore focuses on the task of compiling a catalogue of orthologous and paralogous plant genes for GCP target crops and related model plant species. This task also includes the development of useful (graphical) user interfaces to the catalogue and provisions for (web services) integration with other GCP project data and tools, such as comparative gene expression experiments.

## 2005-32: Development of Crop Gene Expression Database and Data Mining Tools

**Principal Investigator:**
Shoshi Kikuchi, NIAS
**Collaborating Scientists:**
Richard Bruskiewich, IRRI
Hei Leung, IRRI

**Executive Summary**
During the completion of genome sequence analysis in Arabidopsis and rice, many kinds of technologies for comprehensive analysis of gene expression have been developed including microarray, SAGE (Serial Analysis of Gene Expression) and MPSS (Massively Parallel Signature Sequencing), etc. Gene expression data using such technologies have been accumulated and many databases have been opened. But the problem is that the databases have been independently constructed and for the researchers current databases are not easy to access or easy to obtain the data they want.

Shoshi Kikuchi's team in NIAS has been contributing to the establishment of a rice microarray system since 1999. Starting with a 1,265 cDNA-based microarray system, a 8,987 cDNA-based microarray system was finally established in the Rice Microarray Project in Japan (1999-2003). About 60 research groups have joined in the Rice Microarray Project and almost all microarray experiments were performed in the Rice Microarray Centre, established in NIAS, at that time. All gene expression data using the 8,987 microarray system were deposited and accumulated in the Rice Expression Database. Probed cDNA clones originated from the large-scale EST collection of Rice Genome Project (1991-1997). The total gene number of rice has been estimated at 40,000-50,000 and the unique set of EST collection is 11,000. This means the coverage is only one quarter of the whole expressed genes.

To solve the problem and to collect cDNA clones as an intact form of the mRNA, the Rice full-length cDNA project was launched in the beginning of 2000. In this project, 32,127 unique sets of full-length cDNA clones originating from more than 20 different full-length cDNA libraries have been collected, completely sequenced, and opened to the public in July 2003. Sequence information of 29,100 full-length cDNA clones were used for the establishment of the first version of rice oligoarray system. After several rounds of validation experiments, rice 22K oligoarray system ver 1 was commercialised to the world in November 2003 from Agilent Technologies. The first paper using this array system with the gene expression analysis of rice calli treated with ABA and GA was also published in February 2004 and many researchers have started to use the array system. Many kinds of gene expression data using this array system have been accumulated and, based-on the experience in rice comparison of gene expression, data among crops via orthologous genes are currently required.

## 2005-33: Development of an Integrated Decision Support System for Marker-assisted Plant Breeding

**Principal Investigator:**
Subhash Chandra, ICRISAT
**Collaborating Scientists:**
CG McLaren, IRRI
AE Melchinger, University of Hohenheim, Germany
FA van Eeuwijk, WUR
H Mohanty, University of Hyderabad, India
JH Crouch, CIMMYT

**Executive Summary**
Marker-assisted selection (MAS) and marker-accelerated breeding (MAB) require reliable identification and application of simply inherited markers that are in close proximity to genetic factors affecting simple, oligogenic,

and polygenic traits of interest to stakeholders. This can proceed through a mapping-population-based or an association mapping approach, the latter typically based on a sample of unrelated individuals. The mapping-population-based approaches, with or without a linkage map, remain the most popular in plants. As a result, these approaches are relatively well-developed and practical nuances of their application are well understood. The use of association mapping in plants, on the other hand, has only recently started—for example in maize and rice. Association mapping is likely to provide a reduced level of redundancy during the transition from marker identification to application in diverse breeding populations and germplasm. It may be a particularly useful route to follow where the creation of a large enough mapping population and a good linkage map is not feasible due to constraints in the development of these populations or non-availability of sufficient polymorphic markers.

In either approach, the journey from the phenotyping-and-genotyping of individuals to the identification and application of markers in molecular breeding involves the sequential use of a number of different software, each with its own input data format requirement and many alternative choices for data analysis. The use of appropriate experimental design and data analysis is a critical component for successful development and application of marker-assisted breeding systems. Making these choices correctly is a highly specialised function. There is a lack of proper and simple-to-use guidelines for non-specialists, which makes it difficult for them to confidently choose the appropriate design and analysis methods offered by various software. Having a centralised and evolving resource offering biometric inputs required for molecular breeding would be a tremendously valuable asset to the research and breeding community. In this project, we propose to provide simple-to-follow guidelines embedded into the front-end of the system to help users choose the most appropriate experimental design and data analysis methods, and provide them with a regularly updated selection of the most appropriate options at that time. Converting the format of datasets to meet the differing requirements of various software is also an extremely time-consuming process fraught with errors. The system developed in this project will provide automatic transition for data flow between all permutations and combinations of software to be used. This integrated molecular breeding analysis platform (analogous to AgroBase) will be designed to facilitate an integrated, error-free, and appropriate data analysis from the beginning to end of the molecular breeding pathway.

