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para la  
Agricultura  
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Alimentación

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### POTENTIALS AND LIMITATIONS OF BIOTECHNOLOGY IN RICE

By:

**Ronnie Coffman**

International Professor and Chair, Department of Plant Breeding, and Director of International Programs, College of Agriculture and Life Sciences, Cornell University, Ithaca, NY USA

**Susan R. McCouch**

International Professor of Plant Breeding, College of Agriculture and Life Sciences, Cornell University, Ithaca, NY USA

**Robert W. Herdt**

International Professor (Adjunct) of Applied Economics and Management, College of Agriculture and Life Sciences, Cornell University, Ithaca, NY USA

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## 0.0 Abstract

Rice is the first food crop for which complete genome sequence is available. This offers an unprecedented opportunity to identify and functionally characterize the genes and biochemical pathways that are responsible for agronomic performance, adaptation to diverse environments, resistance to biotic stress and consumer quality. Developing rice as a model system is pivotal in the effort to translate the value of information emerging from basic genome research for use in crop improvement.

Plant breeders today are presented with many possibilities for altering the behavior of existing crop varieties using targeted approaches suggested by genomics research. An underlying theme is that information about genes and gene functions is what drives biotechnological applications in plant improvement. Two major applications of biotechnology to rice improvement will be discussed in this paper. One involves the use of molecular markers to facilitate the identification and selection of favorable gene combinations. This approach allows breeders to exploit more efficiently the genetic variation that occurs naturally within a species. The second approach involves the introduction of alien genes using transgenics, referred to as genetic modification (GM). Transgenic technologies under development in rice (no commercial releases have occurred) can be broken out into four categories: (1) herbicide tolerance (2) biotic stress resistance, (3) abiotic stress resistance and (4) nutritional traits. The status and potential of each is discussed.

Most rice is produced and consumed in the same country and domestic considerations are often more important than trade. Some countries that are not net exporters do export a significant amount of rice and may be concerned about the affect of GM rice on their markets. Impacts of GM on rice trade may be that (1) unauthorized technologies that offer a production advantage will spread through the informal sector in most rice-growing countries; (2) high quality markets and/or markets with concerned consumers will require segregated, certified non-GM rice, resulting in additional costs; (3) GM and other technologies will lower the price of rice on the world market; and (4) biotechnologies will be utilized to combine productivity and adaptation with quality traits, affecting the monopoly of certain geographies for certain traits.

The depth of our understanding of the hereditary process has changed, opening an endless array of possibilities for affecting future evolutionary trajectories. How the potential of the human imagination and creative spirit should be nurtured, guided, interpreted and ultimately directed and controlled with respect to biotechnology is a question of profound social, economical and ethical dimensions. It deserves to be discussed, contemplated and digested at all levels of society.

## 1.0 Background and Introduction

The term biotechnology is largely associated with genetic manipulation at the DNA level. However, it is important to note that not all biotechnology involves *genetic engineering*. Biotechnology may refer to specialized forms of fermentation, clonal propagation of plants or animals, embryo splitting or embryo rescue, protein engineering, constructing doubled haploid lines, monitoring recombination throughout the genome or augmenting the efficiency of selection in plant or animal improvement. A large part of what biotechnology represents today is new knowledge about the natural processes of DNA replication, breakage, ligation and repair. This knowledge has paved the way for a much deeper understanding of the mechanics of cell biology and the hereditary process itself.

Beyond the science, a number of important issues are associated with biotechnology, particularly in rice, the world's most important food crop. This paper reviews first the status of the technology in rice, followed by an examination of challenges related to the application of biotechnology to rice including issues related to public perception and awareness, intellectual property, development and commercialization, and the potential impact on trade. Finally, the potential benefits to society are reviewed including benefits to small farmer and the potential for the alleviation of hunger and malnutrition.

## 2.0 Status of the Technology

Rice is recognized as a model system for the study of cereal genomes (Shimamoto and Kyojuka, 2002; Delseny et al., 2001). Its status as a model system arises from several key features, including its small genome size (~430 Mb) (Arumuganathan and Earle, 1991), the availability of whole genome sequence (Yu et al., 2002; Goff et al., 2002; Sasaki et al., 2002; Feng et al, 2002; The Rice Chromosome 10 Sequencing Consortium, 2003; Komari et al., 1998), the large, public germplasm collection (over 84,000 diverse accessions) and the development of several key genomic mapping resources (Chen et al, 2002; Wu et al, 2002; McCouch et al, 2002). In addition, rice is the world's most important food crop -- the primary or secondary staple for more than half the population (Coffman and Juliano 1987).

Rice is the first food crop for which complete genome sequence is available. This offers an unprecedented opportunity to identify and functionally characterize the genes and biochemical pathways that are responsible for agronomic performance, resistance to biotic and abiotic stress and consumer quality. Developing rice as a model system is pivotal in the effort to translate the value of information emerging from basic genome research for use in crop improvement. An important feature of genome science is the understanding that basic information about genes and pathways learned from studying one species can be readily transferred to another species. Thus, the study of rice genomics promises to offer fundamental insights into the genetic architecture and functional significance of genes in many other crop species.

