The Rockefeller Foundation's International Program on Rice Biotechnology

J.C. O'Toole, G.H. Toenniessen, T. Murashige, R.R. Harris, and R.W. Herdt

The Rockefeller Foundation's design of a long-term program on rice biotechnology was the product of a 2-year intensive survey and analysis of the genetic prospects for the world's major food crops conducted in the early 1980s. In late 1984, the Foundation's Board of Trustees approved a strategy for a 10–15-year program. That program was highly speculative and indicated substantial risk with regard to the status at that time of cereal plant molecular biology and rice in particular. During the first 5–7 years, projects supported by the Foundation laid the scientific basis for "rice biotechnology" as we know it today. Early successes were the first DNA molecular marker map of rice, the regeneration and transformation of rice, the use of rice pest genomic information to unravel age-old riddles of host-plant resistance, and numerous other discoveries that changed the way rice geneticists viewed breeding objectives such as insect resistance, abiotic stress tolerance, and hybrid rice. These discoveries culminated in the revelation of rice's pivotal genomic position in the evolution of cereal species. Over the ensuing 7–8 years, the program shifted its focus to the transfer of the resulting biotechnologies to institutions in rice-producing and -consuming countries. This task required the strengthening of both physical and human resources in cooperation with national and international rice research systems in Asia, Africa, and Latin America. The Foundation's program management sought to support further technology generation and application while promoting the program's greatest asset, *international collaborative research-cum-training*. This "win-win" component of the program linking fledgling national rice biotechnology efforts directly to advanced research institutes in the United States, Europe, Japan, and Australia became the hallmark of the Foundation's management strategy. During the program's 17-year lifetime, more than 400 (primarily Asian) rice scientists were trained in this manner. The successful linkage of research in cutting-edge biotechnology with the training of rice scientists often produced long-term collaborative relationships that outgrew dependence on Foundation support and continue today (such as the IRRI-managed Asian Rice Biotechnology Network). Some of these successes were undoubtedly a consequence of the basic research progress in rice plant molecular genomics, which brought greater financial support for rice-centered research as rice became the "model cereal" for genomic research, rivaling even *Arabidopsis*.

The Rockefeller Foundation has a long, complex, and rich history in promoting agricultural development throughout the developing world. The Foundation began its major field-based program in Mexico in the 1940s, which led to the series of technologies, insights, and processes collectively known as the "Green Revolution." During the 1950s, success in Mexico led the Foundation to establish similar country programs in Colombia, Chile, and India. The 1960s saw the Foundation establish, jointly with the Ford Foundation, four international agricultural research centers. In 1971, the Foundation helped establish a consortium of donors to support the international centers, the Consultative Group on International Agricultural Research (CGIAR). Today, 16 CGIAR-supported centers throughout the world have a total annual budget of about $350 million. The resulting growth in agricultural production and farm incomes, together with educational, health, policy, and environmental improvements, helped increase food availability and entitlements and enabled hundreds of millions to escape hunger over the past 50 years.

During the 1970s, many changes occurred in the direction and staffing of the Foundation's Agricultural Sciences Division. In 1982, an external review team intensively examined the Foundation's agricultural program (Kearl et al 1982). Prominent among the suggested future activities was the application of molecular biology to plant breeding. Over the next two years, Foundation officers consulted experts and assessed the relative status and merits of a program focusing on a few or a single crop species. Finally, the decision was made in late 1984 to implement a comprehensive program on rice, ranging from fundamental research through to the application of new molecular-based techniques in rice breeding (Toenniessen and Herdt 1988). The Foundation Board of Trustees approved the program in December 1984 and was aware from the outset of the high risk involved and probable 10–15-year time frame to accomplish the objectives. (At that time, the rice genome was relatively unknown and even its size was considerably overestimated, no DNA molecular markers/maps were available, no cereal had been regenerated from a protoplast, and hence there was no experimental evidence to support the proposal that transformation of rice with novel genes would ultimately become a tool for rice genetic improvement.)

This chapter sets out to chronicle the unique nature of the program's origin, guiding principles, and salient achievements in both scientific progress and capacity building in rice-consuming countries. In addition, we will illustrate the complex nature of an evolving program structure and management experience that fostered international collaborative research, training, and capacity building, focused on rice-consuming countries.

Evolution of program strategy and implementation

In 1984, the lowly position of rice (*Oryza sativa* L.) in the world of plant molecular biology represented a dramatic challenge to Foundation officers charged with generating a rice biotechnology knowledge base. Through a series of strategically placed grants, some of the world's premier laboratories were invited to participate in the program. The early output from these labs and others spurred on by the attention and promise of rice biotechnology was impressive: rice became the first cereal to be re-

generated from a protoplast in 1986-88, a comprehensive molecular (restriction fragment length polymorphism, RFLP) map was achieved by 1988, and the first experimental transformation was accomplished in 1988-90. These rapid developments were heartening and during that period the International Program on Rice Biotechnology (IPRB) goals were modified to include not only the discovery of scientific fundamentals and their transfer to the CGIAR-supported centers, but a more comprehensive and ambitious set of objectives was adopted related to the transfer of the new technology to rice researchers in rice-consuming countries.

Following a review of Foundation-wide development strategies, the IPRB goals were modified into four primary objectives:

1. To assure that the scientific tools of biotechnology were developed for tropical rice;
2. To create sufficient biotechnology capacity in rice-dependent countries to meet current and future challenges to rice production;
3. To better understand the consequences of agricultural technological change in Asia, in part to help in setting priorities for biotechnological applications; and
4. To apply this knowledge and capacity to the production of improved rice varieties and other materials that will enable farmers to produce more abundant supplies of nutritious food while causing less environmental damage.

Setting rice biotechnology research priorities

Setting research priorities for the program using a socioeconomic approach that balanced opportunities for rice productivity gains with costs of research was one of the unique aspects of the program. Herdt and Rieley (1987) pioneered the use of crop-loss estimates, weighted by equity considerations, and a global approach to provide the Foundation's rice biotechnology program with a set of the top-20 priority traits. The use of this mechanism to focus funding on the genetic solution of high-priority traits distinguishes the program and led to very cost-effective decision making by program management staff. The global study of 1986 was followed by several studies, of narrower geographic scale, intended to provide similar guidelines for resource allocation to national agricultural research systems at the country or regional level (eastern India—Widawsky and O'Toole 1990; China—Lin and Shen 1993; Nepal—Upadhyaya et al 1993; for others, see Evenson et al 1996). In addition, in light of changing circumstances and developing science, Foundation economists continued to refine both the methodology and the results used to direct investment in rice research (Herdt 1986, 1987, 1991). The nearly decade-long effort to prioritize rice research targets, with a primary purpose to guide the Foundation's IPRB, culminated in the publication of *Rice Research in Asia: Progress and Priorities* (Evenson et al 1996).

