

Establishment and Application of A Pathogen Molecule Sequence Database in Taiwan (2004)

The purpose of this Center to establish a pathogen molecule sequence database is to fulfill our obligation as the leading disease prevention and control organization in the country by providing research resources to domestic professional laboratories of pathogen research, thus to collect, store, file, integrate and analysis the genetic sequence information of important domestic and international disease-causing agents. These reference databases will be mainly used as important information to sustain policy making in preventive and control infectious diseases in the future. Besides, the genetic information established in this program will be accessible, through an effective management approach, to the biotechnological industry for use. They may take advantage of the local and important communicable disease data combined with the pathogen genetic evolution and epidemiological information to develop relevant vaccines and diagnostic reagents. By such the genetic database can indirectly improve the competitiveness of domestic biotechnological companies. What was achieved by this project in 2004 has three parts. First, we established a sequence laboratory successful in many aspects, such as to save funds, to training people, to provide sequence service for our own laboratories as well as some contract laboratories, to integrate sequence results to announce at the weekly meeting of our center, and to send sequence results to our contract laboratories also weekly. Figure 1. Second, the database collected lots important information about special sequences of viruses or bacteria, epidemiological information of cases and analysis tools of genetic information of viruses or bacteria. This year we are going to maintain the genetic database of enterovirus, influenza virus, dengue virus and Mycobacterium tuberculosis, and build others for Japanese B Encephalitis, HIV, adenovirus and rotavirus in 2004. Finally, the whole database was rebuild to improve TPMGD (Taiwan pathogenic microorganism genome database) infrastructure from re-design and establish of database schema and system architecture. Figure 2. We would focus on the improvements of extension and flexibility in the first version. The second version can accept the whole genome sequences and other genome information from other different pathogens, such as bacteria or different experiment formats. It also added the function of user authority controls and browsing interface. The database is able to exchange information with other external database such as CDC GIS system dynamically and additional powerful analysis programs, which are specific to some pathogens. The main architecture of

system is finished and eight topics have been added to the items of main page. The system test is ongoing nevertheless.

Figure 1

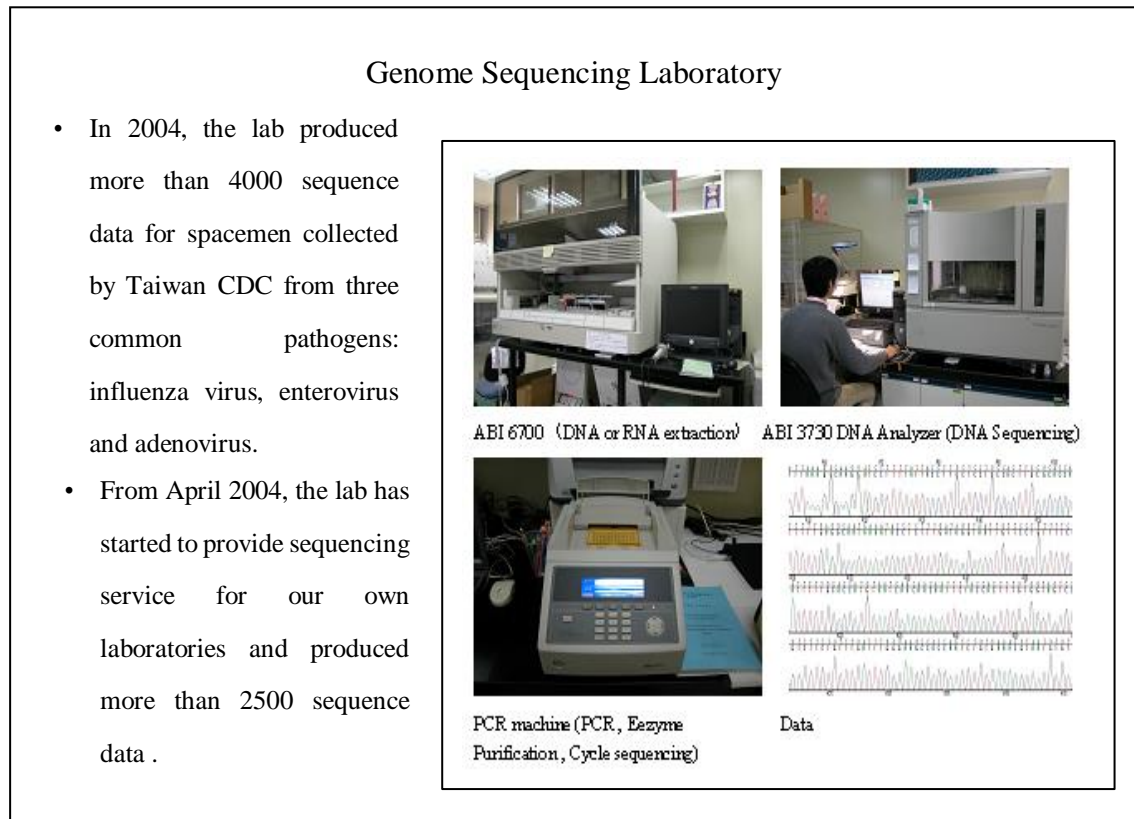


Figure 2

