

Wake-up call for Japan's genomics

A US company's plans to sequence the rice genome in weeks rather than decades should inspire a more venturesome spirit in the Japanese research community.

Last week's news of a newly launched private initiative in the United States to sequence the entire rice genome in only six weeks has sent shock waves through the plant genomics community. It has prompted Japanese researchers engaged in the international Rice Genome Sequencing Project to consider a significant revision of their ten-year initiative planned for completion in 2008.

No doubt those involved in the publicly funded effort are experiencing déjà vu. The private sequencing project, to be carried out by Celera Genomics, the company established by the genome researcher J. Craig Venter, has created a situation very similar to that last year, when he announced plans to sequence the complete human genome, in direct competition with the efforts of researchers at the National Institutes of Health, the Wellcome Trust and elsewhere. Japanese researchers are now having to come to terms with what they consider is a major challenge to their own rice genome project.

Venter plans to create a commercial database containing sequence data of the 430-megabase genome (see page 545). Despite general scepticism over Celera's proposed six-week timescale, the effect of the news has been instantaneous — in a matter of days, Japanese researchers had drawn up plans to accelerate their sequencing effort, including a request for increased funding to purchase DNA sequencers. Researchers realize the urgent need to reaffirm and speed up the publicly funded project, which has so far taken a sluggish path despite rapidly intensifying competition in plant genome research from the private sector. Limited sequencing ability caused by lack of funds is partly to blame for the slow progress of the sequencing effort. Researchers also blame the government for being slow to acknowledge the importance of genome research — as a result, Japan has made a slow start in this sphere of activity, while the United States, prompted by scientists at the National Institutes of Health and

elsewhere (including Venter), enthusiastically embraced such research as a national strategy.

The challenges arising from Venter's initiative will also be an opportunity for the Japanese government to revise its policy on genome-related research. After years of urgent calls from Japanese researchers to promote genome research more energetically on a national level, the government will introduce a new programme this year to promote the commercial application of biotechnology research, particularly in genomics, by increasing funds for basic research and creating public databases of genomic information. But this is scratching the surface by international standards. Japan is far behind the United States and Europe in genome research, and urgently needs to boost not only sequencing capacity and other basic research but also the environment in which research and commerce can jointly thrive. Venture capital needs more encouragement, but the government should also promote rather than, as at present, discourage collaboration between public and private sectors. Japanese researchers themselves would do well to view commercial collaboration more positively than they do now.

Venter's approach will give him a lead in identifying sequences with technological potential. Whether that will in turn result in an appropriate balance between the right to profit from such information and the needs of the world's population is quite another matter, which now requires discussion all the more urgently. But there is nothing to stop publicly funded genome sequencing projects from making their accumulating sequences available to all. Given the obvious commercial and political interests in the sequence for rice, which is the principal food of half of the world's population, the quicker this happens, the better. Rice genome partners — Japan, the United States, the European Union, China and South Korea — please note. □

Xenotransplant caution continues

A ban on clinical trials of transplants from primates shows good judgement. Now we need data.

It's official. Xenotransplants from non-human primates would expose "recipients, their close contacts, and the public at large... to significant infectious disease risk" (see page 549). This strong language comes from the US Food and Drug Administration (FDA), which just three years ago wanted to leave the regulation of xenotransplantation to local institutional review boards. In private, some FDA officials now also argue that the question of whether to proceed with human trials of living parts of any animals is so important that a federal policy ruling is needed.

That it has taken the FDA until now to decide the obvious says much about the reluctance in the United States to regulate if this can be at all avoided. The potential benefits of using primates are tiny — breeding enough clean monkeys or baboons to substantially shorten organ waiting lists is impracticable. The potential cost is the creation of more AIDS, Ebolas or Marburgs.

It would be a mistake to conclude that the FDA's exclusion of primate donors means that other animals, such as pigs, are safe. The benefit side of the equation is better with pigs, but the risk side is largely unknown. The US Department of Health and Human Services is setting up a federal advisory committee on xenotransplantation, to include experts, representatives of other stakeholders and the inevitable bioethicists. The US administration should put human trials of pig organs on hold at least until this committee has had its say.

But it would be unfortunate were the prospect of a moratorium to have the perverse effect of deterring researchers and funders from supporting continued research on xenotransplants outside the clinic. Indeed, perhaps a rule needs to be invented, which says that whenever a government calls a moratorium, it should also make sufficient funds available for research to fill the gaps in knowledge that made it necessary in the first place. □