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[Rice is Life series: 1](#)

Public/Private Partnerships Too Close for Comfort?

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Is the relationship between public and private getting too cosy for comfort in the rice genome sequencing efforts? [Dr. Mae-Wan Ho](#) asks.

Two groups have simultaneously published rough drafts of the rice genome: Yang Huanming and colleagues at the Beijing Genomics Institute (BGI) on the *indica* subspecies, the most widely cultivated in China and most of the rest of Asia, and Stephen Goff's team of the Switzerland-based biotech giant Syngenta on the *japonica* subspecies, grown in Japan and other countries with temperate climates. Just as the publication of the human genome sequence last year was hailed as the "beginning of a new era of biology". The rice genome is expected to transform agricultural sciences similarly.

The publication was marked by controversy over the conditions *Science* is publishing the draft from Syngenta without requiring full disclosure of the sequence (see "Has *Science* compromised science?" this series), as in the case of the human genome sequence. Despite that, there has been much more co-operation between the public and the private groups. The new cosy relationship may suit the scientists involved, but it is not clear how it will affect the rest of society so long as the threat of corporate ownership through gene patenting remains (see CGIAR – science for the poor or procurer for the rich?) The role of the BGI is crucial. China has come up from behind to get its own rough draft of the rice genome (see "Breaching the knowledge monopoly", this issue) and promptly deposited the data on the public database, in line with Yang's insistence that knowledge must be made accessible to all. But Syngenta is already trying to engineer a merger of all the public and private groups on grounds that it would accelerate the completion.

The International Rice Genome Sequencing Project (IRGSP), a consortium of publicly funded laboratories somewhat similar to the Human Genome Project, led by Japan, have been working on *japonica* for nearly 5 years. The projected completion date was 2008. Two years ago, however, the US-based Monsanto announced it had completed a rough draft of the *japonica* genome in conjunction with the University of Washington, Seattle. The company promised to share the data with individual researchers of the IRGSP.

The approach to sequencing taken by both the IRGSP and Monsanto has been rather conventional. This involved mapping the genome first, then sequencing clones located to different chromosomes and piecing them together into contiguous sequences (contigs). Both BGI and Syngenta have opted for the newer whole-genome shotgun approach that enabled them, especially BGI, to complete the rough drafts at "lightning speed". BGI announced its plan to sequence the *indica* subspecies in May 2000, and had the rough draft by October 2001! In the shot-gun approach, the entire genome is broken up into pieces and sequenced. Then through the brute strength of powerful supercomputers and a software program, the sequences are assembled into contigs through ends that overlap. Of course, the fact that a large number of sequences are already mapped and deposited in the public database GenBank means that the task is made much easier.

This shot-gun approach was taken by maverick Craig Venter in

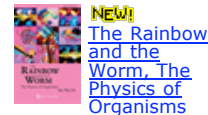
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sequencing the human genome, enabling his private company Celera to beat the public consortium, much to the latter's consternation, and to this day, Venter has been condemned and criticised.

The IRGSP is now worried that funding may dry up before the numerous gaps are filled and errors corrected, which they estimate would take another three years.

Why this interest in the rice genome? Was it because of its importance to the Third World? Actually, it was precisely of its importance to the third world that there has been so little interest in it. Researchers in China and Japan, independently, have begun studying the rice genome almost 20 years ago when no commercial company and few European and American laboratories had any interest. That changed in the early 1990s, when it dawned on researchers that rice is "the Rosetta stone" of cereals, says Chris Somerville, molecular biologist from Stanford University. Rice has the smallest genome size of common cereals, and tend to have the same genes in the same order. So, knowing the rice genome sequence can enable researchers to decipher the much bigger genomes of cereals that are important for rich countries.

Somerville claims no one makes money on rice seeds, and companies are interested because of the potential payoff in the markets for maize, barley, sorghum and wheat seeds. He is wrong. The US is growing and exporting rice, and companies like Monsanto are aggressively targeting the Third World markets for all cereals.

