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NEW SCIENCE

Brings New Hope for People and the Environment

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It is an honor to address this group on a topic that represents one of the CGIAR's greatest aspirations, which is to bring the newest and best scientific insights to bear on some of the hardest realities that human beings have to face: hunger, poverty, and environmental decline.

A large range of work in new areas—marker-assisted selection, functional genomics, and others—is undertaken in the Centers, too much to summarize in a short presentation. I hope you will forgive me if I choose to highlight a few research areas rather than to give an exhaustive review of all of them. I will focus on new breeding methodologies, wide hybridization, gene/QTL mapping, functional genomics, transformation technology, and geographic information systems (GIS).

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New Breeding Methodologies

Many of the innovative breeding methodologies described here resulted when researchers began to examine problems in new ways.

- **Tissue culture/somaclonal variation (grasspea research)**—Few problems have engaged agricultural research in the past decades as much as the search for ways to protect plants from drought. In the case of ICARDA's recent research on grasspea, however, researchers looked for ways to protect people against the ill effects of one of the few food crops that can withstand drought. In so doing, they have saved poor communities from an agonizing choice between starving to death and consuming a food that could result in paralysis.

Grasspea (*Lathyrus sativus*) is a high-protein food crop for poor people in Ethiopia, Bangladesh, Nepal, India, and China. This legume is also extremely hardy under drought, surviving months without rain. When eaten in small quantities, grasspea is harmless, but a steady diet of grasspea causes irreversible paralysis in leg muscles, the result of a neurotoxin contained in the seeds. The paralysis is a familiar occurrence in rural areas affected by long periods of drought. Classical breeding methods had only limited success in reducing the neurotoxin content to safe levels, partly because of the small amount of variation found in grasspea. ICARDA researchers successfully used in vitro culture to generate somaclonal variants of grasspea with low neurotoxin content. The low neurotoxin lines, which are being developed for cropping systems in major grasspea growing areas, will have a great positive impact.

- **Mutator system to combat *Striga* spp. in maize**—The control of *Striga* in Africa's maize production systems depends on the development of integrated weed management strategies that are within the reach of smallholders. In eastern Africa, CIMMYT and several organizations are collaborating on the development of effective short-, medium-, and long-

term alternatives for *Striga* control, including agronomic systems, varietal/host plant tolerance, resistance from wild relatives of maize, and transposon-induced resistance to *Striga*. In 1998, researchers screened 4,000 F₂ families derived from a cross between CML202, a well-adapted line from eastern Africa, and Mutator stocks from the University of California to eliminate the obviously susceptible lines. In 1999, breeders retained 210 out of 4,000 families planted and evaluated in 1998; 23 of them showed a consistently promising level of resistance. Each family was selfed, and the F₃ families were evaluated under very severe *Striga* infestation in 1999. Four of the families were scored as *Striga*-free in the field.

- **Marker-assisted selection (MAS) in the world's three most important food crops**—By now it is well known that DNA markers are linear landmarks in DNA or chromosomes where genotypic differences arise. In breeding programs, they hold great promise for increasing efficiency (e.g., by making advances more rapidly than under traditional breeding schemes) and effectiveness (e.g., through pyramiding useful genes).

At IRRI, multiple genes for resistance to rice bacterial blight and blast have been pyramided through molecular marker technology for durable resistance against these pests. Through the Asian Rice Biotechnology Network, three national institutes (PhilRice in the Philippines, RIFCB in Indonesia, and Punjab Agricultural University in India) used MAS to combine different bacterial blight resistance genes into their local popular cultivars. Advanced lines with good yield and added resistance were developed.

Researchers are also using MAS to increase drought tolerance. This work is underpinned by linkages to worldwide efforts in structural and functional genomics. For upland rice production, researchers evaluated candidate genes for drought tolerance and resistance/defense response for utility in MAS. In rainfed lowland rice, drought and submergence, the dominant problems of the ecosystem, have been difficult to solve with traditional breeding methods. The problems can be addressed through MAS for traits such as root depth, penetration ability, and osmotic adjustment. Researchers have identified mechanisms and are using them to develop screening methods, identify genetic markers, and design MAS methods for these traits.

At CIMMYT, MAS is being used in wheat to screen for resistance to barley yellow dwarf virus and in maize to screen for resistance to maize streak virus, for the quality protein trait, and drought tolerance. The use of molecular markers to promote this approach is being improved by CIMMYT. Breeders have already used MAS to develop maize for drought environments, and CIMMYT is working with national programs in Kenya and Zimbabwe in an innovative experiment aimed at using a single MAS selection step at an early stage of recombination to further speed the development of drought-tolerant materials.

