

► National Institute of General Medical Sciences. It also suggests re-evaluating the special status accorded to the National Cancer Institute, which has an unusual degree of independence from the NIH director.

Many researchers, including former NIH director Harold Varmus, have been calling for greater consolidation, claiming that the current arrangement of the NIH makes it inflexible and causes disparities in research funding. But changes to the status of individual institutes are likely to be opposed by lobbying groups and research organizations linked to the areas of science involved. The report's authors say such difficulties mean that further mergers would be politically impractical.

"Our discussions, correspondence and meetings made it quite clear that there would be very little agreement among these communities on what the right way to organize NIH is," the report's authors write, "and there would probably be dozens of conflicting ideas in play and few clear avenues for narrowing these down."

The authors also address the ongoing effort by the Department of Health and Human Services to centralize or outsource various NIH functions, such as some aspects of grant review. This move won the authors praise from the community for attempting to defend the NIH against interference from Congress and the Bush administration. David Baltimore, president of the California Institute of Technology, describes such behaviour as "gutsy". "They're taking on two big interests here — the administration and the Congress — and I think that's a very good thing," he says.

The question now is what will become of the report. A 1984 Institute of Medicine study, which included similar proposals, was not implemented by Congress. But politicians are currently more interested in the NIH than they were then. The agency is being investigated by Congress over payments to its researchers, for example. Last month, two members of Congress told NIH director Elias Zerhouni that they were beginning an investigation of payments for lectures made to NIH executives by large centres that received NIH money.

On 10 July, the investigation was expanded after an NIH programme administrator told reporters that even though he was removed from his role in 1995, he has since been paid an annual salary of \$100,000 while doing almost no work for the agency. This, together with the fact that Congress requested the report, makes it less likely that the study will be ignored, observers say. ■



Corny question: as the maize genome map nears completion, should a full genome sequence be next?

Maize map sees geneticists split over choice of direction

Carina Dennis

Plant scientists are entering the home straight in their bid to map the genome of maize (corn, *Zea mays*). Weighing in at 2.5 billion base pairs, the genome is about the same size as the human version, and will be the biggest plant genome yet mapped. The data are already accelerating the discovery of useful traits, but could also provide a springboard for a more ambitious effort: the detailed sequencing of the entire maize genome.

Current work is focusing on two maps. A high-resolution genetic map, analogous to a series of signposts showing the relative positions of different genes, was made available last November. A physical map, composed of overlapping cloned gene fragments to give the distances between the genes, is nearly complete and is being combined with the genetic version to create a scaled map of gene positions.

"We have assembled about 95% of the physical map and about half of it has been anchored to the genetic map," says Ed Coe, a geneticist with the US Department of Agriculture and a director of the Maize Mapping Project. Funded by a five-year, US\$11-million grant from the National Science Foundation (NSF), the project involves scientists at the University

of Missouri-Columbia, where Coe is based, and the universities of Arizona and Georgia.

Project scientists predict that the integrated map will be complete in September, but it has already helped researchers. "The map has had an impact on me," says Vicki Chandler, who studies gene control at the University of Arizona. "I now know exactly what the physical distance is between my genetic markers and where my gene is," she says.

For many crop scientists, the sequence of the maize genome is the next logical step. Others disagree, pointing out that the rice genome, which is already sequenced, is similar to that of maize. They argue that the rice sequence, together with the integrated maize map, will provide a good guide for geneticists.

But certain aspects of maize biology, such as the unusual vigour of some hybrid strains, need the genome sequence to be fully understood, some researchers contend. Gene order and the number of genes vary greatly between different strains, and this may contribute to hybrid vigour. "We can't use the rice genome as a reference sequence for understanding the diversity of maize," says Joachim Messing, a maize geneticist at Rutgers University in Piscataway, New Jersey.

Some experts think it would be impractical to sequence maize and other large, repetitive cereal genomes to the same standard as rice. Last September, to address these concerns, the NSF provided \$10 million for a programme to test a gene-enriching strategy for sequencing the maize genome. The project aims to develop a method for filtering out gene-poor areas of the genome, and to uncover ways in which the integrated map can be used to anchor data from sequencing of the gene-rich areas.

It remains to be seen what the private sector will contribute to the maize effort. Several firms, such as DuPont, based in Wilmington, Delaware, have sequenced parts of the maize genome. "At least two of the major players are interested in partnering with us," says Coe. ■