The idea of an international consortium to sequence rice arose from informal discussions in early 1997. That September, Rockefeller foundation supported a small strategy meeting at which a group of molecular biologists decided on sequencing *japonica* because Japan had already started on it since 1991. Five months later, the first IRGSP meeting was held in Tsukuba, Japan. Representatives from Japan, US, UK, South Korea and China drew up guidelines and divided up the 12 chromosomes in the rice genome for sequencing.

Start-up funds were provided to the US lab by Rockefeller Foundation and Syngenta, and the laboratory only won government support in 1999. But no government funding was forthcoming for any other group except for Japan. France, Taiwan and Brazil joined in later to help out.

The first blow to the IRGSP came in April 2000, when Monsanto announced it had sequenced the *japonica* genome in conjunction with the University of Washington and the Institute for Systems Biology in Seattle. Although very incomplete, the sequence was very informative, and Monsanto promised to share the sequence information with academic researchers and with the IRGSP, which it did. This boosted the efforts of the IRGSP, but not enough.

By January 2001, Syngenta reported it, too, had sequenced *japonica*. It had contracted Myriad Genetics in Salt Lake City, Utah, to sequence rice and other cereals for \$30 million.

The real surprise was the BGI, which, from start to finish, took just 18 months to do the job. Yang says that with most of the other efforts focused on *japonica*, "there was a feeling that China should sequence its own rice."

Whereas the Beijing group has made all its data public, depositing them in GenBank, Syngenta is making its sequence available on a rather restricted basis only through its own website and on a CD-ROM. In the meantime, the company's researchers are collaborating with interested researchers, about 65 labs in 11 countries have made use of the information. This compares poorly with the 350 researchers who have used the BGI data since it was deposited in GenBank.

The IRGSP is now under pressure to finish its work, and has said it will produce its own draft by December 2002. It has already placed the data for over 230Mb in the public database, and three chromosomes are nearly finished.

The major worry is how it will affect the poor, for whom rice is

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literally life itself?

What's the rice genome like?

- The *indica* genome has 466 million basepairs (Mb), only 430 of which are in the active functional (euchromatic) regions.
- It is estimated to contain 46 022 to 55 615 genes according to the BGI for the *indica* genome and 32 000 to 50 000 genes according to Syngenta for *japonica*, many more than the 30 000 to 40 000 genes in the human genome
- Repetitive DNA accounts for 42 to 45% of the rice genome. The most abundant repeats are miniature inverted-repeat transposable elements (MITES), there are 98 000 or more copies, which constitutes about 4% of the rice genome.
- Retrotransposons (jumping genes that use reverse transcription) are the most numerous large repeats, they account for more than 15% of the rice genome.
- More than 80% of the genes of *Arabidopsis thaliana* - the smallest dicotyledon plant and the first plant to have its genome sequenced - have counterparts in the rice genome. (Rice is a monocot, the other major division of flowering plants that include all grasses.)
- Genes homologous to 98% of the known maize and wheat genes have been identified in the rice genome.
- Only 49.4% of predicted rice genes had a homologue in *A. thaliana*, in other words, over half of the rice genes are previously unknown.
- Unlike human genes where alternative splicing produce many proteins from the same genes, rice gets its protein diversity simply by having more genes than human.

[Joe Cummins](#)

1. "Rice: boiled down to bare essentials" by Dennis Normile and Elizabeth Pennisi, *Science* 2002, 296, 32-6.
2. "Rice genome sequencers cook up merger" Declan Butler, *Nature* 2002, 416, 573.
3. Yu J, et al. A draft sequence of the rice genome (*Oryza sativa* L. ssp. *indica*). *Science* 2002, 296, 79-92.
4. Goff SA. Et al. A draft sequence of the rice genome (*Oryza sativa* L. ssp. *japonica*). *Science* 2002, 296, 92-100.



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[Rice is Life series: 2](#)

Breaching the Knowledge Monopoly

China Trumps the West in Sequencing Rice Genome

The Beijing Genomics Institute of China has taken the scientific world by surprise. It came up from behind to beat the West at its own game, finishing a draft of the rice genome in just 18 months, and has the potential to change the power politics of agriculture forever. [Dr. Mae-Wan Ho](#) reports on the remarkable scientist who heads the Institute, and his vision of equal and free access of genetic information for all.