All research and capacity-building programs have finite budgets and the Foundation's rice biotechnology program was no exception. The continued use of updated output from "priority-setting" research was a salient component of the IPRB management decision making. In this way, national and international research targets were clearly defined and, when coupled with investments in human resource development (see below), represented a well-integrated and very cost-effective program management structure.

Evolution and implementation of the strategic plan

Evolution and implementation of the strategic plan were based on the Foundation's private mode of operation. This allowed the program to experiment with both scientific and management activities and to be responsive to the needs of grantees while also being opportunistic when appropriate. Figure 1 provides a greatly simplified conceptual model of the IPRB's operational mode.

The program was first of all ***research-driven***. All participants in the program entered only by this route. Few activities were supported that were not directly or indirectly associated with promoting the overall research goals. As illustrated in Figure 1, the benefits of participating in the IPRB were attractive to scientists in both the developed and developing countries. Early in the program's lifetime, it was determined to bring all participants together in periodic international meetings. This venue increased the probability of face-to-face meetings and the evolution of joint ***collaborative research*** proposal development. The Foundation fostered this outcome by providing an array of training opportunities in high-income countries' (HIC) labs and carefully selecting and matching candidates with host scientists based on common research interests and the needs of their home institutions with regard to future human capacity building. The IPRB supported several ***information technologies*** to serve participants' needs; distributed theses, reprints, books, and patents; and published the "Rice Biotechnology Quarterly," a newsletter serving program participants worldwide. At international meetings, participants could be updated on the latest (prepublication) rice biotechnology science as well as the latest in "priorities" established by the social scientists' network. Thus, the international collaborative research and training mechanism supported by the IPRB resulted in excellent synergies and benefits far outweighing the level of financial support available from a single donor organization.

Allocation of funds

Table 1 depicts the allocation of funds over the lifetime of the IPRB. Several trends are noteworthy. Since its inception, IPRB has dispensed almost $105 million, an average of about $6.2 million per year. The breakdown between research and training was

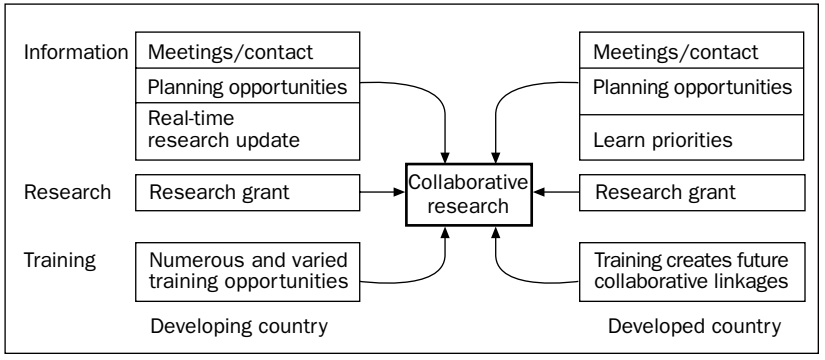


Fig. 1. Research-driven program components.

Table 1. The Rockefeller Foundation's International Program on Rice Biotechnology expenditures × $1,000.

Year	Basic research (HIC)[a]	Applied research (LIC)[b]	International centers	Social science	Meetings/ administration	Fellowships/ training	Total
2000	157	1,400	500	0	64	810	2,931
1999	468	1,689	1,006	55	466	2,266	5,950
1998	561	2,480	729	50	288	2,305	6,413
1997	566	2,068	936	0	523	2,418	6,511
1996	2,073	1,462	1,161	289	346	2,173	7,504
1995	1,974	1,845	1,289	280	240	2,071	7,699
1994	1,263	2,139	1,622	100	614	1,878	7,616
1993	2,400	1,537	1,857	307	176	2,525	8,802
1992	2,474	1,591	1,088	405	499	2,305	8,362
1991	2,081	1,309	800	69	385	2,160	6,804
1990	3,100	1,847	1,092	196	284	2,050	8,569
1989	3,049	2,811	773	181	372	1,038	8,224
1988	1,689	718	655	467	100	635	4,264
1987	4,753	170	621	1,217	100	368	7,229
1986	1,530	125	746	0	155	364	2,920
1985	859	131	15	0	34	427	1,466
1984	2,780	131	50	0	15	488	3,464
Total	31,777	23,453	14,940	3,616	4,661	26,281	104,728

[a]HIC = high-income countries of the industrialized world. [b]LIC = low-income countries of the developing world.

approximately 70% and 30%, respectively. However, as noted above, the training program was well integrated into achieving the research priorities and hence much of the support to training also contributed directly to the research achievements. In the same manner, the apparent allocation of funds to HIC and low-income country (LIC) institutions of 30% and 47%, respectively, is also flawed. Because of the highly integrated program implementation, the remaining 23% was used to create many "bridging" elements, such as meetings and workshops, which, along with the priority-setting research, and integrated *training-cum-research relationships often leading to future international collaboration*, contributed to the close linkages among HICs, LICs, and the international centers.

As noted above, the initial years were devoted primarily to basic research support in HICs. This peaked in 1989-90 with a concomitant increase in funding of LIC research and a sustained increase in training of rice scientists from Asia, made possible by the scientific knowledge base then existing in the HIC laboratories and CGIAR centers after the initial 5–6 years of IPRB support. In addition, although small in magnitude, the funding for social science research on priority setting was sustained from 1987 through 1996, reaching almost all countries participating in the IPRB. The impact on program direction and hence effectiveness was extremely valuable and the training accomplished in research priority setting and management continues to make research more effective across Asia's rice-consuming countries.

Scientific progress and outputs

In the limited space available, we are unable to recount the *many* success stories and scientific achievements associated with the IPRB's comprehensive scheme, long tenure, and many partnerships with associated supporters of rice research. In the following few paragraphs, we will merely touch on a few of the salient research outputs. We apologize to the innumerable researchers and fellows whose work will not be mentioned and trust that relevant reviews will more fully document their work. Here we will emphasize the role of international collaborative research and training that was pivotal to the program's multifaceted scientific and capacity-building output.

The tools of rice biotechnology

When the IPRB began in 1984, little was known about the rice genome at the molecular level and essentially few molecular tools were available for conducting rice biotechnology research. It was unknown then that rice had attributes that would make it especially amenable to genomic research. While initially reluctant to work on what was for them a new plant system, several leading laboratories accepted Foundation funding and quickly began generating results that were at the forefront of plant biotechnology and materials they readily shared with others. Training courses and workshops were sponsored that helped to rapidly transfer these methods and materials across the IPRB network. Rice became the first cereal regenerated from protoplasts and the first cereal transformed via protoplast, particle gun, and *Agrobacterium*-based methods. It was also discovered that rice had the smallest cereal genome, a relatively high percentage of single-copy DNA, and only one small chromosome duplication. By 1988, a molecular genetic map of rice was produced (McCouch et al 1988) and special funding was provided for dissemination of the map and its DNA markers worldwide. In the 1990s, rice became the model plant for cereal genomic research and full-scale rice genome sequencing projects began in Japan and the United States, which have now been combined and expanded to become the International Rice Genome Sequencing Project. And, at the last General Meeting of the IPRB, 20-24 September 1999 in Thailand, an international Rice Functional Genomics Working Group was formulated.