We believe that such an integrated system, based on freely available quality software, will be of profound value to scientists in marker research laboratories and breeders in national programmes and small breeding companies across the developing world. With these end users in mind, the core of the platform will be based on freely available software with the provision of simple-to-use on-line decision guidelines to help users make the right choices of software, experimental design, and data analysis for any given task. We propose to call this integrated system iMAS. To ensure delivery of the system in a realistic timeframe within the available resources, focus will be on crops and marker identification and application systems for which adequate subject matter knowledge, methodology, experience, and free software are already available. However, iMAS will have a built-in flexibility to incorporate new relevant freely available software as it becomes available. It is envisaged that the availability of this system will foster further necessary developments of freely available tools to be integrated into it in future. Also, it is hoped that other parallel GCP competitive projects will support the development of solutions to any fundamental gaps in computational support for molecular breeding for which there are no alternative suppliers of freely available software.

### 2005-34: GenerationCP Software Engineering and Collaboration Platform

**Principal Investigator:**

Thomas Metz, IRRI

**Collaborating Scientists:**

Reinhard Simon, CIP

GCP Scientists as focal points and users of the collaboration platform

**Executive Summary**

This project is a continuation of the commissioned research project 34 from 2005. Two web-based collaborative development systems, one for the development and support of software (http://cropforge.irri.org), and one for the development of textual content (http://cropwiki.irri.org/gcp) were commissioned in 2005 and successfully used by SP4 team members. Currently (09/11/2005) the CropForge server hosts 44 software projects with 93 registered users, and the GCPWiki collaborative web site has about 290 pages and 120 registered users.

The main thrust of this project in 2006 will be to move these collaboration platforms from useful prototypes for early adopters to mainstream collaboration tools for SP4 members, and to extend their use to other subprogrammes as needed. The main investment in 2006 will be in user support in the form of individual helpdesk support, user training, and the production of training materials specially geared towards GCP user needs. In addition, dedicated servers will be deployed to run the collaborative software systems. Outside expertise in the area of open source software development methodology and Community of Practice (CoP) support, as well as in Wiki content organisation, collaboration methodology, and CoP support will be provided.

## 2006-08: Data Analysis Support for Existing Projects in SP2 with Emphasis on Integrating Results across Gene Expression and QTL Mapping Experiments

**Principal Investigator:**

Guy Davenport, CIMMYT

**Co-Principal Investigators:**

Richard Bruskiewich, IRRI
Shoshi Kikuchi, NIAS
Andreas Magusin, JIC

**Collaborating Scientists:**

K. Satoh, NIAS
Masaru Takeya, NIAS
Hei Leung, IRRI
Jose Crossa, CIMMYT
Yunbi Xu, CIMMYT
Ramil Mauleon, IRRI

**Executive Summary**

Current GCP projects do not currently support in-depth analyses of data produced by SP2. The major goal of this project is to further elucidate genes, alleles, mechanisms, and other factors relating to abiotic and biotic stress response across multiple crops through the analysis of available crop gene expression, phenotype, genotype, and QTL mapping data sets across GCP SP2 commissioned and competitive research projects. A dedicated team of expert bioinformatics scientists will pursue the following objectives in collaboration with the providers of the data:

- Consolidate and enhance the organisation, annotation quality, and accessibility of comparative gene expression, phenotype, genotype, and mapping (QTL) from GCP projects.
- Characterise candidate abiotic and biotic stress responsive genes, pathways and processes by the analysis of consolidated GCP data sets and cross-linkage to other publicly available data.
- Document on GCP-hosted web sites the analysis results, methodology, experimental design, and other pertinent best practice parameters of the analysis to facilitate the design and analysis of future experiments and projects.
- Build GCP bioinformatics capacity through direct workshop training of SP2 scientists on data analysis and annotation of SP2 data.

