Scarring following glaucoma surgery may currently be treated with potent anticancer drugs such as mitomycin C, which are applied topically. Such treatments are difficult to administer safely. Their mode of action appears to be to kill fibroblasts and their toxic effects can be sight threatening in themselves. Pre-clinical studies examined the effects of anti-TGFβ_2 mAb on human Tenon's capsular fibroblasts. Subnanomolar concentrations of anti-TGFβ_2 mAb were able to inhibit proliferation, migration and contraction of these cells. In an *in vivo* model of trabeculectomy the anti-TGFβ_2 mAb was successful in preventing surgical failure. In clinical trials, the mAb is being administered at the site of operation pre- and post-operatively with the aim of controlling the development of scar tissue. The Phase I/IIa trial of anti-TGFβ_2 in this indication was started in June 1998 and is expected to be complete in the first quarter of 1999.

David Hughes

Viral intelligence on the Web

Important chemical intelligence on the influenza virus was made available to medical researchers worldwide by Los Alamos National Laboratory (LANL) in New Mexico with the launch of a comprehensive database on the WorldWide Web. The database contains a collection of genetic information about the influenza virus, which scientists will be able to use to better understand how the influenza virus mutates. The obvious impact will be in the development of more-effective new vaccines and putative drugs to combat the disease as well as allowing researchers to track the disease more effectively.

Cohesive research

Los Alamos National Laboratory's Influenza Sequence Database was introduced to prospective users at the American Society for Virology meeting in July in Vancouver, British Columbia. The manager of the database Catherine Macken said that having a central collection point for all the published and unpublished genetic sequences for the virus is the only viable way to get all the information out to the research community. 'With an international repository, we can conduct cohesive analysis rather than patchwork research around the world,' she said.

The new database contains viral sequence data, results from immunological studies, and information on viral protein structures – all crucial components of an investigation into the virus. Importantly, the database will hold unpublished, but nevertheless invaluable, sequence data. Researchers can now add their own information to the database as well as use it to make comparisons of species and strains, that are currently infecting people, with older influenza viruses.

LANL is also working with scientists from the University of California and the Centers for Disease Control and Prevention to expand the database still further. At the moment, the database holds the total influenza sequences held in GenBank, a database managed by the National Institutes of Health. GenBank, however, only collects sequences that have been published in scientific journals. LANL and its institutional collaborators will verify and annotate unpublished genetic data collected around the world and add this to the database.

Working model

It is hoped that the LANL database will act as a working model for similar tools that will be used to track the spread of other deadly diseases, including those that may have been intentionally released. Alan Perelson, head of Los Alamos' Theoretical Biology and Biophysics Group, adds that 'Los Alamos is actively involved in developing new, cutting-edge capabilities to reduce threats to our national security'. He adds that while the influenza database is not directly part of that effort, it does show the kind of expertise Los Alamos can bring to problems of national and global importance.

If the database were just a library of gene fragments it might not have much impact on research, but because it is annotated with background information on how a sequenced virus was grown, for instance, researchers using the information can be more critical of the relevance of particular mutations. This should allow them to assess whether they were the result of problems with culture technique or wild mutations.

Macken and her team are in the process of developing software tools to allow browsers to recognize and analyse characteristic patterns in the sequences. These tools will allow visual and statistical assessments of variations to be made more readily than is possible now. Such developments will arm researchers with information about which strains of influenza are appearing or moving around the world so that health officials can be advised on where to deploy resources. Access to the >3000 influenza sequences in the Los Alamos' Influenza Sequence Database is available on the World Wide Web at: http://www-influenza. lanl.gov/

In this issue, John Oxford and Robert Lambkin (Retroscreen, London, UK) focus on the concept of neuraminidase inhibition in the fight against influenza.

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