Molecular plant pathology

Molecular plant pathology showed perhaps the most significant and rapid research progress and applied product development as well as being a beacon for collaborative research and capacity building. One story that embodies nearly every aspect of the IPRB research agenda as well as the application of rice biotechnology tools was the discovery of the bacterial blight resistance gene *Xa21* and the interesting saga that followed (Box 1). One of the central publications in the series chronicling this effort stated, "Characterization of *Xa21* should facilitate understanding of plant disease resistance and lead to engineered resistance in rice" (Song et al 1995). Indeed, it did both and in this way contributed significantly to plant pathology's understanding of the basis of plant disease resistance (Ronald 1997) and the genetic mechanisms that are the basis of resistance gene family evolution (Song et al 1997, Wang et al 1998, Richter and Ronald 2000).

Box no. 1

The saga of *Xa21*

THE STORY OF BACTERIAL blight disease resistance gene *Xa21* epitomizes nearly all the IPRB program components in Figure 1 and above all the extension of the program goals from knowledge generation to production of improved rice varieties. The following is a brief "telegraphic" coverage of that voyage of discovery and ultimate application for the benefit of Asian rice farmers.

1977 *Oryza longistaminata* lines originating from Mali, Africa, noted to carry broad-spectrum resistance to bacterial blight

198? *Xa21* transferred into *O. sativa* background through interspecific hybridization (Khush et al 1991)

1990 *Xa21* locus RFLP mapped (Ronald et al 1992)

1992-95 Map-based cloning via bacterial artificial chromosome library construction (Wang et al 1995); *Xa21* sequencing and demonstration of engineered resistance of a susceptible genotype (Song et al 1995, Wang et al 1996)

1995 Patent filed and eventual U.S. Patent Number 5,859,339 granted to Ronald et al, 12 January 1999; innovative institution founded (Genetics Resources Recognition Fund—University of California, Davis) to use license fees/royalties to assist science capacity building in developing countries (Ronald PC, personal communication, 28 September 1997)

1997 *Xa21* pyramided with other *Xa* R genes via PCR-based marker-assisted selection (Huang et al 1997, Reddy et al 1997)

1998 *Xa21* experimentally transformed into elite rice varieties (Tu et al 1998, Zhang et al 1998)

1999 Field trials of pyramided *Xa* genes, including *Xa21*, reported in China, India, Indonesia, and Philippines (Rockefeller Foundation 1999)

2000 Commercial hybrid restorer line genetically improved by marker-assisted selection of *Xa21* and resulting hybrid rice demonstrates field-level efficacy (Chen et al 2000)

Over the 17-year period of the IPRB, we estimate that four Predoctoral, four Postdoctoral, and five Biotechnology Career Fellows took part in the above international research collaboration, transferring the basic skills, knowledge, and other materials to their home institutions. In one prominent publication, Song et al (1995), the 12 authors represented four research institutions in China, France, Korea, and the United States. The research background for that publication truly represented unprecedented international collaborative research, training, and capacity building spanning the globe.

Another salient example is that of the research output over approximately 15 years on the rice blast fungal pathogen. In both the bacterial blight and blast disease examples, DNA molecular tools were used, based on a solid 30+ years' foundation of conventional plant pathology and rice genetics, to provide dramatic new and informative insights into host-plant-pathogen interactions (Wang and Leung 1999). In both blast and bacterial blight diseases, DNA marker studies of the pathogens' genomes allowed new information on the geographic array of the pathogens' genetically divergent strains. This information was crucial in both basic understanding of the evolution and distribution of these diseases and in the applied art and science of field screening and "smart" deployment of specific resistance genes to specific geographic zones. Much like the bacterial blight saga (Box 1), the results of the past 15 years' molecular characterization of the blast fungus and the continuous discovery and characterization of blast R genes present in *Oryza* species led to significant basic knowledge of the fungal and rice genomes. This developed a new appreciation and understanding of the fungus's capacity for genotypic variation as well as the evolution of polymerase chain reaction (PCR) markers for specific blast resistance genes and their effective and rapid marker-assisted backcrossing into elite rice varieties. The capacity built by the IPRB in various national rice improvement programs has been used under the Asian Rice Biotechnology Network (ARBN) managed by the International Rice Research Institute (IRRI). Under the ARBN, the relevant PCR markers to genetically manipulate the bacterial and fungal R genes noted above are shared along with increasingly economical lab and field protocols. This international synergy has resulted in the most rapid and targeted deployment of new disease R genes possible. All concerned are to be congratulated!

As noted in the section on priority setting, tungro virus disease and other rice viral diseases ranked high as international and national constraints to rice yield. Again the advent of molecular tools allowed the revelation of an extremely intricate "natural history" story in the case of tungro virus and equally new scientific knowledge of other viruses. The discovery of two nucleic acid forms (spherical = single-stranded RNA and bacilliform = double-stranded DNA) of tungro virus and full sequencing of the virus genomes and the ability to then trace them through the insect vector (green leafhopper) contributed greatly to the understanding of the suite of biological characters responsible for field symptoms of the notoriously episodic damage feared by rice farmers. The high priority placed on viruses by the IPRB prioritization studies also meant that, of the 13 viruses known to attack Asian rice, almost all were partially or fully DNA/RNA-sequenced in the past ten years (Waterhouse and Upadhyaya 1999). With this knowledge in hand, a fruitful scientific dialogue ensued among rice scientists worldwide regarding the most effective way to use this knowledge base for the genetic improvement of rice.

Enhancing resistance to insects

Enhancing resistance to insects is the twin traditional goal of rice breeding with some 100+ species of insects attacking the rice crop. Unlike the study of the pest genome in diseases, insect genomics did not receive as much attention. Nevertheless, as with

viruses, molecular tools made possible a new understanding of both host-plant insect resistance and the natural history of some significant insect pests. In general, the use of molecular markers and the transgenic expression of insecticidal proteins received major attention. Bennett et al (1997) provide an excellent review of the contributions made by various biotechnology tools—interspecific hybridization, molecular markers, and rice plant transformation—toward the goal of enhanced insect resistance. Their review along with that of Mohan et al (1997), which ranges from genome mapping and cross-species synteny to the application of DNA markers in crop breeding, illustrate well the dramatic new genetic resources available to rice breeders regardless of the insect pest being targeted—stem borers, planthoppers, gall midge, or leaffolder.