Consolidated GCP datasets for gene expression and QTL data available for web FTP download will be available by January 2007 and fully integrated and annotated data sets with added value from the results of analysis will be accessible using web browser and service interfaces by July 2007. The list of candidate abiotic and biotic stress

responsive genes will be published by July 2007. Online documentation - including a Frequently Asked Questions (FAQ) resource—about the methodology, experimental design, analysis software, and other pertinent best practice parameters of the data analysis to facilitate the design and analysis of future GCP experiments and projects—will be available by July 2007.

## 2006-16: Development of an Integrated GCP Information Platform

**Principal Investigator:**
Graham McLaren, IRRI
**Collaborating Scientists:**
Guy Davenport, CIMMYT
Reinhard Simon, CIP
Richard Bruskiewich, IRRI
Martin Senger, IRRI
Akinnola Akintunde, ICARDA
Manuel Ruiz, CIRAD
Jayashree Balaji, ICRISAT
Andrew Farmer, NCGR/CIMMYT
Maseru Takeya, NIAS
Jane Morris, ACGT
Natalia Martins, EMBRAPA

**Executive Summary**
This project extends the work of part of SP4 Task 28 – Improvement of Quality of Existing Databases; it continues and focuses the part of that project concerned with the development of an integrated information platform. Work from this part of the project in 2005 concentrated on getting community agreement on a platform architecture and technology to be used in construction of the platform and will result in a prototype platform based on first generation domain models and selected use-cases.

2006 activity will concentrate on improved system integration and interoperability of components, enhanced domain model implementation, and inclusion of a wider range of end user applications including a generalised query interface and result integrator, applications for the analysis and visualisation of germplasm pedigree and genotype information, analysis tools for sequence and expression data, and enhancement of mapping tools and GIS integration.

A network of users will be established to test and provide development direction in response to prototypes to be made available at development and review meetings in March and July.

Prototypes and documentation will also be available for independent download and installation from the collaborative work sites at CropWiki.IRRI.org and CropForge.IRRI.org.

## 2006-17: GenerationCP Data Quality Improvement and Assurance

**Principal Investigator:**
Thomas Metz, IRRI
**Collaborating Scientists:**
GCP Scientists and institutions

**Executive Summary**
This project is a split-off and continuation of the commissioned research project 28 of 2005, with a focus reduced to data quality in 2006. Workshop reports of project 28 are available on the GCPWiki site (http://cropwiki.irri.org/gcp/

index.php/SP4_Commissioned_Projects_2005). For 2006, this project will focus on two sets of data that are crucial in the GCP: genotyping and phenotyping data.

In 2006, the project will focus on producing outputs that are immediately applicable to other GCP partners and collaborators and that can be used as resource materials for training courses. The emphasis will be on publishing existing experiences and practices with a view to generate best-practice solutions and subsequently implement them among GCP partners and collaborators.

The areas affecting data quality that will be specifically addressed are allele assignment in genotyping and digital capture of data in the field and the laboratory for phenotyping data. To support a general approach to data quality control and assessment, a review of resources that are directly applicable to GCP data quality will be conducted. In addition, a guide for using statistical software (preferably free software e.g., R-statistics) for quality control and data quality improvement will be produced. The development of guidelines for the standardisation and quality improvement of specific data types (e.g., nomenclature, georeferences) will be considered.

All results will be published on the GCPWiki site (http://cropwiki.irri.org/gcp), which will serve as a planning, production, monitoring, reporting, and dissemination platform.

## 2006-18: Creation of Institutional Bioinformatics Capacity (CIAT)-2006

**Principal Investigator:**
Joe Tohme, CIAT
**Co-Principal Investigators:**
Fernando Rojas, CIAT
Mathias Lorieux, CIAT
Martin Fregene, CIAT
Matthew Blair, CIAT

**Executive Summary**
This project aims at upgrading and expanding existing bioinformatics skills, continuing with the process of integration of molecular data and genotypic information and the sharing of this information with the scientific community. To achieve this, we will:
- develop new programmes that help with the management of genotypic information (SSR & SNPs markers) in rice and other crops (bean, cassava) such that it flows in an automatic way to the LIMS,
- develop scripts in Perl to establish pipelines for the detection of SNPs (SNP identification pipeline). Some scripts are already available or need to be improved/installed, other still need to be developed,
- complete the molecular markers database in including information for other markers (RAPDs, RFLPs, DARTs) and for other crops (bean, rice),
- increase the use of Web Services technology (BioCase, BioMoby..), and its diffusion and application at CIAT (within the guidelines established in GCP-SP4),
- transfer the knowledge to research assistants and students in the different projects.

