Executive Summaries of Proposals Recommended for Funding

No. 8

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

(IRRI Ref. No. DPPC2004]25)

Proposal

submitted to

Generation Challenge Program

August 2004

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Title: Identifying Genes Responsible for Failure of Grain Formation in Rice and Wheat under Drought

Targeted Subprogramme: SP2

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Participating scientist:

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Participating Institutions: CSIRO, IRRI, NAU, NIAS, TNAU

Submission Date: August 27, 2004

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 continue to increase as it has done 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 the 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.

No. 9
Revitalizing Marginal Lands: Discovery of Genes for Tolerance of Saline and Phosphorus] Deficient Soils to Enhance and Sustain Productivity

(IRRI Ref. No. DPPC2004]26)

Proposal

submitted to the

Generation Challenge Program

August 2004

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Title: Revitalizing Marginal Lands: Discovery of Genes for Tolerance of Saline and Phosphorus-Deficient Soils to Enhance and Sustain Productivity
Targeted Subprogramme(s): SP3 with links to SP2

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Submission Date: August 27, 2004

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.

No. 17

Identifying the physiological and genetic traits that make cassava one of the most drought tolerant crops

A Proposal Submitted to the Generation Challenge Program

By

- **Brazilian Agricultural Research Corporation (EMBRAPA/CNPMF), Brazil**
- **International Center for Tropical Agriculture (CIAT), Colombia**
- **International Institute of Tropical Agriculture (IITA), Nigeria**
- **Cornell University (CU), USA**

Principal Investigator: Dr. Alfredo Alves (EMBRAPA/CNPMF)
Co-Principal Investigator: Dr. Hernán Ceballos (CIAT)
Co-Principal Investigator: Dr. Martin Fregene (CIAT)
Co-Principal Investigator: Dr. Yvonne Lokko (IITA)
Co-Principal Investigator: Dr. Tim Setter (Cornell University)

Submission date: August 2004

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 favorable and unfavorable weather. The general objective of the proposed work is to determine the best traits to be used in breeding programs 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 S_1 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 analyzed 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 programs.

No. 28 (to be funded at 50%)
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 programs in tropical maize and bread wheat

Program

SP4 – Genetic resource, genomic and crop information systems

Lead principal investigator
Fred van Eeuwijk, WUR, The Netherlands
Collaborating scientists
Jean-Marcel Ribaut, CIMMYT, Mexico (Co-PI)
Matthew Reynolds, CIMMYT , Mexico (Co-PI)
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Executive summary

When breeders try to develop adapted genotypes for abiotic stress conditions, i.e., plants with on average superior genetic constitution with respect to yield, they are faced

with the problem that it is hard to get reliable estimates of genetic superiority under stress conditions. Under stress, the phenotype, that what 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 the 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, the genetic correlation 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 characterization 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 analyzing data from abiotic stress trials. The present statistical approaches do not incorporate any explicit physiological knowledge on the part of the genotype nor the environment. We propose the development of an integrated eco-physiological statistical framework, modeling yield responses on both the phenotypic and genetic level in 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 value in the form of deeper insight in 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.

No. 31
Unlocking the genetic diversity in peanut's wild relatives with genomic and genetic tools
Targeted subprogram:
SP3 - Trait capture for crop improvement

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CoPI- David Bertioli, UCB- Universidade Católica de Brasília, Brazil.
CoPI- Serge Braconnier, CERAAS- Centre d’Etude Régional pour l’Amélioration de l’Adaptation à la Sécheresse, Senegal.
CoPI- Jonathan Crouch, ICRISAT- International Crops Research Institute for the Semi-Arid Tropics, Kenya.
CoPI- Pietro Piffanelli, CIRAD- Centre de coopération internationale en recherche agronomique pour le développement, France.
CoPI- Guillermo Seijo, IBONE- Instituto de Botánica del Nordeste, Argentina.
CoPI- Jens Stougaard, Laboratory of Gene Expression, University of Aarhus, Denmark.