Abiotic stresses—flood and drought

Flood/submergence tolerance research focused on studies of the basic response of rice to flooding/submergence and represents a classic example of international collaboration within the IPRB. Collaborative networking included scientists from Australia, Bangladesh, India, Japan, Philippines, Thailand, and the United States working interactively, as well as competitively, for more than a decade (Hossain et al 1996, Huq et al 1999). The studies embraced basic research related to critical gene isolation and regulation in transformed rice as well as molecular marker-assisted selection based on extensive field-level screening (Xu and Mackill 1996, Nandi et al 1997). The output from the various approaches (gene isolation/characterization versus quantitative trait loci identification) has begun to overlap as functional genomics became more pervasive than the "tools × traits" approach to genetic improvement. Those involved in submergence/flood tolerance research are in the forefront of candidate gene searches and international rice sequencing efforts (Normile 1999a). Other examples of the evolution and convergence of rice molecular genetics are widespread among IPRB grantee collaborative networks and illustrate yet another significant outcome of the network. This leads us to ask: Unless these researchers had been collaborating internationally and had a forum to communicate directly, would they be ready for the "next wave" in rice biotechnology—functional genomics and the bioinformatics revolution—now beginning?

Drought tolerance received high priority in the IPRB's earliest priority-setting exercise (1986) and subsequent national exercises further documented its importance. However, water deficit, unlike the abovementioned water excess, is one of crop genetic improvement's least understood genetic traits and is considered intractable by some. Nevertheless, over the past decade, a few dedicated researchers have made significant progress, both from the perspective of molecular marker tagging of traits thought to enhance drought tolerance—root system parameters (Champoux et al 1995, Ray et al 1996, Courtois et al 2000) and osmotic adjustment of tissues (Lilley et al 1996, Zhang et al 1999a,b)—but also in the creation of experimental rice transgenics with increasing levels of stress-inducible promoter and gene construct sophistication, which demonstrate striking responses to water deficit in growth chamber and greenhouse trials (Xu et al 1996, Su et al 1998, Bajaj et al 1999). The considerable accumulation of knowledge, information, and research experience was the subject of two

recent international workshops to plot future research strategy, not only for rice but also for the five major cereals that feed human populations globally (Ito et al 1999, Ribaut and Poland 2000).

The future use of molecular markers to combine or pyramid abiotic stress resistance genes with those of disease and insect resistance, in an efficient and timely manner, could only have been a rice breeder's dream just a decade ago. Today, however, with Internet access to molecular genotype and phenotype databases and the international sharing of many different types of genetic resources (germplasm and DNA-based technologies), even such complex traits and combinations of traits are approachable (Xu 1997).

Comparative genomics

Comparative genomics and the discoveries related to the study of synteny among cereal genomes demonstrated the unequivocal superiority of DNA-based molecular tools for investigating the long-standing questions of cereal evolution. In addition, it demonstrated what has become the ultimate discovery of the rice biotechnology adventure—the central role of the rice genome in understanding and technically accessing the far-larger genomes of such major crops as maize and wheat (Box 2).

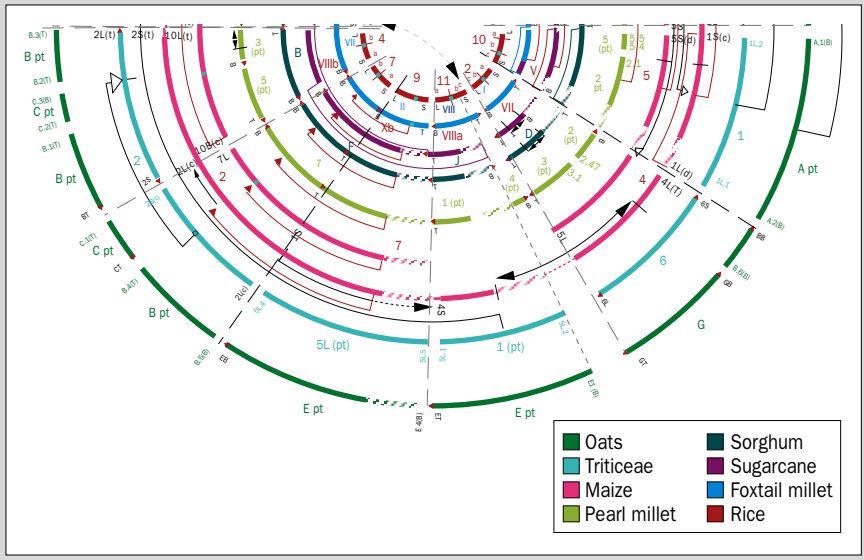
Early in the 1990s, it was apparent that higher plant species must share extensive "colinearity" of DNA markers and presumably genes across genera in both dicots as well as monocots. The prospect of conservation of linearity within linkage groups generated great excitement. For, if this were true, genetic information and related molecular markers might be exploited in related species with less well-developed molecular maps and markers. From 1988 to 1993, numerous papers related the news that indeed colinearity was a fact across species and even genera. However, even more striking and fortuitous for those working with the rice genome was the development of comparative or consensus maps within the cereals (Bennetzen and Freeling 1993). In their conceptual framework, Moore et al (1995) postulated that, based on the alignment of 19 linkage groups/segments from rice, one could form the building blocks of six of the world's major cereal food crops. A flood of research reports followed that not only confirmed the conceptual model but also quickly illustrated how gene discovery in the rice genome, partially because of its small size and saturated molecular maps, could rapidly and effectively be transferred to the other cereals. By 1998, Van Deynze et al (1998) had produced a set of RFLP anchor probes to facilitate comparative mapping across grass genera. Shortly thereafter, the applications forecast earlier began to be apparent. Leister et al (1999) demonstrated the RFLP and physical mapping of resistance gene homologues in rice and barley. Coincidentally, the R genes from rice were the genes with race-specific resistance to blast and bacterial disease noted at the beginning of this section.

These scientific advances, combined with the advent of electronic mail (an equalizer of time, space, and national origin without parallel), added a multiplier effect to the IPRB investment that could not have been imagined 15 years earlier. Researchers worldwide have experienced research synergy unheralded over the past 50 years of rice genetics, as rice, "the pivotal genome," was placed in a unique position along with those researchers who had helped to create the science of rice biotechnology.

Box no. 2

Rice—the pivotal genome

COMPARATIVE GENOMICS HAS revealed a level of conservation in gene content and order within the grasses that surprised even the most experienced geneticists. After the landmark publication of Moore et al (1995), which indicated that all major cereal crop genomes could be represented by 19 segments found in the rice genome, rice has taken a solid position at the *center* of both graphic presentations (adapted from Gale and Devos 1998, this box) as well as research efforts to use map-based cloning for gene discovery and isolation from the much larger genomes of oat, wheat, and maize. The rice genome, with only 400 million DNA base pairs (bp), is about four times larger than *Arabidopsis*, the model dicot. This, coupled with a dense genetic map of >2,500 markers, physical maps of the entire genome, large public collections of expressed sequence tags (ESTs), and the near-term prospect of the complete rice genome sequence, makes rice a model crop for the cereals.



