Editor's note

Learn to fight from the war

In March 2009, a novel type A (H1N1) influenza broke out in North America and rapidly spread all over the world. So far, more than 17000 cases of infection have been reported. The alert level announced by the World Health Organization (WHO) has upgraded sharply to Level 5, indicating that the century long “arms race” between humans and the influenza has entered a new phase.

Just six years ago, the Severe Acute Respiratory Syndromes (SARS) broke out in China. Due to the lack of a mature public infrastructure for emerging infectious disease control and prevention as well as the persistent scientific and medical research related, this sudden epidemic disease of unknown origins presented a massive challenge for medical and life science researchers, government officers and the general public. Eventually, through no small efforts, including massive international collaborations, we won this “war of encounter”. After that, the quality of the medical precaution systems has been greatly improved, along with a dramatic increase in scientific funding for research in infectious diseases. Chinese scientists have published many research articles in international journals, marking the entrance of virology and epidemiology in China into the post-genome era.

The battle has started again. But this time, it is a remerging disease — type A influenza. On 8th May, the Novel Swine-Origin Influenza A (H1N1) Virus Investigation Team published their report in the *New England Journal of Medicine*. They thoroughly investigated this epidemic and the related viruses, and discovered that this novel kind of H1N1 viral strain is a reassortant product of segments from North American swine influenza, avian influenza, Eurasia swine influenza and human influenza. The WHO Rapid Pandemic Assessment Collaboration has also published online their report in *Science* on 11th May. Based on the genetic diversity analysis of the available data, they inferred that the clinical severity appears less than that seen in 1918 but comparable with that seen in 1957. Almost at the same moment, Chinese scientists completed bioinformatics and evolutionary analyses based on the available molecular sequences and the epidemic data. Their research includes the evolution of the H1N1 influenza A virus genomes, the origin and tendency of the viruses, the molecular characteristic of the North American strain, the network structure research of the mutations of the hemagglutinin (HA) gene, the structural modeling of HA protein, and the determination of the hyper-variable and the conserved regions of the HA gene as well as the establishment of the genotyping method. These results were collectively published in this special topic on *Influenza A (H1N1) Virus*, representing a reflection of the research progress made by the scientists in China. To our joy, the corporation between different working areas and institutions began to emerge.

We have to admit that some conclusions reported here are different from or even contradict the foreign research opinions and findings, and will require more supportive data. For example, according to this special topic, the genomic sequences can be classified into the Mexican type, the transition type and the New York type based on their mutations; the obvious differences in the electrostatic potential of the epitope of HA protein for the novel H1N1 flu virus compared to that from previous flu viruses albeit located at the similar position. These conclusions not only reflect the independent research capability of the Chinese scientists, but also may provide a foundation for the control and treatment of influenza as well as the development of related drugs. More importantly, the hyper-variable region-based subtyping by sequencing will provide a fast and specific platform for the clinical diagnosis, epidemic monitoring and molecular evolutionary analysis of type A influenza and it might eventually provide a “gold standard” for the confirmation diagnosis of the influenza A virus and its subtypes.

It is, thus, believed that if we can popularize this kind of “bioinformatics-guided” collaborative research effort and translate these research outcomes quickly in disease prevention, control and treatment practice, the cause of influenza control will be raised to a new level in the near future. With more and more data becoming available through international collaboration, it is expected that more results will be published in domestic and international scientific journals. This will provide us with more support in this “positional warfare” against influenza. It will also promote the development

of virology, molecular epidemiology and the immunology in a post-genomic area, which will eventually assist the “protracted war” in combating all kinds of viral (and even non-viral) epidemics with more knowledge regiments created.

From SARS to the H1N1 influenza, the frequent outbreak of zoonotic epidemic has become a great challenge to scientists. The social globalization requires stricter control over the epidemics but leaves us with little time for preparation. Only by “learning to fight from the war” can scientific and technological researchers within the clinical/medical/public health area continue to progress, which may improve our ability to combat such epidemics and related diseases and to ensure us getting the upper hand in the ultimate battle ground.

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