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## Publication with a pinch of privatization

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LONDON - *Science* has done it again. In 2001, despite opposition from the science community, *Science* published Celera's version of the human genome while allowing the company to restrict access to the genomic data underpinning the publication. On 5 April 2002 *Science* will publish a version of the rice genome, while permitting the researching company Syngenta to keep the data on a private database.

The rules regulating access to the data seem to be simple but many researchers are concerned that these two papers break the long-standing arrangement within the scientific community that if you publish a paper you make all of the relevant data freely available. In addition, some wonder how these rules can operate in practice.

To start with, Syngenta will place its data on its own web site. This breaks the 20-year old convention within genomics research of placing data in GenBank or similar large publicly run databases as a condition of academic publication. *Science* defends the move, saying that it is upholding the spirit of the convention, as academic users can still gain free access to the data. Opponents say that this is creating a situation where data become distributed between different databases, each with different rules of access and use. The consequence could be a hindering of research.

Both *Science* and Syngenta are at pains to stress that academia will not be hindered. Once they have signed relevant letters stating that their intent is not-for-profit research, academics will be able to obtain a compact disc containing the entire genome, publish any results from their work and even seek intellectual property rights over their findings.

Exactly what this means in practice is unclear. Claiming a patent presumably means that you have some intention of commercializing your findings. Asked to clarify this, Editor-in-Chief of *Science*, Donald Kennedy told *BioMed Central* that academics could indeed use their patents to commercialize their work, but Chris Novak a spokesperson for Syngenta, based in Wilmington, Delaware, was more cautious, suggesting that this would need to be checked with their lawyers. It seems that the issue will be straightforward if a not-for-profit laboratory commercializes the findings and ploughs the profits back into the institution. It may be more complex, however, if the research facilities are co-used by a commercial rival of Syngenta.

Commercial users will be able to access the data to verify the conclusions published in *Science*. They will even be able to publish their interpretation of the data. They will, however, need to sign licence agreements with Syngenta if they start to commercialize any findings.

In 2001 Kennedy defended *Science*'s publication of Celera's human genome paper, saying that publishing with restrictions was better than no publication. He also felt that the human genome was an exceptional moment in science and so normal rules of disclosure did not necessarily apply. Some researchers say that the current incident shows how quickly exceptions set precedents, and now Kennedy defends this decision to bend the data submission rules again, arguing that if it was right to publish Celera's human genome paper, then it is imperative to give the world's scientists access to data relating to the world's most important food crop.

Indeed, Syngenta sees the move to publish as a step towards liberating their data, as previously only small groups of highly restricted researchers could use their sequence. Now, says Novak, the data will be open to many more inquiring minds.

As director of the International Rice Research Institute (IRRI) in the Philippines, Ron Cantrell is enthusiastic about the arrangement, saying that it is a symptom of the new world in which privately financed research plays a larger role than the public sector. His experience is that large biotech companies have been generous in their approach to sharing information with non-profit organisations such as the IRRI. "I think this new style of arrangement in publishing is going through an evolutionary process and will take some time to sort out in detail. But we have to view it as a positive thing as this provides information and technologies to the poorest people in the world, the ones we are trying to serve - they are the ones that we don't want to see left behind."

Those worried about the principle of academic data being open to anyone have started to ask how often *Science* will find itself faced with an exceptional circumstance. "I cannot envision another likely exception," replies Kennedy, "But given the volume of high quality, high-throughput basic research now being done in proprietary places, the scientific community needs, over time, to rethink the community standards it applies to sharing of data and materials associated with scientific publication." Cantrell is more Bullish, believing that it will become a standard approach to publication in the near future.

The very thought of this sort of change to the world of academic publishing was sufficient to motivate 20 eminent scientists to write a letter of protest [reprinted below this article], saying that the action poses "a serious threat to genomics research." "I have no great gripe with companies that want to protect data - companies have been doing that since the year dot," says one of the signatories Michael Ashburner, from the Department of Genetics at the University of Cambridge. "My gripe is that they are wanting to have their cake and eat it. They are wanting to publish what is by all appearance a regular scientific paper in what is after all a very respectable magazine, and yet they don't want to adhere to the norms of their community with respect to data release."

He believes that any suggestion that Syngenta is being altruistic is complete rubbish, speculating that rumours of the publication have already aided the company's share price. "Syngenta are taking this route for two reasons. They believe that it will be commercially beneficial and the scientists in their employ want scientific recognition for this... *Science*, too, has taken the decision for commercial reasons - they want people to read their mag."

"Syngenta should be honest and take out a paid advertisement," he added.

For Syngenta, Novak said that there were two benefits to publication. First was the ability to make its data open to more people, and second it gave the company the benefit of having its work scrutinised by the high-level peer-review process.

Another protestor, Sue Wessler, who works at the Department of Plant Biology, University of Georgia, is also angry about the way that Syngenta has managed the public relations side of this project, and the negative impact that has already occurred. "Syngenta has dangled the rice sequence in front of the International Rice Genome Sequencing Project for two years. All this grandstanding has done is hurt the public effort by putting pressure on groups to accelerate the process, cut corners and lower their standards."