Institutional and human resource capacity building[1]

Capacity building is an extremely difficult concept to define. When related to the IPRB, where it refers to national networks and institutions as well as individuals, it can result in a great lack of clarity, which might require a full-length paper to demystify.

[1]This section on capacity building under the IPRB relies heavily on the report "Capacity Building Evaluation of the International Program on Rice Biotechnology (IPRB)," June-October 1999, by Madan Mohan, Leocadio Sebastian, Kangle Zhang, and David Norman. Rockefeller Foundation. 249 p.

For the purposes of this discussion, we will use the following, not as a definition but as the major tools of capacity building under the IPRB.

The major elements of the IPRB that contribute to capacity building are (Toenniessen 1998)

1. Fellowships and courses offering specialized training, skills maintenance, and technology transfer.
2. The enabling environment provided by a network of scientists who are conducting related research and are eager to share ideas and materials.
3. Partnerships with national agencies that assume increasing responsibility for funding and management.
4. Access to relevant information and effective communications systems.
5. A rational process for establishing research priorities.
6. Renewable research grants having application and monitoring processes that place strong public emphasis on the use of rigorous scientific methods and peer review.
7. The emergence of centers of strength capable of playing a leadership role in the future.
8. The work of Foundation field staff scientists located in Asia.

In statistical terms, approximately 700 scientists from more than 30 countries have participated directly in the IPRB. Grantees and fellows came from 12 HIC, 16 LIC, 4 CGIAR centers, and the International Center for Genetic Engineering and Biotechnology. After the "invention of rice biotechnology" phase, the program's primary goal was directed toward building capacity in the rice research institutions of Asia's rice-consuming countries.

The types of institutions

The types of institutions that were contacted by Foundation staff and invited to submit research proposals were a departure from previous "traditional" agricultural research institutions. The fact that a new science was being promoted required the Foundation to include many traditional or basic science institutions in the constellation of institutional grantees. Hence, the IPRB became known early on for its efforts to include nontraditional agricultural institutions, even though the program theme was obviously genetic improvement of rice. However, from the outset it was clear that in the larger countries an intranational network apparatus would be required to achieve the national-level collaboration required for successful application of biotechnologies to rice genetic improvement. Table 2 illustrates the relative frequency of institutional types that eventually made up the intranational and international networks under the IPRB umbrella and the different types of LIC institutions supported by the IPRB. Universities made up 43% of the total, whereas research institutions accounted for 57%. An alternative view is that 47% of the institutions had an agricultural research focus, whereas the remaining 53% did not necessarily share such a focus. Since its inception, the IPRB has awarded grants to 77 different LIC institutions in 16 different countries, 75% of which are in Asia. Institutions in two countries with the largest human populations and rice research systems, China and India, have

Table 2. Types of institutions supported by the Rockefeller Foundation's International Program on Rice Biotechnology.[a]

Country	Type of institution				
	University		Research institution		
	Conventional	Agriculture	Basic	Agriculture	Rice
Bangladesh	1	–	–	–	1
China	3	6	6	5	2
India	8	6	6	2	2
Indonesia	–	–	1	1	–
Malaysia	–	–	–	1	–
Nepal	–	–	–	3	–
Pakistan	1	–	–	1	–
Philippines	1	–	–	1	–
South Korea	1	–	–	1	–
Sri Lanka	–	–	–	1	–
Thailand	3	–	2	–	1
Vietnam	1	–	3	1	1
Latin America	2	–	2	–	–
Total (77)	21	12	20	17	7
Percentage of institutions	27.3	15.6	26.0	22.1	9.0

[a]Only institutions that received research grants were considered.

been the major beneficiaries, together accounting for 62% of the grantees and about the same proportion of total research funds.

The CGIAR-supported international centers

The CGIAR-supported international centers played a primary role from the IPRB's inception. IRRI in the Philippines, the International Center for Tropical Agriculture (CIAT) in Colombia, and the West Africa Rice Development Association (WARDA) in Côte d'Ivoire have as part of their mandate building rice research capacity in developing countries. In 1985, however, these institutions had limited capabilities in biotechnology, as was the case with most international agricultural research institutions. In the late 1980s, Foundation funding enabled IRRI and CIAT to expand their capacities in tissue/anther culture and interspecific hybridization while beginning to develop DNA molecular biology capacity. WARDA followed suit in the 1990s.

By 1990, it was evident that biotechnology would significantly affect rice breeding and IRRI and CIAT began using their core funds to satisfy new staff requirements. Like the national networks' requirement for greater diversity in institutional scientific capability, these international centers now have significant capacity to use biotechnology tools, but they also maintain many international collaborative research partnerships to cover the more sophisticated and costly technologies. The centers have offered a series of training courses for colleagues from national programs. With support from the Asian Development Bank, IRRI began the ARBN in 1996. In this way, IRRI has significantly expanded its capacity to work collaboratively with national centers, many of which were assisted by the IPRB institutional and individual capacity-building process.

Because of the great diversity (scientifically as well as geographically) of institutions involved simultaneously in the IPRB, program management was challenged to provide the full spectrum of research and capacity-building opportunities. However, several of the innovative instruments noted in the following section have proved to be robust across the great institutional and individual diversity embodied in the IPRB.

Formal training

Formal training under the IPRB had six types of fellowships, all of which featured candidates from grantee institutions in LICs who were hosted at an advanced laboratory in an HIC or at IRRI or CIAT:

- Ph.D. Fellowship—Fellow receives training for 4–5 years at an advanced research institution.
- Dissertation Fellowship—Fellow receives Ph.D. degree from home institution but conducts dissertation research at an advanced research institution for 1–2 years.
- Postdoctoral Fellowship—Fellow conducts research at an advanced research institution for 2 years.
- Visiting Scientist Fellowship—Fellow serves as visiting researcher at an advanced research institution for 1–2 years.
- Biotechnology Career Fellowship—Fellow conducts part of collaborative research program at an advanced research institution for 3 months per year over 3 years.
- Technology Transfer Fellowship—Fellow from advanced research institution conducts collaborative research at an institution in a rice-dependent country for 3 months per year over 3 years.

Impact of the formal training program. The impact of the formal training program under the IPRB is extremely difficult to gauge. Table 3 indicates the number of individuals trained by the different number of institutions in the 12 Asian countries and Latin America. China and India clearly have the largest number of institutions in which a broad range of skills and in-depth expertise can be found. Overall, the numbers varied substantially across countries with about 36% of the institutions having five or more people trained, whereas 22% had zero trained under the IPRB. Thus, it appears that the impact of the IPRB formal training program should be greatest in six countries: China, India, Philippines, South Korea, Thailand, and Vietnam.