CoPI – Vincent Vadez, ICRISAT – International Crops Research Institute for the Semi-Arid Tropics, India.

Executive summary

Legumes, unlike other crops, fix nitrogen, need little fertilizer and help maintain the soil productive. 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 soybean. Peanut is sensitive to fungal diseases and drought stress and these factors 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, be 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 peanut, using a wide range of diploid species. So far, four viable synthetic hybrids have been created thus bringing to peanut breeding, for the first time, the genetic diversity of the genomes of eight wild *Arachis* species. 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".

No. 36
MARKER DEVELOPMENT AND MARKER-ASSISTED SELECTION FOR *STRIGA* RESISTANCE IN COWPEA

Targeted Subprogram: SP3

Date of Submission: August 25, 2004

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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 programs. The outcome of this work will be superior-performing, well-adapted cowpea varieties containing pyramided agronomic productivity, 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 favorably on their general livelihoods.

No. 41 (start-up proposal)
Measuring linkage disequilibrium across three genomic regions in rice
Subprogram 1: Genetic diversity of global genetic resources

Dr. Susan McCouch (Lead PI)

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Dr. Michael Thomson (co-PI)
Dr. Endang Septiningsih (co-PI)
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Submission deadline: August 27, 2004

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 Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD) in Bogor, Indonesia. Currently, 250 Indonesian landraces are being analyzed 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.

No. 42
Targeted discovery of superior disease QTL alleles in the maize and rice genomes
Targeted subprogrammes: SP2 and SP3

Collaborators and institutions:
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Submission date: 27 August 2004

Executive Summary
We propose to identify, characterize and utilize 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 proposed work 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 analyzed to identify superior alleles at the loci of greatest potential utility. We propose to characterize 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 analyzed in detail and utilized in the applied breeding programs in which improving disease resistance is a high priority.

No. 45

Development of Low-Cost Technologies for Pyramiding Useful Genes From Wild Relatives of Cassava into Elite Progenitors

A Proposal Submitted to “The Generation Challenge Programme”

Subprogramme 3:
Genetic diversity of global genetic resources – Trait capture for crop improvement

Lead PI:
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Co-PIs:
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• Dr Alfredo Alves (EMBRAPA-CNPMF)
Collaborating Scientists
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Crop Research Institute (CRI), Kumasi, Ghana
National Root Crop Research Institute (NRCRI), Umudike, Nigeria

Submission date:
Aug 27, 2004

Executive Summary

Cassava (*Manihot esculenta* Crantz) is increasing in importance in the tropics due to its hardy nature but it 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, some 30% of total world production, valued at US$1.4billion every year to pests, diseases, and PPD. Wild relatives of cassava are important sources of genes for resistance to pests and diseases and 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 by the development of low cost approaches, expand the gene tagging effort to other traits, and establish a systematic approach of collection, evaluation and use of additional wild germplasm.

No. 47
Exploring Natural Genetic Variation: Developing Genomic Resources and Introgression Lines for Four AA Genome Rice Relatives

Targeted Subprograms: SP1; SP3
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Submission date: August 26, 2004
Total budget requested: 877,200 US $
Submitting consortium member: CIAT
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Executive summary

Cereals provide the majority of calories consumed by humans. Cereal production faces growing challenges due to 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 defenses to endure biotic and abiotic aggressions. These wild relatives represent a valuable source of under-utilized genetic variation that is available to plant breeders and represent an invaluable source of genetic information for modern genomics research initiatives. A systematic approach is required to identify and characterize 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 programs for other cereals (4) analyze 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 Subprograms 1 and 3 by (i) utilizing *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 (iii) making the CSSLs available to breeders and geneticists so that the intersection of their efforts will continue to generate new knowledge.

No. 52
Functional genomics of cross-species resistance to fungal diseases in rice and wheat (CEREALIMMUNITY)

Targeted subprogram: **SP2 Comparative Genomics for Gene Discovery**
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Submission Date 27/08/2004
Cerealimmunity GCP full proposal

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 represents 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 at defining the signalling and effector genetic components involved in non-host resistance in cereals to devise **novel defence strategies** which have the potential **to yield durable resistance against host pathogens in cereals**. This project

aims at implementing existing breeding programs for resistance to blast and rust diseases in developing countries taking advantage of the availability of advanced genomic platforms and technologies.

