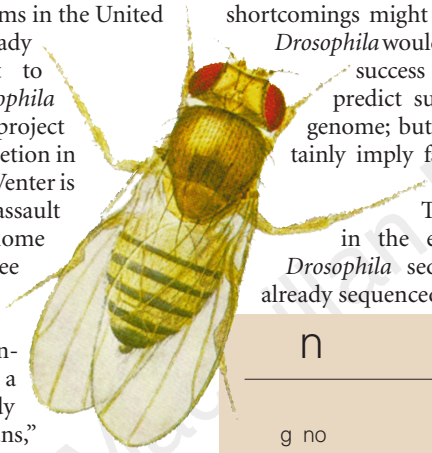
Drosophila set for fast-track sequencing

[LONDON] The humble fruitfly *Drosophila melanogaster* will be the first organism studied by the private fast-track genome-sequencing effort launched jointly earlier this month by J. Craig Venter, founder of The Institute for Genomics Research, and the laboratory equipment manufacturer Perkin-Elmer (see *Nature* **393,** 101 & 201; 1998).

The main objective is to sequence the entire human genome within the next three years. But Venter has announced that he plans to sequence the 120-megabase *Drosophila* euchromatic genome as a dry run.

The project will be carried out jointly with several research teams in the United States and elsewhere already engaged in a project to sequence the *Drosophila* genome. Although this project was scheduled for completion in 2001, the approach that Venter is planning to use for his assault on the human genome should, if successful, see the task completed by next year.



UNIVERSITY OF FREIBURG

"The offer [from Venter] came as a bit of a shock, as we had already drawn up our own plans," says Gerry Rubin of the University of California at Berkeley, leader of the Berkeley *Drosophila* genome project. "But it is in all our interests to see that the genome is sequenced as quickly as possible, and I feel that [this new proposal] is all going to be for the good."

Venter says that a number of potential candidate organisms were investigated for a 'proof of principle' of his sequencing strategy, which uses a 'shotgun' approach to divide the complete sequence into small fragments, each of which is sequenced several times. "We could have used the plant *Arabidopsis*, but we decided that the most useful thing we could do was *Drosophila*."

He says that one of the reasons for the choice was the large amount of work that has already been put into *Drosophila*, particularly the mapping that will allow the isolated sequences to be reassembled in the correct order. "The [existing] cDNA libraries are some of the best in the world," he says.

Sensitive to charges that his human genome efforts will be competing directly with federally funded work (see right), Venter is also keen that the *Drosophila* work should be a genuinely cooperative effort. "I hope that this will serve as a model of how we can work with others in the genome community to get sequencing done."

Rubin says he is pleased that, as part of the collaborative agreement, Venter has agreed to make available to the international research community all the raw trace data obtained from the automatic sequencers. (One bone of contention over the human project has been the conditions under which such data will be made available to other researchers.)

The joint *Drosophila* project has also been welcomed by Francis Collins, director of the National Human Genome Research Institute, the body funding the current *Drosophila* sequencing work at Berkeley and elsewhere in the United States. "I think that we need to learn about the strategy of full genome shotgun sequencing, and what its benefits and shortcomings might be," he says. "Clearly *Drosophila* would be a good test run. Its success would not necessarily predict success for the human genome; but its failure would certainly imply failure for the human genome."

Those who are engaged in the existing international *Drosophila* sequencing, which has already sequenced about 10 per cent of the genome, are aware that collaboration with the Venter/Perkin-Elmer initiative will involve a significant revision of some of their medium-term plans. The repercussions will also be widely felt in Europe, where laboratories in several countries, in particular the United Kingdom, Germany and Greece, are taking part in the sequencing project with support provided through the European Commission in Brussels.

Many of the researchers already engaged in the sequencing also face the prospect of having to overcome the widespread antagonism generated in the sequencing community by the aggressiveness with which news of the Venter/Perkin-Elmer initiative was announced.

A successful, cooperative *Drosophila* sequencing is seen on both sides as one way this antagonism — and the suspicion of the new initiative it has generated — could be diluted by an awareness that the sooner the sequence is completed, the sooner the more interesting work of analysing it can start. "There will still be a significant amount of work to be done," says Rubin. "The sequence is just the beginning."

David Dickson

n o o n

o o ng o . n
g no o n o ng n
. g n n n o
o o n . o n o
o n o o n o n n o n n
n o n g n o n o n no
) n on o n o . no go
n o) o o n o n no o ng ng o
ong o n o on gg ng
o o no n o . go ng o on n o n
n ng o g no o n on . n n
. o n n o g n
o o o og o g o o no .
n o n g no q n o
g o o . o n on)
ong o n g ng o n n o o n
o o n o n n n o
n no o n n g. o on
g o o n gg o
nno n n o n on n
n n o n on ng oo n o o ng
n n o o n n ng on .
q n o o o n o
n g no n n on o n nn)
o). n n n g n o
n o o n o o o o o
n o) o o o on o
o n o n . n n n
n o n o n o
o ong on o g no o n on ng
n o n g o . go n n o
on o on n on n no
o o . o n o o g no o . **Meredith Wadman**