Common problems associated with international training. The common problems associated with international training efforts were addressed in the planning and management of the IPRB using the six primary fellowships above and research grants:

- "Brain drain" or immigration out of the home country was addressed by the incentives of eligibility for a research grant and, after one year of in-country research, eligibility for a Biotechnology Career Fellowship.
- "Irrelevant training" was minimized because fellows were, as much as possible, directed to host labs with similar research interests and, later in the program lifetime, dependent on jointly agreed upon research proposals as a part of the home-institution endorsement and host-institution acceptance.

Table 3. Breakdown of number of institutions by country where formal training was sponsored under the Rockefeller Foundation's International Program on Rice Biotechnology.[a]

Country	Number of institutions according to number of researchers trained[b]						
	>20	15–19	10–14	5–9	3–4	1–2	0
Bangladesh	–	–	–	1	1	–	–
China	–	1	4	4	2	6	5
India	1	1	–	5	7	7	3
Indonesia	–	–	–	1	–	1	–
Malaysia	–	–	–	–	–	1	–
Nepal	–	–	–	1	–	–	2
Pakistan	–	–	–	1	–	–	1
Philippines	–	–	1	1	–	–	–
South Korea	–	–	1	–	–	–	1
Sri Lanka	–	–	–	–	–	–	1
Thailand	–	–	1	1	–	3	1
Vietnam	–	–	1	2	–	3	–
Latin America	–	–	–	–	–	1	3
Total	1	2	8	17	10	22	17

[a]Only institutions that received research grants were considered. [b]The individual column headings reflect the number of scientists trained under IPRB sponsorship.

- "Re-posting" or transfer to an unrelated field of research. The IPRB management had little influence on this matter. But persistent invitations to national and international meetings and indication of eligibility for research funds were occasionally effective in redressing the re-posting issue.
- "Lack of indigenous support" was temporarily overcome with eligibility to apply for a research grant.
- "Nonresponsive home-institution administration" was also little influenced by the IPRB. However, receiving a research grant, invitations to international meetings, and other types of supportive services were often an incentive for institutional administrative personnel to be more responsive to the researcher's needs.

The role of periodic international meetings

The role of periodic international meetings of the entire IPRB network, numbering 350–400+ participants in the final five years, was of immeasurable benefit to the program collaborative research and capacity-building goals. As Figure 1 shows, the international meetings served as a physical venue for networking with colleagues, particularly from other countries, and conducting real-time, face-to-face negotiations of future collaborative research and training plans. The meetings featured well-organized full schedules (day and night sessions); covered extremely wide-ranging biotechnology topics while focusing on a single unifying theme, rice; "forced" accountability took place because a poster and/or verbal presentation was expected along with critical review by peers and Foundation expert advisors; and "think tanks" stimulated future plans to assure that intermediate research products went into the hands of rice

breeders where final products to enhance the productivity and welfare of farmers and consumers could be realized.

Sustainability

In 1999 the Foundation determined that, after 16 years, the IPRB had accomplished its goals and it was time for an orderly closing of the program during 2000. Soon afterward, the news was publicly available (Normile 1999b) and the question of the IPRB's "sustainability" came to the fore. Sustainability of the gains from such a complex and long-term (17 years) international program can be considered for many facets of the IPRB: physical infrastructure and its maintenance, funding for research, maintaining and enhancing the investment in human capital, etc. Indeed, capacity building may be viewed at the individual, institutional, or national level. Much has been written on this subject (Cohen et al 1998, Falconi 1999, Byerlee and Gregory 1999) in recent years. Although the IPRB attempted to incorporate a national perspective, at least for larger countries such as China and India, questions of sustainability are most realistically contemplated at the institutional level. This is indeed a complex issue, but our experience points to one major factor—***leadership***. Institutions in which enlightened and energetic leadership was coupled with a suitable foundation of trained and motivated scientists appear to be well positioned to sustain their research momentum from both national and international sources. Some IPRB participants have used their network linkages to acquire funding from both public- and private-sector sources, thus enhancing their prospects for future support in a public-private partnership world.

The future of rice biotechnology

The past 15 years have so dramatically changed our knowledge of rice genetics that we would like to paraphrase Lander and Weinberg's (2000) recent *Science* article because we can clearly see that the *future of rice biotechnology is now*: "biology enters this century in possession, for the first time, of the mysterious instruction book first postulated by Hippocrates and Aristotle. How far will this take us in explaining the vast complexity of the biological world?".... The solutions to many problems long resistant to attack are now within our reach. The prospects of 21st century biology are surely breathtaking."

We are tempted to point to but a handful of future rice biotechnology outcomes that appear certain to be realized in the relatively near future:

- Rice genomics and functional genomics will demonstrate the enormous benefits of combining traditional (genetics, physiology, biochemistry) and new approaches (bioinformatics) into a fuller understanding of rice biology.
- A major application of the above will be in the regulation of gene expression and resulting manipulation of reproductive development in tandem with the concomitant control of senescence in leaves and other organs.
- Crop response to adverse environmental conditions will see the merger of genomics with rice physiology and biochemistry to more fully understand rice's potential for adaptation to marginal environments and to genetically improve rice for the constraints of the 21st century—water and salinity.

- Transformation of chloroplast genomes will be recognized as a means of containment for such novel genes as herbicide resistance and as such will significantly modify rice farming, especially in rainfed ecosystems.
- The "pocket laboratory" will soon bring PCR, microarrays, and other molecular biology protocols to the greenhouse and field, making marker-assisted selection a powerful practical tool for rice breeders.
- Rice grain quality and nutrition will be addressed to make new rice varieties available that can improve the overall health of rice consumers and generate a multitude of rice-based products for specialty markets.

The foundation laid for these advances, in part through the collaborative research, training, and capacity building accomplished under the IPRB, is only the beginning of the fruits that the world's poor farmers and rice consumers will need if the world's neediest are not to go hungry in the 21st century. These advances in rice biotechnology must be equitably deployed by a strong public-sector agricultural research effort if the ultimate gains are to be shared among those most deserving of them (Conway and Toenniessen 1999).

Concluding remarks

Those of us at the Rockefeller Foundation who have been associated with the International Program on Rice Biotechnology have found it to be an exciting, rewarding, and learning experience. Our grantees, fellows, advisors, and consultants made the important contributions that came together and were readily shared in a highly successful and truly international program. In the process, many became our good friends and colleagues. It was difficult for us to make the decision to bring Foundation funding for the program to a close. However, we are confident that the rice research community, particularly in Asia, now has the capacity to keep rice at the forefront of biotechnology research and to produce the new rice varieties the world urgently needs, as long as the community continues to share and work collaboratively.

References

Bajaj S, Targolli J, Liu L-F, Ho T-HD, Wu R. 1999. Transgenic approaches to increase dehydration-stress tolerance in plants. Mol. Breed. 5:493-503.

Bennett J, Cohen MB, Katiyar SK, Ghareyazie B, Khush GS. 1997. Enhancing insect resistance in rice through biotechnology. In: Carozzi N, Koziel M, editors. Advances in insect control. London (UK): Taylor & Francis. p 75-93.