Geneticists today are often trained to extrapolate information about what individual genes do in a model species observed in a controlled environment to a general understanding of how homologous genes are likely to behave in complex crop genomes in a related field environment. While this approach holds promise for simply inherited traits, the ability to understand the genetic basis of quantitatively inherited traits relies on the use of populations evaluated directly in relevant field environments. Two approaches have been successfully employed in this

endeavor, namely quantitative trait locus (QTL) mapping and linkage disequilibrium (LD) mapping. Both of these approaches provide important information that is immediately relevant to plant breeding about how specific combinations of genes and alleles interact in relevant varietal backgrounds (Flint-Garcia et al, 2003; Remington et al., 2001; Paterson, 2002; McCouch et al., 2001; Tanksley, 1993). Plant breeders today are presented with many possibilities for altering the behavior of existing crop varieties. They may choose to use marker-assisted approaches to facilitate the selection of favorable combinations of genes that occur naturally within a species (Rafalski, 2002; Hittalmani et al., 2003; Zhou et al., 2003; Tanksley and McCouch, 1997). They also have opportunities to adjust particular traits or phenotypes via the introduction of alien genes using transgenics (Nuffield Council on Bioethics, 2004; James, 2003; Ye et al, 2000). In either case, it is information about genes and their functions that drives biotechnological applications in plant improvement.

The completion of the whole rice genome sequence provides an unprecedented opportunity to identify and characterize genes that contribute to evolutionarily and commercially significant phenotypic variation in the world's most important food crop species. Moreover, dissecting the nature of genome diversity in rice will permit a comprehensive analysis of the evolutionary forces that shape rice genes and the rice genome and provides a foundation for comparison with other crop species, such as maize, barley, wheat, soybean and tomato.

## **2.1 Molecular Genetic Analysis**

The use of molecular techniques provides a high-resolution view of genetic differences among individual plants that can be used to address many questions relevant to plant systematics and breeding. Both the products and the processes of evolution and of human selection can be examined on the basis of molecular data.

Most of the characters that plant breeders are concerned with are polygenically controlled. Before the advent of molecular markers, characterization of the genetic factors associated with quantitative traits was accomplished with the aid of classic biometrical procedures. Mapped molecular markers provide the geneticist with powerful tools for identifying the component Mendelian loci of these complexly inherited traits. The number and chromosomal locations of the genetic factors involved in the expression of these traits, as well as the relative size of the contribution made by each locus to trait expression (phenotype), can be determined (Alonso-Blanco and Koornneef, 2000; Yano, 2001; Paterson et al 1988). Although verification of linkage with quantitative trait loci is more laborious and time consuming than for single gene characters, the payoffs are potentially greater. Some traits, such as tolerance for a variety of environmental stresses, including drought, salt, and mineral deficiencies or toxicities (Champoux et al, 1995; Nguyen et al., 2002; Kamoshita et al, 2002; Price et al, 2002; Gregorio, 2002; Flowers et al, 2000), rank as important targets for molecular marker-based selection in rice breeding because they are often prohibitively difficult to screen using classical selection techniques.

### **2.1.1 Marker-Aided Selection**

Marker-aided selection in a plant breeding context involves scoring indirectly for the presence, or absence, of a desired plant phenotype or phenotypic component based on the sequences or banding patterns of molecular markers located in or near the genes controlling the phenotype. The banding pattern of the molecular marker at a given locus is indicative of the presence or

absence of a specific gene or chromosomal segment that is known to carry the desired gene or allele.

Marker-aided selection, based on RFLP, SSR or SNP-tagged QTLs, permits rapid identification of individuals that contain complementary parts of a complex character. Such individuals often defy accurate phenotypic identification because of the complex gene interaction that may govern the trait of interest (Yamamoto et al, 2000; Zheng et al., 2000). Following meiosis in a heterozygote, the set of alleles that governs a complex trait is broken up. Desirable alleles, which are normally located on multiple different chromosomes, are dispersed among the segregating progeny, and the effects of some genes may be masked in the presence or absence of others because of epistatic interactions that govern their expression. When molecular markers linked to those genes (QTLs) have been identified, the opportunity to monitor the presence or absence of each QTL in individual plants is useful in determining which individuals should be crossed in future generations in order to produce a recombinant of interest. The level of resolution afforded by using marker-aided selection in a case such as the one described above can reduce population size and generation time because a breeder does not have to wait for an identifiable phenotype to occur in order to be able to identify promising selections.

DNA, or gene markers can increase screening efficiency in breeding programs in a number of other ways. For example, they provide:

- ◆ the ability to screen in the seedling stage for traits that are expressed late in the life of a plant (i.e. grain or fruit quality, male sterility, photoperiod sensitivity),
- ◆ the ability to screen for traits that are extremely difficult, expensive, or time consuming to score phenotypically (i.e. root morphology, resistance to quarantined pests or to specific races or biotypes of diseases or insects, tolerance for certain abiotic stresses such as drought, salt, or mineral deficiencies or toxicities),
- ◆ the ability to distinguish the homozygous versus heterozygous condition of many loci in a single generation without the need for progeny testing (since molecular markers are co-dominant), and
- ◆ the ability to perform simultaneous marker-aided selection for several characters at one time.