## 2006-19: Creation of Institutional Bioinformatics Capacity (CIMMYT)

**Principal Investigator:**
Guy Davenport, CIMMYT

**Executive Summary**
The Research Informatics Laboratory is now established at CIMMYT. Prototype systems for the management of CIMMYT genomic data will be installed. These systems will used to provide data via web services to the GCP informatics platform. An Access Grid node will be installed at CIMMYT.

CIMMYT has now established a Research Informatics Laboratory, with sufficient capacity and infrastructure to undergo informatics and analysis projects for the benefit of both CIMMYT and the GCP. Projects are now underway to develop integrated databases for genotyping, QTL, and fingerprinting data, funded both by last year's GCP capacity building project and CIMMYT core funding. We propose to continue these projects in 2006, with the installation of prototype systems for the management and analysis of these systems. CIMMYT is also in the process of obtaining internet 2 in order to have high throughput access to biological databases, connection of our HPC to the GCP HPC grid, and multimedia video conferencing for software development across GC centres. In addition we propose to upgrade one of our existing workstations to allow us to set up an Access Grid node that will allow us to have real time developer's meetings between other centres, such as IRRI, CIP, and ICRISAT.

## 2006-20: Creation of Institutional Bioinformatics Capacity (CIP)

**Principal Investigator:**
Reinhard Simon, CIP
**Collaborating Scientists:**
Merideth Bonierbale, CIP
Roland Schafleitner, CIP
Ruth Grene, Virginia Tech
Lenwood Heath, Virginia Tech

**Executive Summary**
This project will concentrate on making new tools available to the GCP on gene-expression analysis. It will collaborate with Virginia Tech on integrating the EXPRESSO analysis pipeline (http://bioinformatics.cs.vt.edu/~expresso/) into the Generation Challenge Programme Pipeline. It will also add new tools from systems biology (metabolic control analysis, MCA).

During 2005 gene expression data became available at CIP under the GCP that are currently being analysed. Also, in 2006 CIP expects to realise n one or two new projects. Thus, further expertise and tools will be needed to make best use of the generated data. It is anticipated that under a new activity in SP4 (task 23) new expertise (personnel) will become available such that this project intends to complement this by leveraging software tools.

## 2006-21: Creation of Institutional Bioinformatics Capacity (ICARDA)

**Principal Investigator:**
M. Singh, ICARDA
**Collaborating Scientists:**
M. Baum, ICARDA
K. Chabane, ICARDA
G. Peiguo, ICARDA
A. Akintunde, ICARDA
K. El-Shamaa, ICARDA
H. Abed; ICARDA

**Executive Summary**
Bioinformatics support to the GCP activities under SP1- SP3 is critical to ICARDA's commitment. We aim to continue to develop and exploit molecular and phenotypic databases, LIMS, and other specialised software for data analysis and interpretation, and share bioinformatics and biometric tools with in-house scientists and NARS scientists. To meet the need of bioinformatics at ICARDA, we intend to develop our capability further during 2006 by attending training courses, workshops, and conferences, and exploring the possibility of eventually recruiting a full-time bioinformatician. With the limited funds of US$16,500 we present in the following table our workplan, which reflects only a small part of our activities.

## 2006-22: Creation of Institutional Bioinformatics Capacity (ICRISAT)

**Principal Investigator:**
Subhash Chandra, ICRISAT
**Collaborating Scientists:**
Jayashree B, ICRISAT
Dave Hoisington, ICRISAT

**Executive Summary**
For quality genomics research to take place, it is critically important that (a) Genomics researchers are trained in information management, and in the access of publicly available data resources and tools; (b) Advice and support is readily available to them to help organise and analyse data; and (c) Appropriate information systems and analysis tools are developed, maintained, and regularly updated to facilitate proper management, analysis, and use of genomics data. Accordingly, the project during 2006 aims to (1) Conduct bioinformatics training in (a) simple programming for data management for scientists, (b) in-silico marker development, and (c) Association Mapping; (2) Provide advice and support to genomics researchers; and (3) Develop, maintain, and regularly update appropriate information systems and analysis tools. These will be tailored to meet the current and near-future on-the-job needs of genomics researchers at ICRISAT.

