NEWS

Big money for cancer genomics

WASHINGTON DC

The US National Institutes of Health (NIH) has launched the pilot phase of its controversial Human Cancer Genome Project, which aims to catalogue the genetic changes associated with cancer.

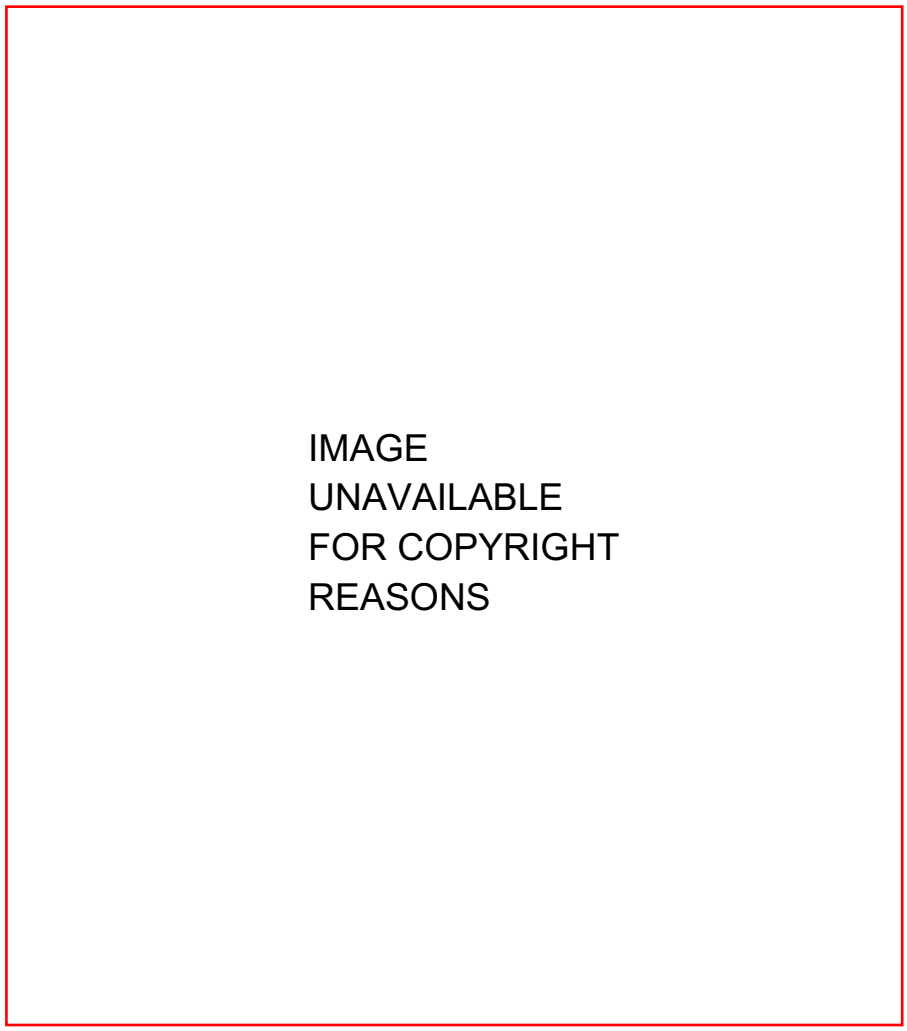
The project is a potentially huge undertaking that could take 10 years and cost US$1.5 billion. Its proponents say that tallying up all the genetic mutations in cancer cells may reveal new drug targets.

But opponents argue that cancer biology is too poorly understood to make such a cataloguing approach viable and say that the money would be better spent on basic research into how cancer functions.

The NIH pilot project, announced on 13 December, is itself a major endeavour. Its budget of $100 million over three years is high, considering that the agency's budget for 2006, which has not yet been finalized, is likely to stay flat or even drop. But Francis Collins, director of the National Human Genome Research Institute (NHGRI), says it would be a mistake to wait. The NHGRI and the National Cancer Institute — both based in Bethesda, Maryland — will split the cost evenly.

"The chance to apply this incredibly powerful engine called genomics to cancer is extremely compelling, and to say, 'Budget times are tough, we're gonna have to wait a while,' would be unacceptable," says Collins.

The pilot plan has five stages. First, the agency will pick two or three types of cancer to study and collect samples of their tumours. Second, it will award money to centres that can do high-throughput analyses, such as gene-expression experiments, on the tumours. Third, the agencies will ask its genome sequencing centres to resequence about 2,000 genes in each tumour. This is part of a larger shift in focus at the NHGRI towards repetitive sequencing of genes associated with disease (see *Nature* **437,** 1233–1234; 2005). The cancer project's scientific advisory board has not yet decided which genes will be resequenced. The fourth and fifth components will be grants for technology development and for bioinformatics systems.



Is this the answer? The NIH is giving strong backing to genomics in cancer research.

TEK IMAGE/SPL

The genome project was proposed by the National Cancer Institute's board of advisers earlier this year. But supporters point to earlier success from a similar but smaller effort — the UK Cancer Genome Project at the Wellcome Trust Sanger Institute in Cambridge. In 2002 it turned up a gene called *BRAF* that is mutated in most melanomas and is now a target for drug development (*Nature* **417,** 949–954; 2002). Many cancer researchers and cell biologists, though, say the big-science tactic could suck money away from other grants for years to come. Others caution that the project may not generate useful information unless it includes tests that are not currently planned, such as functional assays that could identify mutations crucial for cancer-cell survival.

Stephen Elledge, a geneticist at Harvard Medical School in Boston, Massachusetts, co-wrote an open letter in October calling on the National Cancer Institute to set up clear standards by which the pilot project can be judged (S. J. Elledge and G. J. Hannon *Science* **310,** 439–441; 2005). "I would really like to have the sequence of all the cancer genomes, but it may not be that useful and cost-effective," Elledge says. "They need an independent panel of scientists who can evaluate the data and really have the possibility that they will change the way the project is going to go forward."

Collins says that the project's scientific advisory board is looking at this very question and that the agencies will take any recommendations seriously. "We will have very explicit goals," Collins says, adding that finding drug targets should be one of them. And, he says, scientists can apply for money for functional-screening projects as part of the pilot. The pilot will be a crucial test for the institute, and for all genome scientists, as they try to make the case that they can make a difference to medicine. ■

Erika Check