Of the two papers in *Science* that announce the draft sequence of the rice genome, one is from Beijing Genomics Institute (BGI), the other from the biotech giant Syngenta.

Media attention has focussed on Syngenta, but the Chinese effort is the real landmark. If Yang Huanming, Director of the Beijing Genomics Institute, has any say in the matter, it could spell the beginning of the end for the knowledge monopoly held by the west and its transnational corporations.

China is the almost the only developing country in the genomics race, and the only one to make its mark. It has all the usual disadvantages, lack of finance, of supporting technologies and scientists. Whereas the United States and Japan have about 70 researchers and engineers per 10,000 population, China has only six. Despite that, she has come out well ahead of the west. And instead of hording the data on its own website like Syngenta, the BGI has deposited the rice genome data promptly into the public database GenBank that can be accessed by all. As the two versions of the rice genome are almost identical, there is no need for Syngenta's data, except for the groups that are sequencing the rice genome itself. China has breached the knowledge monopoly in a big way. And it is surprising that none of this was even hinted at in the seven commentaries that accompany the scientific papers in *Science*.

How did China manage this mission impossible? It is definitely thanks to Yang and his team, featured in a special profile in *Science*. University of Washington geneticist Maynard Olson, who helped train many BGI scientists, recalled how Yang led a sceptical collection of scientists from around to world to see a completely empty, two-storey brick building in the northern reaches of Beijing, which was the then Beijing Genomics Institute. Yang said that the sequencing machines and employees were "on the way", but neglected to mention that he had money for neither.

Today, the Beijing Genomics Institute, relocated to a much bigger building with a floor area of 10 000 square meters, has a staff of 500 that "grows by a dozen or so every month". It also has more than 80 latest model automated sequencing machines, and four of the fastest computer in China. "It's pretty startling", Olson remarks, "When you think of being a support center for a scientific program in a developing country, you don't expect them to become 10 times bigger than you are, in less than 4 years, and to start publishing in *Science*." His colleague, Mary-Claire King remarks, "the Beijing Genomics Institute would be a miracle, except that the BGI guys make genomics miracles routine."

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Yang's ability to translate his vision into reality is put down to his ability to tap "the increasingly diversified sources of support in a reform-minded China."

But the most important factor for Yang's success may be his ability to inspire young colleagues with his idealist vision of knowledge for the benefit of all, which provides a far stronger motivation than money could ever buy. This should be a lesson for policy-makers who place far too much emphasis on wealth-creation and the importance of the private sector for science.

Yang earned his Ph.D. in genetics at the University of Copenhagen, Denmark, then spent six years mapping genes on the X-chromosome in the CNRS Immunology Centre in Marseilles, France, in Harvard Medical School in Boston, and then University of California, Los Angeles. He returned to China in 1994 with the idea to start sequencing genes at high efficiency and low cost.

His first target was the international human genome sequencing effort, already well underway, and his intended vehicle, the Human Genome Centre, part of the Chinese Academy of Sciences (CAS) Institute of Genetics. But, like maverick Craig Venter in the United States, he broke from the Academy, because its "rules and traditions" would slow them down. And the original centre – the brick building shown to the visiting foreign scientists – never got off the ground.

Instead, Yang and three colleagues who had worked with Olson, took advantage of new laws, and in spring 1999, set up the BGI as a private, nonprofit research organisation. Seed money came from the CAS, the Institute of Genetics, Yang's hometown municipal government, and even loans from employees, family, and friends. CAS also designated BGI as its Genomics and Bioinformatics Institute, although less than 10 members of BGI are employed by CAS.

BGI bought their first batch of sequencing machines on an installment plan and trained its staff on sequencing a heat-loving bacterium, *Thermoanaerobacter tengcongensis*, isolated from a hot spring in Tengcong, China. In September that year, Yang made his bid to sequence the human genome. There was only one hurdle. "Do you have the money?" "I lied" Yang admits, "We didn't have the money, but I was sure we would get it."

