Genomic approach to seasonal and pandemic influenza viruses

Nobuyuki Fujita*

Department of Biotechnology, National Institute of Technology and Evaluation (NITE), Japan

ABSTRACT

Influenza is one of the most serious infectious diseases, infecting roughly 10% of the population and causing hundreds of thousands of deaths worldwide every year. To combat this disease, World Health Organization (WHO) established global surveillance network in which National Institute of Infectious Diseases (NIID) in Japan plays a major part as one of the four international WHO collaborating centers. NITE has been participating in the surveillance, in collaboration with NIID and prefectural and municipal public health institutes, by massively sequencing some of the genes, those related to viral antigenicity and drug resistance, of seasonal influenza viruses clinically isolated in Japan and other Asian countries. The data are shared globally and used for the selection of vaccine strains and the monitoring of drug-resistant viruses.

A new H1N1 influenza virus of swine origin emerged early this year. Worldwide spread of the virus prompted WHO to declare pandemic phase 6 in June. As the virus is new to human, it is possible that the virus may rapidly accumulate mutations in the course of its adaptation to human host system, and develop higher virulence, higher transmissibility, or resistance to antivirals. It is also a concern that the virus may exchange genetic components with other circulating viruses leading to unexpected drastic changes (a phenomenon called reassortment). For close monitoring of these mutations and reassortments, whole genome sequencing would be a definitive method of choice. As of this writing, we have determined complete coding sequences of more than 90 isolates of the pandemic H1N1 virus. The data so far obtained, together with those obtained in

* Corresponding author. Tel.: 81-438-20-5760
E-mail: fujita-nobuyuki@nite.go.jp
other countries, indicate that i) the virus is relatively homogeneous in terms of the genomic sequence, ii) although mutations have been accumulating in all viral genome segments, no mutation or reassortment potentially associated with higher virulence or transmissibility has been found, iii) there is no evidence that oseltamivir (Tamiflu) resistant virus is circulating, albeit some sporadic cases were reported.