## 2006-23: Creation of Institutional Bioinformatics Capacity (IITA)

**Principal Investigator:**
Dong-Jin Kim, IITA
**Collaborating Scientists:**
Trushar Shah, ILRI/BECA
Andrew Farmer, NCGR

**Executive Summary**
Recent progress in genomics research provides tremendous amounts of bioinformation to the individual scientist. In order to utilise these resources, various bioinformatics tools have been developed and many are freely available to the community, but a customised platform is usually necessary for an individual project. This project proposes to hold a three-day workshop for participants from NARS, Universities, and CG Centres in the Nairobi area to assist them to access and utilise the information. In the workshop we will cover basic topics such as downloading sequences from NCBI, Blast analysis, SSR finding, and Primer Design. We will put these tools into a comparative genomics and COS marker development context. A workshop website will provide the communication platform for participating scientists. Public bioinformatics tools for COS marker design will be linked and a message board will provide a mechanism for feedback after the workshop.

## 2006-24: Creation of Institutional Bioinformatics Capacity (IPGRI)

**Principal Investigator:**
Samy Gaiji, IPGRI
**Collaborating Scientist:**
Milko Skofic, IPGRI

**Executive Summary**
This project is intended to further support the target activities involved in implementing the Subprogramme 4 workplan. Eligible activities include the recruitment of additional bioinformatics staff as well as sustaining existing bioinformatics experts. IPGRI proposed to allocate the funds within this project to support the recruitment of a Bioinformatics Senior Scientist to be based at IPGRI HQ in Rome (Italy). This person would be dedicated to the

Generation CP Bioinformatics activities led by IPGRI as well as to providing leadership and support in the overall Generation CP Subprogramme 4 platform and implementation design.

## 2006-25: Creation of Institutional Bioinformatics Capacity (IRRI)

**Principal Investigator:**
Graham McLaren, IRRI


**Executive Summary**

Bioinformatics capacity building for 2006 will continue to fund NRS bioinformatics staff at IRRI to expand the capability of the bioinformatics team. Documentation and software will continue to be added to the libraries of bioinformatics resources available at IRRI. Bioinformatics staff will have the opportunity to attend GCP meetings, bioinformatics training, and international bioinformatics meetings during 2006.

The capacity building project is required to enhance bioinformatics capacity at IRRI by providing staff resources, an effective literature resource, and software required for bioinformatics analysis to support GCP and IRRI research projects.


## 2006-34: Installation and Implementation of the ICRISAT LIMS at the Biosciences Eastern and Central Africa (BecA) Facility and IITA-Ibadan

**Principal Investigator:**
Dave Hoisington, ICRISAT
**Collaborating Scientists:**
Etienne de Villiers, ILRI
ME Ferguson, IITA
Sarah Hearne, IITA
Santie de Villiers, ICRISAT
Rosemary Mutegi, ICRISAT


**Executive Summary**

SSR genotyping is a major activity in most crop genomics laboratories. The laboratory workflow needs to be organised and the large amounts of data that are produced during high throughput genotyping need to be managed. During 2005, the existing ICRISAT MS-Windows based LIMS has been re-coded as a platform independent, multi–user Laboratory Information Management System (LIMS) that manages workflow and information in the Applied Genomics Laboratory (AGL) at ICRISAT-Patancheru. The AGL-LIMS can be broken into two main functional areas: laboratory management and data management. Laboratory management includes sample tracking –from the time that DNA is extracted to the time that capillary electrophoresis is complete and the output uploaded into the system. Data management includes management of reagents and protocols, storage of sample information, gel images, textual, graphical, and chromatogram files, implementation of data quality measures, and report generation.

The LIMS has been developed as a three-tier application. Our experience with an earlier two-tier system indicated that one of the key challenges lies in coping with constant changes required by the user, since researchers continually refine existing procedures or introduce new ones. The advantage of having a three-layered architecture is that each layer is completely independent of changes introduced in the other. The LIMS was also developed as modules, thus any number of modules may be added depending upon the needs of the laboratory using the application. The current version of the LIMS has functional modules on experiment set-up and sample tracking that includes DNA extraction, quantification, dilution, PCR setup, marker selection for PCR, capillary electrophoresis, file uploading, and checking for allele binning quality. In addition, there are visualisation or display modules, data management, and storage modules. Given its modular structure, the LIMS can be adapted to the needs of almost any genotyping laboratory.