In some cases, simultaneous marker-aided selection could offer an opportunity to screen for a character, or characters, that could not be included in the program because of cost or difficulty of traditional screening procedures.

Both pyramiding and multiline construction have been suggested as ways to provide more durable forms of disease and insect resistance in rice (Yoshimura et al., 1992, Yoshimura et al 1995; Hittalmani et al, 1995; Blair and McCouch, 1997; Ndjiondjop et al., 1999; Davierwala et al, 2001; Su et al., 2002; Conaway-Bormans et al., 2003; Lorieux et al., 2003; Hayashi et al, 2004). Construction of such lines via backcrossing is efficient if the genes of interest have been cloned or tagged with molecular markers. The ability to select accurately for rapid return to parental type, and for minimal linkage drag associated with the target gene, or genes, are two important features of marker-aided selection during backcrossing (Tanksley 1993; McCouch et al, 1997).

Marker-based selection is also helpful in attempts to transfer genes from exotic germplasm into cultivated lines. Several workers have used RFLP and SSR markers to monitor introgression of brown planthopper resistance from *O. officinalis* (Kochert et al 1990), bacterial blight resistance from *O. longistaminata* (Ronald et al., 1992) aluminum tolerance or yield and quality related traits from *O. rufipogon* (Nguyen et al, 2002; Thomson et al.,2003; Septiningsih et al., 2003 a & b) or from other wild species such as *O. glumaepatula* (Brondani et al., 2002) or *O. glaberrima* (Jones et al., 1997; Lorieux et al., 2003) into cultivated *O. sativa* backgrounds. Linkage drag between a desired character and one or more highly undesirable characters is a common problem in such wide crosses, and identifying the recombinants with the least amount of donor DNA flanking the genes of interest is enhanced by the use of molecular markers (Takeuchi et al., 2003; Blair et al., 2003; Monna et al., 2002). Thus, whole-genome, marker-based selection offers new opportunities to make efficient use of the wealth of useful genetic variation that exists in wild species of cultivated food crops.

### 2.1.2 Potential Applications

The availability of complete genome sequence of rice has opened the door for many applications of DNA markers in plant breeding. Though the number of agronomically important genetic loci that have been cloned or tagged via linkage to molecular markers is still limited, work toward this end is accelerating rapidly. To take advantage of the potential that complete genome sequence information represents, a great deal of time and effort must be devoted to identifying the genetic loci and specific allelic variants that are responsible for the tremendous array of characters that breeders are concerned about in population or variety improvement programs. Much of this effort involves analysis of breeding lines and specially designed crosses to determine which genes or combinations of genes determine a favorable phenotypic outcome. Further, given the complexity of quantitative traits, many different lines or crosses must be carefully analyzed over different years and environments in order to unravel the important components of gene interaction and to clarify the effect of environment and genetic background on the expression of individual alleles (Li et al, 2003; Hittalmani et al., 2003; Zheng et al, 2000).

To provide rice breeders with a useful repertoire of new tools, the genome sequence must be annotated with information about which genes and alleles are associated with phenotypic characters of agronomic importance and the complex interactions among genes must be enumerated in the context of specific breeding populations or gene pools and the environments to which they are adapted. Furthermore, information resources targeted at the breeding community must be developed so that the overwhelming amount of information about genes, alleles and natural genetic variation can be funneled into a useful tool for breeding applications. This will involve a very different approach to information resources than that currently employed by the large, genome databases that are oriented toward genomics researchers and molecular biologists rather than the breeding community. Nonetheless, a few examples offer beacons of inspiration in this area, including the emerging IRIS database (Bruskiewich et al, 2003; <http://www.icis.cgiar.org/>) the GeneFlow database ([www.geneflow.com](http://www.geneflow.com)), the marker-assisted selection wheat (MASwheat) database ( <http://maswheat.ucdavis.edu/> ) and software such as RealTime QTL ( <http://zamir.sgn.cornell.edu/Qtl/Html/home.htm>).

As the multiple dimensions of genome sequence analysis begin to take shape and new technologies give rise to new types of genetic markers and new possibilities for understanding the genetic basis of complex phenotypes, opportunities for effectively integrating molecular

analysis of genetic variation into existing plant improvement programs become increasingly apparent.

## **2.2 Transgenic Technologies**

It is challenging to locate specific information about the status of transgenic technologies in rice but some insight can be gained from patents and field trials. Transgenic technologies under development in rice (no commercial releases have occurred) can be broken out into four categories: (1) herbicide tolerance (2) biotic stress resistance, (3) abiotic stress resistance and (4) nutritional traits.

### **2.2.1 Patents**

Brooks and Barfot (2003) reviewed the patents filed for rice through 2002 and identified 307 rice biotechnology patents from 404 organizations. DuPont/Pioneer held by far the largest number of patents (68) followed by Monsanto (33), Syngenta (32), and Bayer (19). Specific numbers were not provided for other organizations but the Japanese public sector, along with Japan Tobacco, were mentioned as significant.

### **2.2.2 Herbicide Tolerance**

Herbicide tolerance has been the priority trait for the major companies as evidenced by the number of field trials conducted. Brooks and Barfot (2003) reported that, in the U.S., Monsanto and Aventis (now Bayer) accounted for more than 80 percent of the rice field trials with a concentration on herbicide tolerance. They also report testing in Europe (Italy), South America (Brazil and Argentina), and Japan. While specific documentation is not available, it is reasonable to assume that this technology has been tested in China.

