

Foreword

Performing Laboratory Network Surveillance to Monitor the Emergence and Spread of Infectious Diseases

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Laboratory systems are one of the pillars in the infrastructure for infectious disease control and prevention — surveillance, early warning, and emergency response capacities are a priority to public health. Laboratory based monitoring provides essential support for infection diagnosis, pathogen identification, spread tracking, and outbreak warning, especially for emerging infections caused by newly recognized pathogens and clusters of unknown diseases. In response to coronavirus disease 2019 (COVID-19) outbreaks, laboratories have played critical roles for virus discovery, infection diagnosis, carrier screening, epidemic trend analysis, transmission chain identification, source tracing, vaccine and drug development, and intervention effect assessments. Many clinical laboratories were rapidly equipped with the abilities of molecular diagnosis and virus genome sequencing, which provided data for public health decision-making.

Infection diagnosis and analysis of pathogens from human, animal, and environmental sources are necessary. Since the pathogens can be transferred from one region to new regions, a laboratory-based network for surveillance should be established and the laboratory data shared for the purpose of joint surveillance and response. Besides laboratory tests, information techniques are necessary for the rapid sharing of data within the network. Traditional tests such as cultures and bio-typing of pathogens, antibody measurements, and molecular detection of genes have been commonly performed. Genome sequencing has been used progressively, which generated a vast ocean of sequence data for pathogen gene/genome detection and alignment. The era of microbial big data has come.

Some laboratory-based surveillance networks have been implemented as international or countrywide surveillance, such as PulseNet International (1), which is a global laboratory network for bacterial food-borne diseases. In the Netherlands, a national antimicrobial resistance (AMR) laboratory system was developed for the surveillance and control of antimicrobial resistance (2). In China, to improve the surveillance and response abilities of infections and outbreaks, the Chinese Pathogen Identification Net (China PIN) was established in 2017 and has acted as a national laboratory-based surveillance and early warning network for bacterial infectious diseases. It is derived from the PulseNet China, a member of PulseNet International, and it currently still conducts the tasks of PulseNet China. China PIN is comprised of four levels of network laboratories in the disease prevention and control institutions, including national, provincial, prefectural, and county levels. It integrates laboratory techniques, database, information platform, and workflow management into the system.

China PIN functions to carry out pathogen identification, outbreak detection, and source tracing through laboratory surveillance. In this special issue, we organized six analysis articles and application reports from the laboratories of China PIN to illustrate the missions and roles of the network. We presented a brief introduction of China PIN to summarize the organization, mission, and progress of the network (3). Emerging pathogen identification is one task of China PIN, one paper reported two cholera outbreaks caused by the Serogroup O5 strains of *Vibrio cholerae*, which is a new serogroup causing cholera outbreak, though it does not carry cholera toxin genes (4). Another paper in “Outbreak Reports” reported the rare *Anaplasma bovis* infections in humans and pathogen carriage in ticks in environment, which corresponds to the role of China PIN in source tracking of infection with integrating of environmental monitoring (5). A field laboratory monitoring mode, which metagenomic sequencing and sequence analysis was performed in the mobile biosafety laboratory in the field, was reported to show the practicability of work mode and unexpected finding of pathogens (6), corresponding to the tasks of pathogen identification by metagenomic next-generation sequencing (mNGS) and animal source investigation of China PIN. A typhoid fever outbreak caused by extensively drug-resistant (XDR) *Salmonella* serovar Typhi was reported (7) based on the etiological and genome sequence evidences. China PIN performed genome sequencing in transmission monitoring and source tracing of AMR strains. In one article of worldwide spread analysis of the *mcr*-carrying plasmids, the effect and role of resistant plasmid tracing using the complete plasmid

sequences were shown (8), which showed the necessity of complete plasmid genome sequences in AMR transmission monitoring.

All the papers are representations of the missions of China PIN. Some laboratory findings have been used to launch joint investigations in the network laboratories in China PIN. These laboratory-based investigations and analyses applied genome sequencing in the monitoring of infectious diseases from the aspects of human, animal, and environment, showing the roles of laboratory surveillance networks under the framework of infectious disease control and the One Health approach.

doi: 10.46234/ccdcw2022.057

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Submitted: March 21, 2022; Accepted: March 22, 2022

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