## 2006-35: Data Analysis Support for Existing Projects in SP1 with Emphasis on Sampling Germplasm (DASSP1)

**Principal Investigator:**
Marco Bink, WUR
**Co-Principal Investigators:**
Hans Jansen, WUR
Fred van Eeuwijk, WUR
Xavier Perrier, CIRAD
**Collaborating Scientists:**
Paula Hurtado, CIAT
Claire Billot, CIRAD
Reinhard Simon, CIP

**Executive Summary**

The project on development of Decision Support System (DSS) for germplasm sampling was aimed at developing new algorithms for selection of germplasm and implementing these in an environment that would allow widespread use. These objectives will be reached at the end of 2005.

However, SP1 scientists strongly expressed a need for support in using these algorithms. We therefore define this new project that is targeted to provide that support, and most of the project budget will be used for support. This support may include the following activities: the creation of a web page (under the GCP portal) with general descriptions of procedures, an email-based helpdesk, and possibly face-to-face consultations. Nevertheless, during the previous projects additional prerequisites to sampling and association analyse were identified, which require further algorithm development and software implementation; this will become a minor task in this project (not more than 20% of the budget).

We will build on existing partnerships, but will try to involve new partners when needed in order to fill gaps in current expertise. To warrant our project from delays, only SP1 projects that have their datasets completed by early 2006 will be included in this project.

# SP5 COMMISSIONED GRANTS

### 2005-CB13: The Institute for Genomic Diversity's Interactive Resource Center

**Principal Investigator:**
Theresa Fulton, Cornell University


**Executive Summary**
One of the many challenges for scientists in the international community, particularly in developing countries, is getting personalised, interactive support in addressing the needs specific to their own research programmes. The lack of access to trained personnel, key literature, and a support system can be limiting factors in the progress of scientists' research programmes. At the Genetic Resources Challenge Programme's Stakeholders Meeting in Alexandria, January 2003, one of the recommendations of the Working Group on Capacity Building was to create an Interactive Resource Centre (a "helpdesk") to support scientists involved in the Challenge Programme.

The IGD is in a key position to take the initiative in setting up this Resource Centre. Our location at Cornell University gives us access to important resources, including facilities and faculty, that could play an important role in addressing the needs of scientists all over the globe. Nearby facilities include many large libraries (and networked resources), information technologies such as the Cornell Theory Centre and the new Computational Biology Support Centre. These resources, together with IGD's combined expertise in research and education, make it possible for our Institute to have a significant positive impact, particularly as a capacity-building contribution to the Challenge Programme. Many international scientists have taken advantage of these resources while on training visits to the IGD; establishing a Resource Centre will allow us to extend our resources to scientists that do not have to opportunity to visit in person.

Targeted for, but not limited to, the international CGIAR centres, National Agricultural Research centres and their clients, users of the Resource Centre would include scientists around the world working on plant genetic resources and needing support. Support given could be in the form of answering questions about experimental design, laboratory protocols, data management, laboratory maintenance, funding, training possibilities, software specifics, statistics questions, making literature available, etc. The goal is not necessarily to directly answer each question, but to be able to direct the client to the appropriate person or place that will be able to address the question.


### 2005-CB15: Distant Policies: A distance learning module for scientists on genetic resource policies and their implications for freedom-to-operate

**Principal Investigator:**
Niels Louwaars, WUR


**Executive Summary**
The purpose of this project is to provide a basic and practical distance-learning module to help GCP scientists understand the importance of limitations of the rights to use plant genetic resources and tools, methods, and products protected by intellectual property rights.

The course introduces scientists from GCP consortium members, partners, and stakeholders on topics concerned with access, benefit sharing, and intellectual property matters at a rather basic level, but in such detail that they are well-prepared to understand the impact of the relevant rights systems on their projects and on the implications of the use of materials and research tools for the availability of the output of their work for target intermediate and end-users. The course will include a test to verify that the course participants have sufficiently understood the issues. It may include a possibility to follow the course at two levels.

The GCP is a collaboration among researchers, breeders, and social scientists from a wide variety of institutions, serving an equally broad group of potential users. Much of the success of the programme depends upon a clear freedom to operate on the materials, tools, and methods. Scientists commonly are not sufficiently concerned with the legal implications of the use of materials and tools that are developed by others in their research. This is particularly true for scientists in institutions that primarily produce public goods.