### **2.2.3 Biotic Stress Resistance**

Biotic stress resistance is a high priority for rice as it would mitigate some of the major constraints to production. According to Brooks and Barfot (2003), Chinese sources (Wang and Ma, 2003), and findings of the Cornell University – USAID Agricultural Biotechnology Support Project (ABSP) II (Anonymous, 2003), work is underway by various (mostly public) institutions focused on resistance to bacterial leaf blight (*Xa21*), rice blast, rice hoja blanca virus, rice tungro spherical virus, rice yellow mottle virus, rice ragged stunt virus, the brown planthopper, and yellow stem borer. Among these, only stemborer resistance (*Bt* rice) is reasonably close to commercial development.

### **2.2.4 Abiotic Stress Resistance**

Work in the laboratory of Dr. Ray Wu of Cornell University, as reported by Garg, et al (2003), has resulted in transgenic rice plants that produce trehalose at 3-10 times the normal rate, resulting in tolerance to drought and/or salinity. This trait has not been field tested and is not yet in a genetic background satisfactory for commercial development. Work on submergence tolerance has also been reported but specific information is not available.

### **2.2.5 Nutritional Traits**

Proof of concept has been demonstrated for rice to produce and accumulate pro-Vitamin A (beta-carotene) in the seed endosperm tissue (Beyer, et al, 2002) through genetic engineering. Some of the constructs, genes, promoters and selectable markers used in the initial development of Golden Rice were unsuitable for the commercial development and regulatory clearance and required re-engineering. This has been going on for the last few years and new material is in the pipeline that is said to contain more than 10 times the level of pro-Vitamin A compared to the original material. These lines are also reported to be “clean” events without cross-border transfers or antibiotic markers. If all goes well, this material reportedly will be ready for backcrossing and field testing later in 2004. The accumulation of pro-Vitamin A in Golden Rice under field conditions is still unknown and field trials will need to be performed under different environmental conditions to ascertain that the gene is stable and the expression consistent. Finally, studies are underway or planned, in the Philippines, China and the USA, to test the absorption and bioavailability of pro-vitamin A in rice. Until these tests are completed in 2005, the precise amount of pro-Vitamin A that Golden Rice can supply will not be known. In addition, the acceptance of Golden Rice remains an open question. What is certain, however, is that even a modest amount of the recommended daily allowance of pro-Vitamin A would lift millions of people out of sub-clinical vitamin A deficiency and thus contribute to the alleviation of widespread suffering.

The effectiveness of rice with high iron bioavailability in reducing anemia in women has been demonstrated (Haas et al 2000). Work is underway to enhance rice for bioavailability through transgenes and/or molecular assisted breeding (Bouis et al 2003). Brookes and Barfot (2003) project an 89 percent probability that this technology will be deployed during the 2006 to 2008 timeframe.

### **3.0 Challenges to the Application of Biotechnology on Rice**

While the ability to manipulate the hereditary process is not new, the depth of our understanding of this process has changed and the knowledge we have gained has opened up an endless array of possibilities for affecting future evolutionary trajectories. How the potential of the human imagination and creative spirit should be nurtured, guided, interpreted and ultimately directed and controlled with respect to biotechnology is a question of profound social, economical and ethical dimensions. It and related questions are being discussed, contemplated and digested at all levels of society.

People want to know why we should now start using plant biotechnology in agriculture when traditionally bred crop varieties have provided food for the human population for thousands of years. People also want to know who will benefit from the use of plant biotechnology. What are the risks and who will take responsibility for the problems that are sure to emerge? Will a few big multinational companies use the intellectual property regime to capture all the gains from biotechnology or can some applications be reserved for the public good? If new transgenic rice varieties with the traits talked about above are developed, will farmers adopt them? What might be the effect of international trade considerations? These are reasonable questions that need to be addressed.

### 3.1 Public Opinion

Public opinion surveys have demonstrated that while many people are initially uncomfortable with the prospect of using biotechnology to transfer genes between organisms, those reservations can be overcome if they perceive a particular benefit that they deem ethically or morally persuasive. For example, in a study of 600 residents of New Jersey conducted by Hallman (1996), the use of genetic engineering to produce insect resistant corn was given a 65% approval rating but when the same people were asked how they felt about using genetic engineering to create more nutritious grains to feed hungry people, approval ratings were 85%. An even greater percent (95%) approved of the use of genetic engineering of microbes to produce pharmaceuticals such as insulin or antibiotics, where there was a clear benefit to consumers. But people were much more suspicious about the use of genetic engineering on animals, and most anxious about its application to humans. For example, when the same 600 residents of New Jersey were asked about using biotechnology to improve the beef quality of cows, only 40% approved. A 1997 study by Frewer, Howard and Shepherd reported that many consumers were concerned about the “trivial” use of biotechnology, especially when conventional alternatives already existed and perceived risks to themselves or something they valued appeared to outweigh the advantages. The more a biotech application was judged to be useful for society, the more it was seen as morally acceptable. Hallman (1996) noted that “People want those who employ biotechnology to use its extraordinary power to create products that promise real benefits for consumers, not merely big profits for companies.”