Bennetzen JL, Freeling M. 1993. Grasses as a single genetic system: genome composition, collinearity and compatibility. Trends Genet. 9:259-261.

Byerlee DE, Gregory P. 1999. Agricultural biotechnology and rural development: options for the World Bank. Biotechnology Task Force, World Bank, Washington, D.C.

Champoux MC, Wang G, Sarkarung S, Mackill DJ, O'Toole JC, Huang N, McCouch SR. 1995. Locating genes associated with root morphology and drought avoidance in rice via linkage to molecular markers. Theor. Appl. Genet. 90:969-981.

Chen S, Lin XH, Xu CG, Zhang Q. 2000. Improvement of bacterial blight resistance of 'Minghui 63', an elite restorer line of hybrid rice, by molecular marker-assisted selection. Crop Sci. 40:239-244.

Cohen JL, Falconi C, Komen J. 1998. Proprietary biotechnology inputs and international agricultural research. ISNAR Briefing Paper No. 38. The Hague (Netherlands): International Service for National Agricultural Research.

Conway G, Toenniessen GH. 1999. Feeding the world in the twenty-first century. Nature 402(suppl):C55-C58.

Courtois B, McLaren G, Sinha PK, Prasad K, Yadav R, Shen L. 2000. Mapping QTLs associated with drought avoidance in upland rice. Mol. Breed. 6:55-66.

Devos KM, Gale MD. 2000. Genome relationships: the grass model in current research. Plant Cell 12:637-646.

Evenson RE, Herdt RW, Hossain M, editors. 1996. Rice research in Asia: progress and priorities. Manila (Philippines): International Rice Research Institute, and Wallingford (UK): CAB International. 418 p.

Falconi C. 1999. What is agricultural biotechnology research capacity in developing countries? ISNAR Discussion Paper No. 99-10. The Hague (Netherlands): International Service for National Agricultural Research.

Gale MD, Devos KM. 1998. Plant comparative genetics after 10 years. Science 282:656-658.

Herdt RW. 1986. Information needs for research resource allocation. Prepared for the workshop on Biotechnology for Crop Improvement, 13-17 Oct. 1986, International Rice Research Institute (IRRI). Los Baños (Philippines): IRRI. 32 p.

Herdt RW. 1987. Equity considerations in setting priorities for Third World rice biotechnology research. Dev. Seeds Change 4:19-24.

Herdt RW. 1991. Research priorities for rice biotechnology. In: Khush GS, Toenniessen GH, editors. Rice biotechnology. Manila (Philippines); International Rice Research Institute, and Wallingford (UK): CAB International. p 19-54.

Herdt RW, Rieley Jr. R. 1987. International rice research priorities: implications for biotechnology initiatives. Prepared for the Rockefeller Foundation Workshop on Allocating Resources for Developing Country Agricultural Research, 6-10 July 1987, Bellagio, Italy. 78 p.

Hossain MA, Huq E, Grover A, Dennis E, Peacock WJ, Hodges TK. 1996. Characterization of pyruvate decarboxylase genes from rice. Plant Mol. Biol. 31:761-770.

Huang N, Angeles ER, Domingo J, Magpantay G, Singh S, Zhang G, Kumaravadivel N, Bennett J, Khush GS. 1997. Pyramiding of bacterial blight resistance genes in rice: marker-assisted selection using RFLP and PCR. Theor. Appl. Genet. 95:313-320.

Huq E, Harrington S, Hossain MA, Wen F, McCouch SR, Hodges TK. 1999. Molecular characterization of *pdc2* and mapping of three *pdc* genes from rice. Theor. Appl. Genet. 98:815-824.

Ito O, O'Toole J, Hardy B, editors. 1999. Genetic improvement of rice for water-limited environments. Proceedings of the Workshop on Genetic Improvement of Rice for Water-Limited Environments, 1-3 December 1998, Los Baños, Philippines. Manila (Philippines): International Rice Research Institute. 353 p.

Kearl B, Adkisson P, McNamara R. 1982. A review of the Rockefeller Foundation Conquest of Hunger Program. New York (USA): Rockefeller Foundation.

Khush GS, Bacalangco E, Ogawa T. 1991. A new gene for resistance to bacterial blight from *O. longistaminata*. Rice Genet. Newsl. 7:121-122.

Lander ES, Weinberg RA. 2000. Genomics: journey to the center of biology. Science 287:1777-1782.

Leister D, Kurth J, Laurie DA, Yano M, Sasaki T, Graner A, Schulze-Lefert P. 1999. RFLP and physical mapping of resistance gene homologues in rice (*O. sativa*) and barley (*H. vulgare*). Theor. Appl. Genet. 98:509-520.

Lilley JM, Ludlow MM, McCouch SR, O'Toole JC. 1996. Locating QTL for osmotic adjustment and dehydration tolerance in rice. J. Exp. Bot. 47:1427-1436.

Lin J, Shen M. 1993. Rice production constraints in China: implication for biotechnology initiative. Prepared for the 6th Annual Meeting of the Rockefeller Foundation's International Program on Rice Biotechnology, 1-5 Feb. 1993, Chiang Mai, Thailand. 33 p.

McCouch SR, Kochert G, Yu ZH, Wang ZY, Khush GS, Coffman WR, Tanksley SD. 1988. Molecular mapping of rice chromosomes. Theor. Appl. Genet. 76:815-829.

Mohan M, Nair S, Bhagwat A, Krishna TG, Yano M, Bhatia CR, Sasaki T. 1997. Genome mapping, molecular markers and marker-assisted selection in crop plants. Mol. Breed. 3:87-103.

Moore G, Devos KM, Wang Z, Gale MD. 1995. Grasses, line up and form a circle. Curr. Biol. 5:737-739.

Nandi S, Subudhi PK, Senadhira D, Manigbas NL, Sen-Mandi S, Huang N. 1997. Mapping QTLs for submergence tolerance in rice by AFLP analysis and selective genotyping. Mol. Gen. Genet. 255:1-8.

Normile D. 1999a. U.S. adds $12 million to global sequencing push. Science 286:24-25.

Normile D. 1999b. Rockefeller to end network after 15 years of success. Science 286:1468-1469.

Ray JD, Yu L, McCouch SR, Champoux MC, Wang G, Nguyen HT. 1996. Mapping quantitative trait loci associated with root penetration ability in rice (*Oryza sativa* L.). Theor. Appl. Genet. 92:627-636.

Reddy JN, Baraoidan MR, Bernardo MA, George MLC, Sridhar R. 1997. Application of marker-assisted selection in rice for bacterial blight resistance gene, *Xa21*. Curr. Sci. 73:873-875.

Ribaut J-M, Poland D, editors. 2000. Molecular approaches for the genetic improvement of cereals for stable production in water-limited environments. A strategic planning workshop held at CIMMYT, El Batán, Mexico, 21-25 June 1999. Mexico, D.F.: International Maize and Wheat Improvement Center. 172 p.