- **Markers for genomic grouping**—At IITA the introduction of RAPD (random amplified polymorphic DNA) markers has facilitated genome composition studies in *Musa* spp. Plantain and banana originated from intra- and interspecific hybridization between two wild diploid species, *M. acuminata* and *M. balhisiana*, which contributed the A and B genomes, respectively. Polyploidy and hybridization have given rise to a number of diploid, triploid, and tetraploid clones with different permutations of the A and B genomes. Thus dessert and highland bananas are classified as AAA, plantains as AAB, and cooking bananas are ABB. Other more complex genome permutations including AB, AAAB, and ABBB also exist. Classification of *Musa* into genome groups has been based on morphological characteristics. A plant's morphology can be altered by environmental factors and such a system of morphological classification would be inconsistent. Additionally, some characteristics are expressed at maturity and these traits can be measured only after 18-24 months. Therefore, easier, more stable, and reliable techniques are needed to determine genomic groups in *Musa*. This study identified RAPD markers for the A and B genomes. Eighty 10-mer Operon primers were used to amplify DNA from *M. acuminata* clone Calcutta 4 (AA genomes) and *M. balbisiana* clone Honduras (BB genomes). Three primers (A17, A18, and D10) that produced unique genome-specific fragments in the two species were identified. These primers were then tested in a sample of 40 genotypes representing various genome combinations. The RAPD markers were able to elucidate the genome composition of all genotypes. The results showed that RAPD analysis can provide a quick and reliable system for genome identification in *Musa* that could facilitate genome characterization and manipulations in breeding lines.

Wide Hybridization

(Wide Crosses)

The hybridization of crop species with distant relatives (wild species) has clear advantages: it broadens the genepool and permits the transfer of alien genes that confer positive benefits, such as stress tolerance, which lead to higher yields. At IRRI, genes for resistance to brown planthopper, bacterial blight, and blast have been transferred across genetic barriers from wild species into rice.

CIMMYT has drawn on genetic diversity from wheat's wild relatives to develop synthetic hexaploid wheats that have proven remarkably resistant to diseases including leaf blights, Septoria, and Fusarium head blight (scab), as well as to stresses such as heat and waterlogging. This resistance is extremely valuable, given that scab alone has been reported to cause losses of billions of dollars and millions of tons of grain in the US and China alone. To date, CIMMYT has formed almost 800 synthetics, and of these several lines have shown very high levels of resistance to scab (e.g., infection rates of only 5–10%, compared to 45–60% in susceptible checks). New materials show even higher levels of resistance.

Maize/*Tripsacum*/teosinte combinations also have potential for apomixis and for *Striga* resistance. For apomixis, a large step forward was taken with the development of apomictic maize-like plants; crossing and screening will continue with these plants until a true apomictic maize is

produced. For *Striga*, researchers are evaluating teosinte and *Tripsacum* accessions for resistance; some promising materials have been identified. Maize-*Tripsacum* hybrid derivatives coming from a potentially immune material were also evaluated. Plants backcrossed three times to maize were first evaluated in the fields and showed zero *Striga* emergence. They were further evaluated in the lab in Sheffield University, UK, and showed both a reduced level of *Striga* emergence and poor growth of the attached *Striga* plants. One accession has been selected for further analysis, based on both field response and the availability of advanced backcross generations to maize.

Gene/QTL Mapping

Geneticists can accelerate breeders' work in the field by identifying plants that carry the useful gene(s) or sets of alleles called quantitative trait loci (QTLs). Research at CIMMYT has recently identified three quantitative trait loci (QTLs) that contribute to scab resistance. These QTLs individually account for 10%, 15%, and 20% of the total variation of FHB resistance. A simple tabulation of these percentages, however, does not provide an accurate picture of their actual influence, because some of their resistance activity almost certainly overlaps or results from interactions between the genes. Further statistical analysis is planned to ascertain the actual combined effect of the three QTLs, but it is estimated that they account for 30–40% of the resistance. Researchers eventually hope to account for 60–70% of the resistance. Mapping these genes is the equivalent of adding another brick to the foundation needed for building higher levels of resistance to this important disease.

Functional Genomics

Functional genomics holds great promise for helping researchers understand the genetic basis of expression of complex traits by enabling them to assign specific biological functions to DNA sequences.

The objectives of this area of research in the CGIAR are to identify new genes controlling complex traits; identify sources of genes for crop/animal improvement; and facilitate access to products and technologies by partners in national research programs. The importance of partnerships in this effort cannot be understated. CIMMYT and Pioneer Hi-Bred International have initiated an effort to use functional genomics to understand the genetic basis of drought tolerance in maize. Each partner brings important contributions to this research alliance. CIMMYT provides well-characterized germplasm, proven field protocols, and a segregating/QTL population. Pioneer offers high-throughput capacity, genomic technologies, and candidate gene testing.