It would appear that much of the public could be convinced about the value of biotechnology if those who develop and introduce biotechnological products demonstrated a sincere commitment to achieving socially relevant objectives and were willing to enter into an honest dialogue with the public. Those who stand to profit from biotechnology need to demonstrate that the advantages of any particular product to themselves or others outweighed the risks associated with it and that a rational system has been put in place to ensure the equitable distribution of both the costs and the benefits of the technology. If the public were convinced that biotechnology was being productively engaged as a tool to alleviate hunger and poverty, help small-scale farmers in developing countries, protect biodiversity, help clean up the environment, enhance ecological stability, and improve food and health quality, many people would be far more receptive to its use than is the case today.

A few large multinational companies have come to dominate the applications of plant biotechnology in agriculture through their aggressive purchasing of companies that produce and sell seeds. In the wealthy countries regulatory systems and the widespread availability of information creates an environment in public interests and those of the companies are balanced. Farmers participated in the process and make informed decisions about the use of transgenic seeds. Opposition to the deployment of transgenic seeds has led the companies to claim they are developing such technologies for the benefit of poor farmers and malnourished people in the developing world while the obstacles to deploying the technologies are formidable.

### 3.2 Intellectual Property Issues

The perception that the biotechnology industry has been greedy in the face of a worsening economic situation for small-scale farmers in both developed and developing countries has worked against gaining public acceptance for the technology. Intellectual property rights on key components of transgenic technology often require complex licensing agreements. This can be a formidable challenge to a public sector institution with little experience in negotiating such agreements. Nonetheless, there are a small but growing number of examples where private corporations have collaborated with national agricultural research institutions in the developing world to extend the technology to crops such as potato, sweet potato, banana, sugarcane and rice (Rivera-Bustamante, 1995; Wambugu, 1999).

Still, there are valid concerns that industry's current expansive approach to number and breadth of patents will ultimately limit the future involvement of the public/non-profit sector in plant improvement and will jeopardize the utilization of our germplasm resources for the welfare of humanity (Barton, 1997; Bragdon and Downes, 1998). Specifically, mechanisms must be sought for reducing the barriers that impede access to agricultural biotechnology for subsistence and minor crops. These crops do not attract the attention of the private sector because they hold no commercial interest, but they face problems that may benefit from applications of biotechnology and are essential to the welfare of millions of people in the developing world.

Several innovative ideas have been proposed to reduce IP barriers that limit access to valuable agricultural technology. One involves the creation of a clearinghouse to advise researchers, administrators, and technology managers about practical IP management strategies that will result in quicker decisions, lower transaction costs, and ultimately, the development and dissemination of plant varieties using biotechnology that address hunger (subsistence crops) or contribute to more vibrant state economies (minor commercial crops). Unification of the public sector may become a significant factor. A group of research university presidents (Atkinson et al, 2003) is attempting to unite public sector institutions to conserve the right to utilize their collective intellectual property for humanitarian purposes. They have expressed their intent to form the Public-Sector Intellectual Property Resource for Agriculture (PIPRA) for the purpose of (1) reviewing public-sector licensing practices, (2) creating a collective, public, IP asset database, (3) pooling specific IP to form shared technology packages and (4) inviting broad participation by other public-sector institutions. These and other innovative partnerships between public or other non-profit institutions working to improve the livelihoods of low income farmers and consumers and private institutions whose investments have helped create valuable new technologies offer some hope for expanding the market potential of small-holder crops and facilitating access to a range of technical solutions for problems faced by small-scale farmers.

Success of a venture like PIPRA is predicated on the following assumptions: (1) intellectual property rights (IPR) are here to stay and globalizing; (2) most key inventions have occurred and will continue to occur in the public sector at research universities; (3) public funding should maximize public benefits and food security is an important public benefit; (4) international agricultural research centers and national agricultural research systems throughout the world need help with access to IPR; (5) the private sector will not serve poor farmers; (6) private companies have IPR that they are willing to donate and pooling IPR creates added value; (7) most university scientists would like to see their work benefit needy people; (8) a portfolio of public IPR supplemented by case-by-case licensing can provide freedom to operate and sharing that will benefit humanity.

A different approach argues that the patent system for genes and varieties has gone too far and needs radical reform -- that continuation of variety development for crops like rice depends to a large extent on the policies that we evolve for the management of intellectual property related to crop improvement. Sears (1998) pointed out that the free exchange and utilization of germplasm has been the foundation for all plant improvement efforts since crops were first cultivated over 10,000 years ago. He draws the analogy to a book (which may be copyrighted) and words (which may not be copyrighted). If words were copyrighted, only the few who owned them could communicate and our society would be harmed. Genes are analogous to words in that they allow the creation of new plant cultivars just as words allow the creation of a book. Everyone in society should have the right to use genes. Cultivars (novel genotypes or combinations of genes), not genes, should be eligible for patenting. It is now clear that the current system of patenting genes restricts the playing field so that a handful of companies will have a major influence on the global food system. While in a broader context, the debate over the patentability of 'discoveries' such as naturally occurring genes is an age old one, key interpretations now being made by the U.S. patent and Trademark Office (Cowley and Makowski, 2003) will determine whether the recent trends are reinforced or curtailed.