No. 54

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

A Proposal Submitted to
Subprogramme 3 – Trait capture for crop improvement

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Submission Date: August 27, 2004

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 North China and the rainfed areas of South/Southeast Asia. Developing drought tolerant (DT) rice cultivars is the most efficient way to stabilize rice production and alleviate food insecurity and poverty in China and Asia. In the proposed project, we propose to develop high yielding and DT rice cultivars for the 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 program 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 characterized DT IR64 lines, our goal is to discover and characterize 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 characterized in the elite rice backgrounds; (2) development of

superior high yielding and DT rice cultivars for the 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 its modern breeding systems that fully integrate the molecular tools with the current breeding programs for genetic improvement of major crops in China.

No. 64
Development of informative DNA markers through association mapping in maize to improve drought tolerance in cereals

Targeted Subprogram: 2

Lead PI: Jean-Marcel Ribaut (Genetic Resources Program, CIMMYT, Mexico)
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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, although allowing genetic progress, crops need to be fully evaluated in every environment, which is costly and time consuming. Association studies, proposed in this project, are based on correlation between a gene sequence and plant performance for target traits, and represent a powerful approach to evaluate 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 maximizes 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, it is that any discovery can be rapidly converted to improved breeding materials without the societal and regulatory obstacles of transgenics materials. Because of the genetic and physiological commonalities among cereal crops, this knowledge gathered in maize can be applied to all other cereal crops.

No. 66

Characterization of genetic diversity of maize populations: Documenting global maize migration from the center of origin.

Targeted Subprogram: 1

Lead PI: Marilyn Warburton (Genetic Resources Program, CIMMYT, Mexico)
Collaborating Scientists and Affiliated Institutions:
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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. Populations introduced into other countries, originally from the center of origin in Central America but following a complicated pattern of introductions, have become 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 characterization 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 one that 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 analyzing maize populations from geographic regions that have been underrepresented in previous studies, and representatives of the wild ancestor of maize (teosinte). Structural characterization will occur at the molecular

level using SSR markers. The populations containing the most unique alleles at the SSR loci will then be characterized for markers associated with drought tolerance, as these are the populations most likely to contain new alleles in general and potentially for drought related loci. The genetic characterization data will provide useful information for utilizing these populations in genomic studies and breeding efforts to create drought tolerant maize.

No. 67
Determination of a common genetic basis for tissue growth rate under water-limited conditions across plant organs and genomes.

Targeted Subprogram: SP2

Lead PI: Mark Sawkins (Genetic Resources Program, CIMMYT, Mexico)
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Executive Summary

The effort to minimize 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 centers 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 characterizing environmental conditions in all experiments (including those for genomics), and analyzing 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 over the world and how does that correlate with yields? And, What combinations of alleles optimize 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 vigor, high light interception or maintenance of reproductive development.

No. 69

Isolation and Characterization of Aluminum Tolerance Genes in the Cereals: An Integrated Functional Genomic, Molecular Genetic and Physiological Analysis

Subprogram: SP2 – Comparative Genomics for Gene Discovery
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Project Period: January 1, 2005 – December 31, 2007 (36 months)
Funds Requested: $900,000 / 3 years
Submission Date: August 27, 2004

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 humanity-derived reasons. On acid soils, regardless of their source, toxic levels of aluminum (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 characterize 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 aluminum 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 program 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.

No. 74
Allele Mining Based on Non-Coding Regulatory SNPs in barley germplasm.

Targeted Subprogramme: Subprogramme 1: Genetic diversity of global genetic resources

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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 endeavor. 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 harbor 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 characterize a series of genes identified and 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 create a high quality collaborative network of researchers delivering new knowledge on genetic diversity and translatable outputs for the Developing World.