## 2005-CB16: IP Matters: An Intellectual Property and Access & Benefit Sharing Helpdesk and on-line resource for the GCP community, partners, and stakeholders

**Principal Investigator:**

Victoria Henson-Apollonio, IPGRI

**Executive Summary**

The objective of this project is to provide a practical on-line service desk for assistance, clearing-house activity, and feedback to GCP consortium members, partners, and stakeholders on topics concerned with intellectual property matters in the broadest sense. This project will field questions related to GCP agreement requirements, access issues, asset identification, and product development and delivery that will be responded to by a network of IP and ABS professionals. In addition, information that is relevant to IP management, ABS experiences, and IPRs will be provided as original material and in links to other on-line IP sites.

The GCP is a collaboration among researchers, breeders, and social scientists from a wide variety of institutions, serving an equally broad group of potential users. Much of the success of the programme depends upon having agreements, plans, and other tools in place that encourage communication among scientists, provision of the necessary materials (including germplasm), participation of end-users in project design and implementation, as well as effective product development, distribution, and uptake. Negotiating agreements, access to materials and information, obtaining the necessary licenses/permissions to use 3rd party technologies, etc, can be daunting tasks, even for experienced administrators or technology transfer personnel at advanced research institutions. We believe that providing a facility to help GCP participants with Freedom-to-Operate management would be very useful and timely. This service desk would assist GCP institutions, scientists, and staff with fulfilling GCP IP management requirements, complying with national legislation, answering questions related to IP issues, while also providing additional information on IP and ABS topics that may be of further interest to the GCP community. The "IP Matters" facility would be modeled, in part, on the "IPR-Helpdesk," available at the URL: http://www.ipr-helpdesk.org/index.htm.1. In addition, this facility would look to the SP5 GCP-sponsored technical (scientific) helpdesk, hosted by Cornell University, located at URL: http://irc.igd.cornell.edu/, for materials and methods.

## 2005-CB17: Reporting for Product Distribution: An asset inventory system for the Generation Challenge Programme

**Principal Investigator:**

Victoria Henson-Apollonio, IPGRI

**Executive Summary**

The purpose of this project is to develop a practical on-line service that will facilitate the production of a dynamic inventory of 3rd party materials used by GCP scientists and products produced by GCP research. The GCP is a collaboration among researchers, breeders, and social scientists from a wide variety of institutions, serving an equally broad group of potential users. Much of the success of the programme depends upon having GCP assets and products used and taken up by as broad a user-base as possible. This requires that an inventory of GCP products be created and also that 3rd party materials used in the production of these assets be reported as well.

CAS-IP has developed several reporting tools over the past several years that can be used as the basis for developing this GCP reporting system. In addition, a CAS-intern is currently working on a project to make this reporting system more efficient, informative, and easier for the scientist-originators to use.

### 2006-09: Training Course on Phenotyping

**Principal Investigator:**
François Tardieu INRA

**Executive Summary**
Phenotype analysis is a critical issue for quantitative genetics, analysis of mutants, and association genetics. The parallel between "phenotyping" and "genotyping" implies that phenotyping should aim at high-throughput, cheap, and automated characterisation of a large number of genotypes. However, phenotyping for complex traits such as drought tolerance also involves methodological and technical choices (including the number of studied genotypes) which will eventually determine the quality of the whole phenotyping process. Three topics are proposed: stress characterisation, choosing and measuring the appropriate phenotypic traits, and data analysis and modeling. We propose to deal with these three topics with a combination of lectures, computer sessions aimed at providing methods of analysis and reasoning, and practical sessions about methods of measurements.

### 2006-11: Establishment of training materials for a course in association study/linkage disequilibrium mapping (TM_AS)

**Principal Investigator:**
Marco Bink, WUR
**Co-Principal Investigators:**
Hans Jansen, WUR
Fred van Eeuwijk, WUR
**Collaborating Scientists:**
Marja Thijssen, WUR
Ed Buckler, Cornell University
Ian MacKay, NIAB
Claire Billot, CIRAD

**Executive Summary**
This project aims at developing and gathering comprehensive training materials in association study/linkage disequilibrium mapping intended for an audience of scientists with a background in germplasm management, biology, and genetics. Furthermore, the audience is expected to have working knowledge of the application to plant and agricultural sciences. Preferably, they will have a fair understanding of plant breeding and QTL detection for trait dissection.

The materials are meant as a guide to alternatives to conventional linkage mapping and they become useful when dealing with (1) collections of crop germplasm, or (2) crops not amenable to obtaining progenies from controlled crosses, or when other limitations exist to the development of appropriate populations for segregation analyses.