### **3.3 Seed Production and Farmer Adoption**

The availability of GM rice varieties will depend on the aggressiveness of public sector actors in pursuing their development and dissemination. It is unlikely that private companies will take the lead in developing GM rice varieties. Farmers save their own rice seed so opportunities for sales are limited. A truly superior GM trait could be incorporated in a hybrid that would provide a private company the incentive to jump in, but the public sector seed system will need to carry the ball for non-hybrids.

Experience shows that Asian farmers adopt new rice varieties when there is an advantage to them. When transgenic varieties are ready for release, the pace of their adoption will depend on the advantages conferred by the trait in combination with all others. The bigger the advantage to farmers, the faster and more complete the adoption, other things being equal. A recent study of Bangladesh rice farmers found a steady rate of adoption of new rice varieties since 1970 (Hossain 2002). By 2000, 80 percent of dry season rice and 50 percent of wet season was planted to new, modern varieties. Dry season yields of modern varieties were three times those of wet, while value of output per hectare was 2.6 times as great. The farmers invested an average of \$393 per hectare to produce modern varieties and \$172 per hectare to produce traditional in the dry season but the higher costs of production were more than offset by the greater value of output and, on average, farmers were left with \$308 per hectare return over costs for modern varieties and \$38 per hectare for traditional varieties. Differences between the two types of varieties were smaller in the wet season -- modern varieties returned \$290 per hectare over costs and traditional \$154. Because the difference was much smaller in the wet season, farmers used the new varieties on only 50 percent of their land.

A variety carrying a trait that confers a nutritional advantage to consumers is unlikely to be adopted by farmers unless it also provides advantages to the farmers -- a higher yield or higher price than varieties without the trait. The persistence of some "old" varieties for decades after their release and first adoption testify to this. Between 1967 and 2000 over 600 new varieties of rice were released in India although by 2000 only 309 were still being grown by farmers (Janaiah and Hossain 2002). In that year nearly one-third of India's rice area was occupied by the seven

most popular varieties. About 15 percent of the area was planted to varieties released before 1980, one-quarter was planted to varieties released in 1981-85 and about 28 percent was planted to varieties released since 1991. Farmers continued to plant traditional varieties (TVs) on 19 percent of the area.

### **3.4 International Trade**

Most rice is produced and consumed in the same country and, for most countries, domestic considerations are more important than trade. However, some countries that are not net exporters do export a significant amount of rice and may be concerned about the affect of GM rice on their markets. These might include (based on metric tons exported in 2001) Thailand (7.5M), Vietnam (3.6M), the USA (2.6M), Pakistan (2.4M), China (1.9M), India (1.6M), Uruguay (0.8M), Egypt (0.7M), Myanmar (0.7M) and Australia (0.6M).

Significant importing countries (metric tons) during the same year were Nigeria (1.6M), Indonesia (1.3M), Philippines (1.2M), Iraq (1.0M), Saudia Arabia (0.9M), Senegal (0.9M), Ivory Coast (0.7M), Japan (0.7M) and Malaysia (0.6M). On a regional basis, Asia (6.6M), Africa (6.4M), the Middle East (4.0M), Latin America (1.9M), North America (1.1M) and Europe (0.6M) are the significant importers.

Europe and the Middle East import significant amounts of high quality rice. Given the strength of anti-GM feeling in Europe and the potential for that to spill over to other countries it seems unlikely that European and wealthy Middle Eastern countries would import rice from countries that grow GM crops even if the WTO eliminates outright bans on GM food. Countries exporting rice to those anti-GM markets are unlikely to approve GM rice for production. On the other hand, governments cannot really control the informal movement of seed, including GM. Satisfying high quality markets such as the Middle East and Europe will be the challenge of growers who derive a premium from that market. Growers aiming at markets with consumers indifferent to GM will certainly utilize GM if a production advantage exists.

In the near to medium term, impacts of GM on rice trade may be as follows:

- ◆ Unauthorized technologies that offer a production advantage will spread through the informal sector in most, if not all, rice-growing countries, including exporting countries;
- ◆ High quality markets and/or markets with concerned consumers will require segregated, certified non-GM rice, resulting in additional costs that will need to be borne by the buyers, sellers and marketers of that rice;
- ◆ GM and other technologies will lower the price of rice on the world market;
- ◆ Eventually, biotechnologies will be utilized to combine productivity and adaptation with quality traits, reducing the premium for quality traits and affecting the monopoly of certain geographies for certain traits.

## **4.0 Potential Benefits of Rice Biotechnology for Society**

In addition to the limitations discussed above, one must recognize other obstacles to the transfer of modern biotechnologies to resource poor farmers. Included are: covering regulatory costs, partitioning markets with both commercial and small farmer applications, developing transformation protocols for non commercial crops like cassava, provision of training, establishing and monitoring oversight, such as may be needed for delaying resistance development when using *Bt*, and managing the tradeoff between costs and the maintenance of genetic diversity when multiple local varieties are being grown. This last issue is particularly relevant to producers with the poorest and most heterogeneous soil/water resources, and it is they who can be expected to suffer the most if denied access to cost reducing technologies while crop prices fall as producers elsewhere in more favorable circumstances adopt those same technologies. However, we believe that overcoming the challenges will produce benefits for resource-poor farmers that make it worthwhile.