And he did get the money four months later. CAS agreed to fund three Chinese sequencing centres to do 1% of the human genome, and BGI received slightly more than half the total award. China completed its share of the draft on time, despite being the last to enter into the public consortium (see below), and has recently closed the gaps and corrected errors in the draft sequence.

This success helped Yang to convince the Hangzhou municipal official to provide a rent-free building and enough money to set up a sister centre, the Hanzhou Genomics Institute.

The youthful enthusiasm at the two institutes is impressive. The average age of the 100 authors on the *Science* paper is in the mid-20s. Wang Jun, who leads 150 programmers and computer scientists, entered Beijing University at 16, and is now 26. Heading the 100-person sample preparation and sequencing group is 29 year-old 'police woman' Deng Yajun, a former forensic investigator for the police department in her hometown of Xi'An.

BGI was able to save a lot of money by using home-grown technologies. For example, the 96-well plastic plate used in preparing DNA samples were imported at first at a cost of \$2.54 each. But a local glassmaker provided it for just 36 cents. Similarly, the institute was barred from acquiring US supercomputers, so they relied on Dawning, a home-grown supercomputer company. Particularly crucial was the assembler, a piece of software to piece together the sequence of fragments. That, BGI developed in-house, starting from the assembly program used in the public Human Genome Project.

So, from start to finish, the BGI took an incredibly brief 18 months, using the latest, whole-genome shot-gun approach (see "[Pubic/private partnership too close for comfort?](#)", this series).

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And watch this space for further developments.

I first met Yang at a conference organised by the World Health Organisation in Bangkok, Thailand in July 2001. That was when I became aware that China was a party to the international public consortium to sequence the human genome, and I had no doubt, even then, as to who was responsible for bringing China into the project. Yang has the youthful energy and infectious enthusiasm of a person much younger than his 50 years, and is immensely charming and likeable.

Yang gave by far the most challenging and entertaining talk in the conference, which was to explore Genomics and Health, especially for the Third World.

Yang was motivated by his concern that there should be "equal and free access to the basic information of the human genome" and that "ownership and benefit-sharing of genetic resources" should be secured for developing countries. The only way to achieve those objectives, he decided, was to establish genomics research capacity in a developing country - China.

He takes social responsibility of geneticists very seriously, and firmly believes that scientific advance should bring health care for all. China, he said, has strong desires to have innovative research and new technology, and is very sensitive to sharing the achievements from the Human Genome Project for improving health. Like Gro Harlem Brundtland, Director General of WHO, he finds it "ethically unacceptable" that "most biotechnology research is carried out in the industrialized world, and is primarily market-driven".

"The human genome is in danger", Yang said, of being "confiscated" by a few countries or companies". That was why China became the latest contributor to the Human Genome Project. Despite being the latest to join, China was among the top 10 contributors when the working draft was announced in the journal *Nature* on 15 February, 2001. China finished the complete sequence map of the region of the human genome she has claimed in record time. That too, was a miracle.

"Immediately after joining the Human Genome Project Consortium in September 1999, China began to persistently call for the international effort to protect the human genome, as the unique member state from the developing world in the Consortium." Yang recalled. He submitted five proposals to UNESCO, the first of which was to draft a statement "for the protection of the human genome sequences, **to ensure the equal and free access to the genome sequence data by all**". This was the prelude to the statement released by Clinton and Blair in March 2000, followed by other statements that culminated in the United Nations Millennium Declaration (19 September 2000):

"To ensure free access to information on the human genome sequence."

But that did not mean the human gene sequences could not be patented, as Clinton and Blair were quick to 'clarify' immediately after making their joint statement. Gene patents are overwhelmingly from the US, Western Europe and Japan. Yang roundly condemned the biopiracy of genetic resources up to and including the genes of people in developing countries.

To China's horror, newspapers in the United States revealed that hundreds and thousands of human genetic samples have been taken and exported, without informed consent, and under the pretext of providing "free check-up" and "free treatment". China has become the main provider of human tissues for several US companies, and several traditional medicinal herbs have also been patented in the north.