The materials will be designed as an educational resource or reference tool that can be used as a self-tutorial or will serve as a course curriculum appropriate for a one-week course incorporating key references, photographs, illustrations of concepts, examples, and suggested applications.

The materials should serve as the basis for training of scientists involved in the GCP, in particular those engaged in SP1 research projects. They will be made available to GCP partners and scientists in a repository of training materials accessible through the GCP web site. The materials will be derived through close collaborations with leading plant breeding scientists in the area of association analysis.

### 2006-15: Fellowships and Travel Grants

**Principal Investigator:**
Carmen de Vicente, IPRGRI

**Executive Summary**

The Generation Fellowship awards were established to facilitate innovative research related to the central theme of the Generation Challenge Programme, i.e. unlocking genetic diversity of crops for the resource-poor. The Fellowship programme is aimed at scientists who want to conduct research outside of their home countries/ institutions for a period of three months to one year. The Generation Fellowship places primary emphasis on research in the four thematic subprogrammes: 1) genetic diversity of global genetic resources, 2) comparative genomics for gene discovery, 3) trait capture for crop improvement, and 4) genetic resources, genomic, and crop information systems. Up to 8 fellowships per year are awarded, and the maximum award per fellow will be up to US$25,000, which is intended to cover travel, living expenses, laboratory consumables, and conference participation.

Proposals should deal with at least one of the following GCP crops (rice, maize, barley, wheat, sorghum, millet, cassava, chickpea, sweet potato, cowpea, beans, and groundnut). In addition, proposals must be linked with ongoing research supported by the GCP, either by competitive or commissioned grants. (See the GCP Research Page for information on competitive and commissioned grants: (http://www.generationcp.org/reserach.php?da=0634417).

Applications are invited from crop science researchers from developing country research institutions (National Agricultural Research Systems), who hold at least a Master of Science degree (MSc), or equivalent, in a relevant subject area. Applicants should demonstrate they are engaged in a related ongoing research activity in their home country. Priority is given to scientists from National Agricultural Research Systems already involved in GCP research projects. For more information on the Fellowships programme and to access the application materials, please see the GCP Capacity Building Corner: (http://www.generationcp.org/reserach.php?da=0531908).

The Generation Travel Grant Programme is a key component of the GCP Capacity Building Subprogramme (SP5). Sixteen Travel Grants are available per year to cover the expenses of developing country National Programme scientists working at or in collaboration with a GCP Consortium Institution (list of GCP Consortium Institutions: (http://www.generationcp.org/consortiummembers.php). The purpose of the Travel Grant Programme is to encourage and promote collaboration between the GCP and NARS institutions, foster linkages within current GCP projects, and provide training opportunities for developing country scientists. The grant may be requested to visit a GCP Consortium Institution or any other Advanced Research Institution to get training in concepts and/or techniques necessary for the advancement of the GCP research (first priority), to participate in any training event organised by the GCP (second priority), to participate in the annual GCP research meeting (limited number of spaces available), or to participate in conferences whose subject is relevant to the work of the GCP. Preference will be given to applicants with links to current GCP projects and for whom the travel grant will be used as a learning experience.

The maximum grant award will be $5,000 USD, which is intended to cover travel, accommodation, and conference participation, if applicable.

The selection criteria to request a GCP Travel Grant are the following: 1) The applicant should belong to an institution from a developing country (NARS or academia) that is either a member of the GCP Consortium or is working in collaboration with a GCP Consortium Institution. 2) He/She should work in research related to the running theme of the GCP (any of the Subprogrammes) with one of the GCP crops (rice, maize, barley, wheat, sorghum, millet, cassava, potato, sweet potato, yam, Musa, chickpea, cowpea, beans, lentil, pigeon pea, soybean, coconut, and groundnut). 3) The applicant should justify the objectives of the travel and benefits to his/her research and home institution.

A Generation Travel Grant Committee evaluates all applications and selects the recipients. The deadline for travel grant applications is the 20th of each month. Winners are notified early the following month. Applications are evaluated as they are received until all 16 grants are awarded.

### 2006-28: Regional PGR Courses

**Principal Investigator:**
Marja Thijssen, WUR

**Executive Summary**
The project creates a curriculum for regional courses on institutional genetic resource policies in order to create awareness, extend relevant knowledge, and share experiences among scientists and science managers, which will allow them to develop or strengthen institutional policies and tools for handling Freedom to Operate on IPR and ABS in partner institutions of the Challenge Programme.