### **4.1 Benefits for Small Scale Farmers**

The use of biotechnology has tremendous potential to provide genetic resistance to pests, diseases and tolerance to numerous soil and environmental stresses that constrain the production of many crops in both the tropical and temperate zones. Pests and diseases are especially problematic in the tropics, where most rice is cultivated, because of climatic conditions that favor their year-round growth and reproduction. Small-scale farmers, representing many diverse cropping systems and growing environments, are typically least able to afford the means of combating both biotic and abiotic stresses because of the high cost of purchasing pesticide, fertilizer or other soil amendments and access to irrigation water. The first generation of transgenic varieties has been developed primarily for field crops grown on large acreage under temperate cropping conditions. This focus illustrates the power of large markets to attract the interest of agri-business. However, opportunities to develop genetically engineered varieties to address the constraints faced by small-scale rice farmers in the tropics is an option.

### **4.2 Alleviation of Hunger and Malnutrition**

While many people today enjoy a diet that is more abundant and more varied than ever before in human history, this is in stark contrast to the reality of millions of others who confront profound food insecurity on a daily basis. Because food availability on a global scale is largely determined by purchasing power rather than proximity to, or direct involvement in, the food production process, the concerns of the world's poor who have little voice in the marketplace are much less likely to be heard than are the concerns of people whose decisions are registered by how they spend their money. While some segments of the population are vociferously opposing the use of biotechnology in agriculture and aim to restrict or completely suppress the use of genetically engineered crop varieties, the potential of biotechnology may represent an opportunity to respond to urgent issues of hunger and malnutrition for people who are hungry. The development of rice that has been genetically engineered to minimize the impact of anti-nutrients and enhance the uptake of iron and other essential minerals, or to produce provitamin A (B-carotene) in the endosperm (Ye et al, 2000) are examples of products that have the potential to directly improve the quality of life for millions of human beings who suffer from iron and vitamin A deficiency. People who suffer from malnutrition generally lack essential levels of micronutrients because they lack the purchasing power to obtain sufficient diversity in their diet.

The impact of delivering those essential micronutrients through enriched “Golden Rice” is parallel to fortifying milk with vitamin D, salt with iodine, or orange juice with calcium in industrialized countries. It is not seen as an alternative to maintaining a healthy diet, but this transgenic rice does offer immediate assistance to people in need and as a staple food, it has a built-in delivery system that is one of the best ways of getting the nutrients to those who need them most. Is it ethical to refrain from using biotechnology to improve the nutritional status of hungry people, while those with purchasing power condone the use of the same technology to extend their life expectancy by producing pharmaceuticals?

### **4.3 Beneficial Transgenic Traits**

Major companies presumably are “sitting” on herbicide tolerance in rice pending arrangements that would allow them a favorable return on investments. Brooks and Barfoot (2003) project an 80 percent probability of release of varieties with this trait during the 2003-2005 time frame. They project a similar probability for the release of Bt rice (resistance to stemborers) and bacterial blight resistant rice. Bt rice will probably be released first in China where it has been widely tested in large-scale field trials (Wang and Ma, 2003).

In terms of impact, herbicide tolerance probably will be an enormous benefit for farmers but a detriment to workers hired to weed rice fields. Labor displacement may be significant where hired weeding still prevails but herbicide resistance will allow farmers to do a better job of controlling weeds in situations where they are unable to hire the necessary labor. The impact of Bt rice is uncertain due to the compensating capacity of the rice plant in the face of stemborer damage. The impact of Xa21 is not expected to be significant as Xa-21 is a native rice gene and this technology is already available in conventionally bred varieties.

### **4.4 Biosafety and The Environment**

For any transgenic variety to be released commercially, the biosafety regulations in place in each country must be followed. Being specific to individual countries, regulations vary, but include laboratory and field tests designed to reveal any possible danger to human health or the environment. Despite the lack of any demonstrated effect of genetically engineered crops on human health, the possibility of some unanticipated effects cannot be ignored. Authorities in countries that have not yet adopted biosafety regulations therefore have generally taken the precautionary stance that no genetically engineered crops should be grown until biosafety regulations are in place.

The use of pest resistant rice varieties can help decrease the dependence on pesticides. Whether resistant varieties are obtained through traditional crossing and selection or via genetic engineering, the resistance itself derives from the presence of specific genes whose expression renders the plant capable of discouraging or protecting itself from pest attack. Both transgenic and non-transgenic resistant varieties are important tools in a pest management strategy and, if used responsibly, represent an ecologically sound and economically viable way to reduce the use of externally applied pesticides. While minimizing the use of pesticides represents a critical step toward restoring environmental integrity and improving human health, the long term management of resistance requires careful consideration.