IRRI's work on functional genomics aims to generate genetic resources for applications of genomic databases to discover new genes and traits; enhance ecosystem-based varietal improvement programs with new genes and bioinformatics tools; and promote accessibility of genomic databases, tools, and genetic resources to national agricultural research systems (NARSs) in developing countries. Researchers engage in several interrelated

activities: development of genetic resources, phenotyping, and application of genome-wide, high-throughput genotyping.

A variety of genetic resources, including mutants, introgression lines, and mapping populations segregating for particular traits, are being produced for functional analysis. Elite breeding lines developed from cycles of selection for specific traits become part of the resources that reveal new functions through application of genomic tools. These materials serve distinct purposes in gene discovery based on their phenotypic expression.

Phenotyping activities concentrate on genetic variation and characteristics that are most relevant under field conditions. Work is underway in evaluating disease resistance, tolerance to submergence and drought, and morphological variations in the genetic stocks produced. As the work progresses, this approach will be extended to other important agronomic traits such as plant architecture, yield, and grain quality.

IRRI is acquiring high-throughput equipment to conduct reverse genetics, rapid genotyping, and discovery of candidate genes in metabolic pathways. The initial investment includes robotic workstations for DNA extraction, polymerase chain reaction (PCR), and library arraying. A plan is in place to establish a microarray facility. Eventually, IRRI plans to provide research capacity and training for national research systems in high-throughput facilities. Handling and interpretation of data (e.g., gene expression profiles) will be part of the training.

In bioinformatics, IRRI's immediate objective is to build a public database to link phenotype data with sequence

information from the international sequencing groups. This database will eventually provide information on gene function, genotypes of elite lines, and phenotypic expression of specific genotypes.

At ILRI, researchers have launched an ambitious program to decode the DNA of one of Africa's most destructive cattle parasites. The availability of detailed genetic information about the parasite that causes East Coast fever (a leading cause of death in African cattle) should speed the development of a cost-effective vaccine. Decoding the parasite's genetic structure could cut ten years off the time needed to produce a cost-effective vaccine. The research should help immunologists to identify the proteins that enable the parasite to invade the cow's white blood cells. Over the longer term it may also assist researchers working to develop a vaccine against malaria and improve science's understanding of human cancers. The project is being conducted by the Nairobi-based International Livestock Research Institute (ILRI) and the Institute for Genomic Research (TIGR). Biotechnologist Craig Venter, who chairs TIGR's board of trustees, donated all of the US\$ 100,000 in prize money he received as the winner of this year's King Faisal International Science Prize to this multimillion dollar project. The project is expected to sequence the parasite genome within a year. ILRI scientists estimate that 24 million head of cattle are at risk of contracting the disease. A vaccine would inject up to US\$ 300 million annually into the economies of the 11 countries where the disease is widespread.

Transformation

Transformation, which permits the introduction of novel genes in purified form, has probably excited more controversy in plant breeding than any other innovation in recent memory. Readers do not need a review of the many issues that surround the development and deployment of transgenic organisms; instead I will focus on some of the directions that this kind of research has taken within two CGIAR centers.

IRRI has been using transformation technology in efforts to develop improved resistance to rice stem borer, bacterial blight, and sheath blight, but the most well-known example of rice transformation research is Golden Rice, which has been genetically modified to contain more iron and vitamin A. Researchers from the Swiss Federal Institute of Technology's Institute for Plant Sciences inserted genes from a daffodil and a bacterium into rice plants, enabling them to produce grain with beta-carotene (which is converted to vitamin A in humans). To double the iron content in rice, the research team added a gene from a French bean. The Swiss research was conducted with funding from governments and not-for-profit organizations. If the numerous intellectual property issues surrounding Golden Rice can be untangled, the new rice will be freely available to national and international agricultural research centers, and IRRI will adapt, develop, and conduct nutritional and environmental testing on rice varieties for the tropics.

At CIMMYT, transformation technology forms part of a series of conventional and novel breeding strategies designed to increase resistance in maize to stem borers, which are particularly pernicious in Africa. Once inside a maize stalk, borers are impervious to conventional insecticide applications and cannot be removed by hand. In Kenya, it has been estimated that borers damage as much as 15% to 40% of the national maize crop. A CIMMYT research team has inserted *cry1B* and *cry1Ac* genes into a tropical maize background. This maize resists southwestern corn borer (SWCB), sugarcane borer (SCB), and fall armyworm (FAW). A synthetic *cry1E* gene and a translational fusion *cry1B-1Ab* gene were also introduced into tropical maize and have shown resistance to FAW, SWCB, and SCB.