Craig Venter of Celera said, "With a significant portion of the world's plant, animal and human genetic diversity located in China, access to this diversity will be fundamental in Celera expanding its genomic information."

In Yang's view, no nation can afford not to have biotechnology. "It would be more expensive", he said, "you would be charged unreasonably high prices because you cannot do it yourself!"

Indeed, two Chinese laboratories struck a deal with a foreign-owned company in the spring of 2000 in which the labs agreed to pay US \$225 000 to sequence a prawn virus, and also ceded one-third of the intellectual property rights on the 300kb sequence. Yang is adamant that genetic material in China and in every other country must be shared, and the only way to assure that is "to develop our own research capacity!"

I remain very doubtful over the potential of human genomics research to contribute to health (see [Inside human genomics and genetics](#) series, *Science in Society* 13/14, February 2002 www.i-sis.org.uk). But rice genomics is something else (see "Significance of the rice genome", this series).

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1. Normile D. From standing start to sequencing superpower. *Science* 2002, 296, 36-9.
2. Yang HM. Genomics & health – a regional or national perspective, WHO Multi-regional consultative Meeting, Bangkok, 23-25 July, 2001.



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Significance of the Rice Genome

The rice genome is in many respects much more significant than the human genome, because the potential to use (and hence abuse) it is much greater. [Dr. Mae-Wan Ho](#) and [Prof. Joe Cummins](#) report.

For crop improvement and basic science

It offers real opportunities for scientific studies and selective breeding of monoculture crops, neither of which is feasible, nor morally acceptable in human beings (see "[Inside human genomics & genetics](#)" series, *Science in Society* 13/14, February 2002). Whether it can contribute to improving local varieties is much less clear.

The rice genome is the smallest of all cultivated cereals, 466 million bases (Mb), compared to the 3 billion Mb in the maize genome, 4.9 billion in barley genome and 16 billion in wheat genome. Evolution is very conservative among the cereals. They tend to have the same genes in the same order - a condition called synteny. Therefore, knowing the rice genome sequence can enable researchers to decipher the much bigger genomes of other cultivated cereals.

Whole genome comparisons, or expressed sequence comparisons can be done using gene chips that could allow identification of genetic markers for important traits such as yield, drought resistance, or flowering time in relation to day length, thereby speeding up conventional breeding of desirable varieties. In fact, many scientists and biotech companies have suggested that such marker-assisted breeding may render it unnecessary to make transgenic crops.

The rice genome data is also invaluable for basic research, such as working out evolutionary relationships of living species and studying plant development.

There is a distinct danger, however, that the scientific elite may take research in directions that are of no benefit for the farmers and worse, displace indigenous varieties with more monocultures and transgenic crops controlled by corporations. It is all the more important for scientists and farmers to work in partnership towards making agriculture more sustainable and to resist corporate takeover.

Social and political

Rice has been domesticated by human beings for 5000 years. It is grown in 100 countries, but nine-tenths of the world's crop is produced in Asia, providing four-fifths of the calories consumed in South-East Asia, which have some of the world's poorest countries.

When biotech giant Syngenta announced the rice genome sequence in January 2001, it triggered alarm from Action Aid, the hunger charity. There were already hundreds of patents on rice, and it is feared that the diet of the world's poorest will become the preserve of big business.

Indeed, if the present intellectual property rights regime were to continue, poor farmers may be prevented from using their own varieties, let alone generating new varieties or saving and exchanging rice seeds.

The publicly funded International Rice Research Institute (IRRI), one of the 16 research centres belonging to the Consultative Group on International Agricultural Research (CGIAR) has been subject to fierce criticism from the poor farmers whom it is supposed to serve, as has the CGIAR itself (see "[Science for the poor or procurer for the rich?](#)", this series). In a commentary congratulating "BGI and Syngenta on their milestone contribution

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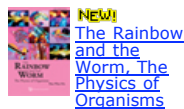
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science and human kind", IRRI advocates " broad collaborations" between "the public and private sectors", and is completely silent on the intellectual property rights issue.