Richter TE, Ronald PC. 2000. The evolution of disease resistance genes. Plant Mol. Biol. 42: 195-204.

Rockefeller Foundation. 1999. Proceedings (abstracts) of the meeting of the International Program on Rice Biotechnology. Phuket, Thailand, 20-24 September 1999. 388 p.

Ronald PC. 1997. The molecular basis of disease resistance in rice. Plant Mol. Biol. 35:179-186.

Ronald PC, Albano B, Tabien R, Abenes L, Wu K, McCouch S, Tanksley S. 1992. Genetic and physical analysis of the rice bacterial blight resistance locus, Xa21. Mol. Gen. Genet. 236:113-120.

Song W-Y, Wang G-L, Chen L-L, Kim H-S, Pi L-Y, Holsten T, Gardner J, Wang B, Zhai W-X, Zhu L-H, Fauquet C, Ronald P. 1995. A receptor kinase-like protein encoded by the rice disease resistance gene, *Xa21*. Science 270:1804-1806.

Song W-Y, Pi L-Y, Wang G-L, Gardner J, Holsten T, Ronald PC. 1997. Evolution of the rice *Xa21* disease resistance gene family. Plant Cell 9:1279-1287.

Su J, Shen Q, Ho T-HD, Wu R. 1998. Dehydration-stress-regulated transgene expression in stably transformed rice plants. Plant Physiol. 117:913-922.

Toenniessen GH. 1998. Rice biotechnology capacity building in Asia. In: Ives CL, Bedford BM, editors. Agricultural biotechnology in international development. Wallingford (UK): CAB International. p 201-212.

Toenniessen GH, Herdt RW. 1988. The Rockefeller Foundation's International Program on Rice Biotechnology. Presented at USAID-sponsored conference on Strengthening Collaboration in Biotechnology: International Agriculture and the Private Sector, 17-21 April 1988, Washington, D.C. p 291-317.

Tu J, Ona I, Zhang Q, Mew TW, Khush GS, Datta SK. 1998. Transgenic rice variety 'IR72' with *Xa21* is resistant to bacterial blight. Theor. Appl. Genet. 97:31-36.

United States Patent No. 5,859,339. 12 Jan. 1999. PC Ronald, G-L Wang, W-Y Song. Nucleic acids, from *Oryza sativa*, which encode leucine-rich repeat polypeptides and enhance *Xanthomonas* resistance in plants.

Upadhyaya HK, Pokhrel TP, Shivakoti GP, Vaidya SN, Bimb HP. 1993. Rice research in Nepal: current state and future priorities. Prepared for the 6th Annual Meeting of the Rockefeller Foundation's International Program on Rice Biotechnology, 1-5 Feb. 1993, Chiang Mai, Thailand. 40 p.

Van Deynze AE, Sorrells ME, Park WD, Ayres NM, Fu H, Cartinhour SW, Paul E, McCouch SR. 1998. Anchor probes for comparative mapping of grass genera. Theor. Appl. Genet. 97:356-369.

Wang G-L, Leung H. 1999. Molecular biology of host-pathogen interactions in rice diseases. In: Shimamoto, K, editor. Molecular biology of rice. Tokyo (Japan): Springer-Verlag. p 201-232.

Wang G-L, Holsten TE, Song W-Y, Wang H-P, Ronald PC. 1995. Construction of a rice bacterial artificial chromosome library and identification of clones linked to the *Xa-21* disease resistance locus. Plant J. 7:525-533.

Wang G-L, Ruan D-L, Song W-Y, Sideris S, Chen L, Pi L-Y, Zhang S, Zhang Z, Fauquet C, Gaut BS, Whalen MC, Ronald PC. 1998. Xa21D encodes a receptor-like molecule with a leucine-rich repeat domain that determines race-specific recognition and is subject to adaptive evolution. Plant Cell 10:765-779.

Wang G-L, Song W-Y, Ruan D-L, Sideris S, Ronald PC. 1996. The cloned gene, *Xa21*, confers resistance to multiple *Xanthomonas oryzae* pv. *oryzae* isolates in transgenic plants. Mol. Plant-Microbe Interact. 9:850-855.

Waterhouse PM, Upadhyaya NM. 1999. Genetic engineering of virus resistance. In: Shimamoto K, editor. Molecular biology of rice. Tokyo (Japan): Springer. p 257-281.

Widawsky DA, O'Toole JC. 1990. Prioritizing the rice research agenda for Eastern India. New York (USA): Rockefeller Foundation. 86 p.

Xu D, Duan X, Wang B, Hong B, Ho T-HD, Wu R. 1996. Expression of a late embryogenesis abundant protein gene, *HVA1*, from barley confers tolerance to water deficit and salt stress in transgenic rice. Plant Physiol. 110:249-257.

Xu K, Mackill DJ. 1996. A major locus for submergence tolerance mapped on rice chromosome 9. Mol. Breed. 2:219-224.

Xu Y. 1997. Quantitative trait loci: separating, pyramiding, and cloning. Plant Breed. Rev. 15:85-139.

Zhang J, Nguyen HT, Blum A. 1999a. Genetic analysis of osmotic adjustment in crop plants. J. Exp. Bot. 50:291-302.

Zhang J, Zheng HG, Ali ML, Tripathy JN, Aarti A, Pathan MS, Sarial AK, Robin S, Nguyen TT, Babu RC, Nguyen BD, Sarkarung S, Blum A, Nguyen HT. 1999b. Progress on the molecular mapping of osmotic adjustment and root traits in rice. In: Ito O, O'Toole J, Hardy B, editors. Genetic improvement of rice for water-limited environments. Manila (Philippines): International Rice Research Institute. p 307-317.

Zhang S, Song W-Y, Chen L, Ruan D, Taylor N, Ronald P, Beachy R, Fauguet C. 1998. Transgenic elite indica rice varieties, resistant to *Xanthomonas oryzae* pv. *orzae*. Mol. Breed. 4:551-558.

Notes

Authors' addresses: J.C. O'Toole, Senior Scientist and Field Representative, Food Security, The Rockefeller Foundation, Suite 1602, Central Chidlom Tower, 22 Soi Somkid, Ploenchit Road, Bangkok 10330, Thailand; G.H. Toenniessen, Director, Food Security, The Rockefeller Foundation, 420 Fifth Ave, New York, NY, USA; T. Murashige, Senior Scientist (Retired), Food Security, The Rockefeller Foundation, New York; R.R. Harris, Senior Program Associate, Food Security, The Rockefeller Foundation, New York; and R.W. Herdt, Vice President for Program Administration, The Rockefeller Foundation, New York.

Citation: Khush GS, Brar DS, Hardy B, editors. 2001. Rice genetics IV. Proceedings of the Fourth International Rice Genetics Symposium, 22-27 October 2000, Los Baños, Philippines. Los Baños (Philippines): International Rice Research Institute. 488 p.