For wheat, transformation research at CIMMYT focuses on developing improved disease resistance in wheat, especially resistance to the rusts, the most economically important wheat diseases worldwide. Recent significant improvements in the wheat transformation rate at CIMMYT have taken researchers much closer to achieving this goal. In 2000, researchers inserted a gene that confers complete immunity to rust diseases in rice into wheat, with striking results. Transformed plants were infected with one of the more virulent races of rust found in Mexico and showed only a modest level of infection, compared with highly lethal infections on the control plants. Although it is unlikely that the rice gene represents a magic bullet (with truly novel characteristics) against rust, it could still be a valuable asset when stacked or pyramided with other resistance genes.

Geographic Information Systems

Geographic information systems (GIS) literally bring new science “down to earth” by enabling researchers to integrate, process, analyze, and manipulate data in an explicitly spatial manner. The CGIAR centers have taken advantage of GIS in their own work and have also developed a number of extremely useful, practical tools and applications that have brought the analytical power of GIS to researchers who may not even have had desktop computers five years ago.

Over the last 5 years, IRRI has developed a fully functioning GIS laboratory and has established links with advanced research institutions engaged in developing and maintaining global databases. Researchers have developed crop models and a GIS-based methodology for environmental characterization. IRRI focuses its GIS capacity on analyzing rice production and socioeconomic systems, as well as biophysical and socioeconomic constraints; targeting and prioritizing research; assessing potential rice supply and demand; and determining optimal land use options.

FloraMap®, a computer tool on CD-ROM from CIAT, is the product of more than two decades of research and testing. The main uses of FloraMap are to guide the collection of wild plant species as well as to investigate their taxonomic and genetic variation. The program has also helped researchers to plan gene-conservation strategies and to map crop pests and their natural enemies. For example, an international research team

used the pilot version of FloraMap to map the probable distribution of five Andean species of passion fruit (*Passiflora* spp.). Before this research project was undertaken, only a relatively small number of passion fruit specimens had been systematically gathered and conserved, and little was known about the genetic variation and climatic adaptation of commercially important passion fruit species in South America. The research team organized prospecting expeditions, reviewed the taxonomic literature, and obtained data for nearly 400 accessions of five *Passiflora* species. The spatial coordinates were input into FloraMap to identify other areas where specimens might be collected. Results also allowed the scientists to compare differences in climatic adaptation with genetic variations demonstrated through isozymes. IPGRI, which is interested in FloraMap for its conservation work, is extending the use of this software to national programs and to IPGRI staff around the world.

CIMMYT has used GIS to target sites for farmer participatory research both in Zimbabwe and in Mexico. In Zimbabwe, site similarity studies were conducted for prospective research sites to ensure that analyses of farmers' risk management strategies in the research site would be relevant over a wider area and for a large number of farmers. In Mexico's Mixteca region, one of the poorest yet most culturally and biologically diverse regions of Mexico, researchers work with farmer groups to identify and solve their problems. A series of site similarity analyses were used to guide a farmer tour through other parts of the Mexican altiplano so that farmers could view relevant technologies used or being developed elsewhere.

Conclusion

These short descriptions of the ways that new scientific strategies are used in our research system provides only a minimal introduction to their great potential in helping us to fulfill our mission. These strategies are promising; they are exciting; but like any innovation, they present challenges and uncertainties that will require many things from us. They will require great vigilance to ensure that concerns about equity, human health, and environmental welfare remain at the forefront of decisions about how to accomplish our research objectives. They will require great perseverance—both from researchers, who must deal with all of the unknowns that accompany new research directions, and from research managers, who must negotiate their way through an environment in which controversy increasingly limits consensus about how the new science should be used. And finally, these research strategies will require (and inspire) immense creativity in our research community.

We must not forget that it is our science that gives substance to our mission. It is worth asking whether we would have been able to engage in so many innovative research areas if our colleague Ismail Serageldin had not believed in our potential to achieve results, and convinced others of that potential. The tremendous scientific dedication and energy within the CGIAR are fitting tributes to his own dedication and energy in acting as an advocate on our behalf. His efforts are helping our research to bear results, and I can think of few better legacies for humanity.

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Acronyms and Abbreviations

CGIAR	Consultative Group on International Agricultural Research
CIAT	Centro Internacional de Agricultura Tropical (International Center for Tropical Agriculture)
CIMMYT	Centro Internacional de Mejoramiento de Maíz y Trigo (International Maize and Wheat Improvement Center)
FAW	Fall armyworm
GIS	Geographic information systems
ICARDA	International Center for Agricultural Research in the Dry Areas
IITA	International Institute of Tropical Agriculture
ILRI	International Livestock Research Institute
IPGRI	International Plant Genetic Resources Institute
IRRI	International Rice Research Institute
MAS	Marker-assisted selection
NARSs	National agricultural research systems
QTL	Quantitative trait loci
RAPD	Random amplified polymorphic DNA
SCB	Sugarcane borer
SWCB	Southwestern corn borer
TIGR	The Institute for Genomic Research