More worrying is the message from another commentary co-authored by a scientist from IRRI, the intention to "tap" into the "over 100, 000 accessions of traditional rice varieties and wild species...collected from a broad range of geo-climates" and held in trust in the IRRI Genebank. IRRI runs the risk of officiating largescale biopiracy of indigenous rice varieties from around the world, and delivering the poorest to corporate serfdom, lock, stock and barrel, unless patenting of research using its collection is banned.

Ismail Serageldin, chair of the CGIAR, bombards us with statistics on the present woes of the world that science must address, including poverty and inequality. He went as far as to call for different kinds of science and technology, though all that amounts to is, "We need more examples like Quality Protein Maize (QPM) and vitamin-A-rice (Golden Rice)".

Serageldin notes the special challenge of dealing with the emergence of private sector-driven science, "which increasingly poses the problem of how to protect intellectual property rights without impeding free access to research tools and the equitable sharing of benefits with the poor who cannot afford to pay". Although the CGIAR has called for a moratorium on patenting research results and material held in its centres, it has failed to ban it. **Now is the time to take decisive action.**

Sources:

1. Cantrell RP and Reeves TG. The cereal of the world's poor takes center stage. *Science* 2002, 296, 53.
2. Serageldin I. World poverty and hunger - the challenge for science. *Science* 2002, 296, 54-



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The Consultative Group on International Agricultural Research (CGIAR) is the world's largest and most influential agricultural research network that is supposed to help the poor. Dr. Mae-Wan Ho questions its role in safeguarding genetic resources held in its trust.

The CGIAR is an association of 58 public and private institutions, sponsored by the FAO, UN Development Programme, UN Environment Programme and World Bank. It supports 16 agricultural research centres worldwide. CGIAR's US\$304 million (1998 figures) annual budget represents between 4-10% of the South's agricultural research funds and contributes to the training of almost every agronomist in the Third World. It is estimated that foreign aid flows to the CGIAR of \$300 million per annum yield an unacknowledged return (to the North) of not less than \$5 billion. CGIAR estimates that its research feeds at least 1 billion people, and its high yield research has reduced farmland requirements by as much as 40% while keeping staple food prices low for the urban poor. But CGIAR's claims are hotly contested by its critics, the strongest among whom are the poor farmers CGIAR is supposed to help. As much as 70% of the South's most important food crops are based upon CGIAR germplasm enhancement. Its 16 International Agricultural Research Centres (IARCs), among which, International Rice Research Institute (IRRI), play a key role in research policy development throughout the South.

Despite recent improvements, the South continues to be a marginal player in the development of CGIAR's research policies that profoundly impact national economies.

The CGIAR holds the world's largest international *ex situ* collections of plant genetic resources, the GeneBanks, containing more than 500,000 accessions that are vital for crop improvement worldwide. These are held "in trust for the benefit of the international community, in particular developing countries", and subject to conditions contained in agreements signed by the research centres and the UN Food and Agriculture Organization (FAO) in 1994. These agreements specify that neither the CGIAR Centres nor recipients of designated germplasm will seek any intellectual property rights (such as patents) over that germplasm or related information. Despite that, many biotech patents are based on genetic resources from the CGIAR's GeneBanks.

Under pressure from non-government organisations, CGIAR called for a moratorium on intellectual property claims on seeds held in its collections in February 1998. CGIAR Chair, Dr. Ismail Serageldin, a supporter of agbiotech, reiterated the CGIAR's "strong and unequivocal support" for the 1994 agreements, which seek to guarantee that access to these resources will not be restricted. He called upon all recipients of designated material to honour the spirit of the agreements with FAO and to refrain from applying for intellectual property rights.