Sue Mayer of the independent genetics think-tank GeneWatch raises a different issue. She believes that the move could damage the public reputation of science. "Scientists should work to foster public confidence and trust, and these sort of restrictive agreements will only serve to damage that relationship," she said.

In addition, asks Mayer, "how is the situation going to be policed?" Novak acknowledges that policing will be difficult, and that the data will effectively be given on trust. Kennedy admits that they haven't got a compliance system in effect. Indeed, any enforcement could become a lawyer's paradise because it will be very difficult to prove which bit was inspired by Syngenta's data once a researcher's work has drawn information from a number of different sources. "Maybe the threat of legal action from a huge company will be enough, but in that case it could simply push another obstacle in the path of some sectors of progress," fears Mayer.

The whole issue, claims Novak, will be very short-lived. According to best predictions a complete version of a rice genome will probably be lodged with GenBank in the next 18 months. Once this occurs, the data will be free to all, effectively nullifying the current contracts. The general issue of data-ownership is, however, not going to go away so quickly.

## The text of the letter of protest sent to Science 's editorial advisers:

## Dear Colleague

We write to you as an editorial advisor to Science.

In February 2001 *Science* published the human genome sequence paper from Celera Genomics. This was not only a major scientific event but also caused very considerable disquiet since, exceptionally, the authors were permitted not to deposit their data in "GenBank", the internationally recognised database for nucleic acid sequence data since the early 1980's.

At that time we, and many other colleagues, expressed dismay at this action, because of the absolute necessity for genomic research of having all of the public sequence data available from one place. [In fact "GenBank" is an international collaboration between the European Institute of Bioinformatics in the UK, the National Center for Biotechnology Information (NIH) in the US and the DNA Data Bank of Japan in Mishima. It is not, therefore, "owned" by any single body or government, thus ensuring its independence and commitment to free access.]

We are very happy to share with you now the arguments then made, and they remain as valid now as then, as to why deposition of sequence data in GenBank" is so important for the scientific community at large. It is, indeed, for this reason that all good scientific journals demand data deposition as an absolute condition for publication. This is from the instructions for authors to Nature:

"Papers reporting protein or DNA sequences and crystallographic structures will not be accepted without an accession number to Genbank/EMBL/DDBJ, Brookhaven, SWISS-PROT or other appropriate, identified, publicly available database in general use in the field that gives free access to researchers from the date of publication (see *Nature* 1998, **394**:105 and *Nature* 2000, **404**:317). Accession numbers are provided directly to authors by these databases on deposition of data, and must be included in the *Nature* paper before publication."

*Science* has a similar statement, but with this critical final sentence: "In selected cases, other repositories that allow free access to the data for purposes of verification and replication may be acceptable with the approval of the Editor-in-Chief."

We might add that, in the case of the Celera human sequence data, the condition of "free access" has not been met (see http://www.celera.com/genomics/academic/ home.cfm?ppage=pricelist&cpage=default).

Be that as it may, the National Academy of Sciences has convened a meeting on February 25th to discuss these and more general matters concerning data access.

The matter is important now, for there are strong rumours in the field that *Science* is considering allowing the publication of papers from commercial companies on the rice and mouse genomes, without demanding the submission of the data in "GenBank" as a condition. If this is so, then it represents a very serious threat to genomics research. Even if the rumours are false, the sentence that we have quoted above allows potential authors a let out, and one they may attempt to exploit if the Editors of *Science* think that their paper would have very high visibility.

We ask you to make your views known to Dr Don Kennedy (kennedyd@leland.stanford.edu) and urge *Science* to change their policy and bring it in line with the accepted norms of the field.

Yours sincerely,

Michael Ashburner, Department of Genetics, University of Cambridge.

Ewan Birney, European Bioinformatics Institute.

David Botstein, Department of Genetics, Stanford University.

Graham Cameron, European Bioinformatics Institute.

Mike Dexter, The Wellcome Trust.

Richard Durbin, Wellcome Trust Sanger Institute.

Sean Eddy, HHMI & Washington University, St. Louis.

Richard Henderson, MRC Laboratory of Molecular Biology, Cambridge.

Aaron Klug, MRC Laboratory of Molecular Biology, Cambridge.

Richard McCombie, Cold Spring Harbor Laboratory.

Susan McCouch, Department of Plant Breeding, Cornell University.

Rick Myers, Stanford Human Genome Center, Stanford University.

Paul Nurse, Cancer Research UK.

Maynard Olson, University of Washington Genome Center, Washington.

Bruce Roe, Advanced Center for Genome Technology, University of Oklahoma.

John Sulston, Wellcome Trust Sanger Institute.

Janet Thornton, European Bioinformatics Institute.

Bob Waterston, Genome Sequencing Center, Washington University, St. Louis.

Jean Weissenbach, Genescope, Evry, France.

Sue Wessler, Department of Plant Biology, University of Georgia.

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