In the context of ecological stability and environmental impact, the use of transgenic resistant varieties should be evaluated from many angles. The possibility that transgenes will be

transmitted to wild relatives growing in the vicinity of crop plants should be investigated on a case by case basis. It is reasonable to ask whether a specific transgene(s) would affect the fitness of a wild species population if it were transmitted. Where a gene is expressed at some physiological cost to the plant, it will be eliminated from a wild population by natural selection unless it confers a real advantage in the wild. For example, a transgene that protects a crop variety from insect or disease attack may be of little consequence when transmitted to wild relatives if the fitness of the wild population is not affected by the specific pest or disease. Further, it should be acknowledged that successful transmission of genes through pollen requires the presence of a sexually receptive partner. Many crop plants are grown far from their center of diversity in areas where sexually compatible wild relatives are not part of the natural ecosystem. Thus, in cases such as soybeans in Europe, North and South America, or maize in the northern US, Europe or Asia, concerns about geneflow to wild relatives are not always relevant. In cases where crops are grown in a relevant center of diversity and where transmission of a transgene is likely to be ecologically disruptive, strategies for genetically engineering the chloroplast genome (which would preclude pollen transmission) may provide a way of managing the risk of gene flow. Genetic forms of resistance are a critical component of any reliable pest management plan and if transgenic resistant varieties can be used responsibly, this application of biotechnology should not be ignored as a way of helping to minimize the use of synthetic pesticides and clean up the environment.

#### **4.5 Protection of Genetic Diversity**

One of the specters of modern agriculture is that it represents a vast movement toward uniformity. This has profound ecological and dietary implications for all people. An important feature of industrial agriculture was to alter the environment in an effort to optimize conditions for crop production. In the process, the diversity inherent in our agricultural production systems followed a declining curve as fewer and fewer species were planted over larger and larger areas and variety development and seed production were increasingly consolidated in a few, large multinational corporations. Wild flora and fauna have been increasingly threatened as human populations continue to expand and industrial agricultural systems are pushed to the limit in an effort to maximize global food production. Some people argue that the high productivity of industrial agriculture and the application of new techniques aimed at making it more efficient, including biotechnology, serve to protect wild lands that would have been converted to farmland had the system been less productive (Swaminathan, 2000). Yet, throughout the world, people are questioning the methods, technologies and philosophies underlying the current food production system upon which all humans have come to depend. In the midst of these discussions, it is often assumed that the use of biotechnology in food production will inevitably lead to further ecological disruption and economic disparity without benefiting consumers.

This perspective should be challenged. There are many forms of biotechnology and many ways in which it could be used to augment productivity while benefiting consumers and the environment. In rice, it has been demonstrated that wild relatives of crop species can harbor favorable genes that are not expressed in the phenotype of the parent (Tanksley and McCouch, 1997; Lorieux et al., 2000; Moncada et al., 2001; Brondani et al., 2002; Septiningsih et al 2003 a & b; Thomson et al., 2003; Xiao et al, 1998) For example, genes that enhance the yield characteristics of cultivated rice can be introgressed from low-yielding wild relatives using traditional crossing and selection coupled with the use of molecular maps and markers. This use of biotechnology allows the simultaneous identification of regions of the genome containing

unexpectedly favorable alleles and the more efficient generation of improved varieties. While this is accomplished without the use of genetic engineering, identifying the genes underlying the traits of interest provides information about the DNA sequence of those genes, which in turn can be used as the basis for identifying novel variation in additional wild and exotic germplasm. This use of *knowledge derived from* genomics and biotechnology provides a strong case for preserving wild species because of the direct and far-reaching value the germplasm may bring to future plant improvement efforts. Nature offers an invaluable window on the combinatorial problem of what works in the “real world” and modern biotechnology offers tools to understand, mechanistically, how and why things work.

The array of biological solutions observed in nature brings renewed interest in preserving natural forms of biodiversity. From an economic perspective, the tools of biotechnology make it possible to identify distantly related organisms that share evolutionarily conserved genes or biochemical pathways and use the information to generate new solutions to old problems. In agriculture, this includes the quest for new solutions to problems of enhancing yield, nutrient use efficiency, weed competition, pest resistance, etc. Whether through cross-breeding, tissue culture-assisted propagation or through genetic engineering, agriculturalists currently use biotechnology to incrementally adjust the essential species backbone provided by nature, tailoring new varieties from the original landraces provided by traditional farmers. Good ideas abound but well-planned and well-executed field tests are still required to assess the value of novel phenotypes for addressing global agricultural problems. By increasing the appreciation of the value of genetic diversity *per se* and the value of the knowledge that can be derived from studying it in the context of agriculture, biotechnology argues strongly in favor of continued efforts to protect and conserve wild and domesticated forms of biodiversity.

## 5.0 Conclusion

To achieve a more productive and sustainable rice production system and a more equitable distribution of the benefits in the years ahead, we must nurture both our innate creativity and our deepest sense of ethical and moral connections to each other and to the earth. We must ensure that we are all as well-informed as possible in the technical, social, economic and ethical realms so that our considerations of the future are not limited by the perspectives and accomplishments of today. We must incorporate an understanding of how we grow and develop as a species so that we evolve a visionary concept of where we want to go. In doing so, it is imperative that people seek to maintain an awareness of and respect for the diversity of human situations and the diversity of possible solutions to the problems we face collectively. Clearly, not all people have the same choices nor will they express the same preferences even if given the same choices. Careful consideration and creative exploration of different options for rice production and distribution systems and of the risks and benefits that different systems present to different groups of people are essential as we face the challenges ahead.

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