In November 2001, a new treaty was agreed - the International Treaty on Plant Genetic Resources for Food and Agriculture - by delegates from 116 countries. It would facilitate the free flow of genetic material to plant breeders (against the restrictions of the patents regime), but it fell short of banning patents on genetic resources. "We think it is good that there now is a treaty, though

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a number of issues have been left unresolved and in some areas it is weaker than we would have hoped," said Peter Rosset, co-director of the US based non-government organisation Food First. Among the major weaknesses are the unresolved issues of farmers' rights and intellectual property rights. Unless farmers' rights are settled in the farmers' favour, and the principle that public resources should not be patented is upheld, "then much of the potential benefits will be lost". It could be worse. For unless the tide of rampant patenting of genes and plant varieties is stemmed, this treaty would simply open up CGIAR's GeneBanks to exploitation by biotech companies, and make it impossible for indigenous communities to safeguard their *in situ* genetic resources as well. Sources: "RAFI COMMUNIQUE on the CGIAR's Third External Review" 17/9/1997 <http://cgiar.rafi.org>

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2. "FOOD ANTI-PATENT PACT HAILED DESPITE WEAKNESSES" By Emad Mekay, Inter Press Service, November 16, 2001, Friday



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Has Science Compromised Science?

Once again, the journal *Science* has allowed a private company to publish a scientific paper in its pages while withholding data from public view for commercial reasons. [Dr. Mae-Wan Ho reports.](#)

Just as Celera got away with denying public access to its human genome data, Syngenta too, is refusing to deposit its rice sequence data in the public database GenBank. Instead, Syngenta is making the data available through its own website (tmri.org) or on a CD-ROM.

According to *Science's* own report, Scientists can use the raw sequence without strings attached for research, and Syngenta will permit researchers to publish paper and "have Syngenta deposit a gene's worth of DNA data in GenBank without negotiation." Larger amounts will require a specific agreement. The company seeks no "reach through" intellectual property rights, but scientists doing commercial work must negotiate their own data-access agreements. The raw data include only minimal notes, such as labels on DNA likely to be "nonrice in origin", and is of no use to most researchers.

According to a news report in *Nature*, access to Syngenta draft sequence is very restrictive. Up to 15 000 bases at a time, and no more than 100 000 bases per week. If more is required, then a statement has to be signed that no commercial use is to be made of the sequence.

Science's deal with Syngenta is similar to that struck with Celera for the human genome sequence the journal published last year. Celera gives noncommercial researchers free access to raw DNA sequence but charges a fee for access to its annotated gene database. It had sparked off a furore among the scientific community. The journal had compromised the ideals of open science by allowing that precedent.

This time around, a score of leading researchers, including Micheal Ashburner of Cambridge University UK, David Botstein of Stanford University, circulated a letter stating that failure to deposit the data in GenBank constituted a "very serious threat" to genomes research. The value of GenBank is that diverse sequences from bacteria and worm to rice and human, are all accessible in one database, making it possible to carry out studies on evolutionary relationships and thorough searches for homology of gene sequences.

Science's editor-in-chief, Donald Kennedy, defended his decision, stating that, "the public benefit of bringing this importance science out of trade secret status greatly outweighs the cost of granting the exception". Many scientists would disagree.

Reaction from the scientific community has been relatively muted. *Science's* reporter thinks that it is because Syngenta has promised to work closely with public funded groups to produce more complete draft, and pointed out that Monsanto's draft of *japonica*, completed two years ago but unpublished, has also been made available to publicly funded groups, with the result that 30% of the data released to GenBank has originated from the company. So, much of Syngenta sequence is likely to end up in GenBank over the next "12 to 18 months" mixed with data from public groups, says Steven Briggs, head of Syngenta's Torrey Mesa Research Institute in San Diego, California.

All the signs are that the scientific establishment is getting far

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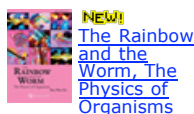
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One positive reason for the muted response from the scientific community may be that, thanks to Yang and the Beijing Genomics Institute, (see "[Breaching the corporate monopoly](#)", this series), the rice genome draft of *indica has* been deposited in the GenBank. This alone might have persuaded both Monsanto and Syngenta to make their sequences more available.

The problem is not just access to scientific information, it is how the information could be used for public good when the interests of the scientists and corporations are too closely tied up.

Source: "A deal for the rice genome" by Eliot Marshall, *Science* 2002, 296, 34.



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