Retrospective Studies: Excellent Tools to Complement Surveillance

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(See the major article by Takahashi et al on pages 816–27.)

Emerging infectious diseases pose an important challenge to public health globally. The identification of an etiologic pathogen responsible for an emerging infection in humans can be a major task. The time required to isolate and characterize a new infectious agent sufficiently to adopt control measures and, when possible, to select and make available curative and preventive treatments can be considerable and take years. If the novel pathogen exhibits rapid pathogenesis, causing serious illness and death in a significant percentage of infected individuals, in addition to efficient transmission and spread, serious consequences for the human population can be readily observed. The race between the spread of a high-consequence pathogen and the deployment of adequate public health measures can hardly be satisfactory from a public perspective, because it is a reactive chain of events to the initial spread of the infectious agent.

Predicting the emergence of infectious diseases months or years in advance would be a perfect solution but for now has remained a theoretical concept. Improved surveillance systems to detect emerging infectious diseases and new technologies using algorithms specifically developed to isolate and identify causative infectious agents have been emphasized to minimize public health emergencies related to emerging infections. Enhanced surveillance and detection is one of the most significant improvements to regional and global public health of the past several decades. For example, several regional or national networks, such as the Global Public Health Intelligence Network in Canada and the Global Disease Detection program of the Centers for Disease Control and Prevention network in the United States, are informing and cooperating with international networks, such as the Global Outbreak Alert and Response Network developed by the World Health Organization [1–3]. Unfortunately, surveillance and detection methods are region specific, and many regions are currently not being actively monitored. Regions under surveillance often make use of different technologies and approaches that are not yet standardized, thus creating many potential holes in the global network intended to detect new pathogens before they cause damage. More work will be required before these newly developed systems are ideal, but the recognition of their importance and usefulness is a critical step toward enhanced preparedness and response and ultimately prevention.

Viruses are responsible for a significant proportion of emerging infectious diseases, the numbers of which may be on an increasing trend overall [4, 5]. It is clear that surveillance and identification of unknown pathogens has greatly improved in the past decade, which has resulted in the concomitant rise in the number of new pathogens being discovered each year. Again, this increase has occurred despite the fact that the detection and identification of previously unknown pathogens currently depends on heterogeneous surveillance systems of variable sensitivity and precision. Regardless, heightened surveillance, detection, and identification of emerging pathogens are currently active and prolific fields of research. Whether there exists a real or apparent increase in the number of viruses emerging in the past 50 years, compared with the number that emerged 50 or 100 years earlier, there is certainly an increasing number of viruses being detected and identified in recent years. A PubMed search using the term "emerging viruses" revealed that the number of scientific articles published on the subject of emerging viruses has jumped from <10 per year in the early 1990s to nearly 70 in the early 2000s and up to 220 per year during 2011–2012, reflecting a

growing interest from the scientific community and public health officials. Many new viruses potentially capable of endangering public health have been identified in approximately the past 10 years: SARS coronavirus, Middle East respiratory syndrome coronavirus, Lujo virus, and severe fever with thrombocytopenia syndrome virus (SFTSV) are just a few examples of a rapidly expanding list.

SFTSV is the subject of a study by Takahashi et al [6] in this issue of the *Journal*. SFTSV is a *Phlebovirus* in the family *Bunyaviridae* that was first isolated in China and reported in 2011 to be a novel bunyavirus [7]. The virus is likely transmitted by ticks and was reported to be unique to China, with only 1 case reported elsewhere (in Dubai, in a patient from an area of North Korea that borders a region of China where SFTSV was epidemic) [8]. Human-to-human transmission has been described and attributed to close contact with infected blood [9–12]. SFTSV causes a febrile illness with a case-fatality rate initially reported to be around 30% and later revised to an average of 17% [7, 13]. Consequently, SFTSV infection can lead to serious disease that approximates the severity of other high-consequence pathogens.

The study by Takahashi et al describes the first case of SFTSV isolated from the serum of a female resident showing SFTS-like disease in Japan and retrospective diagnoses of further cases dating back to 2005. The authors studied the relationship between the Japanese and the Chinese viruses by phylogenetic analysis. According to the study, SFTSV has been endemic to Japan for some time, with the earliest known case dating back to around the same time as the first documented case in China (2005 in Japan and 2006 in China). In addition, this study indicates a wider spread of the virus than previously thought and raises the possibility that it may be in regions beyond China and Japan. The recent identification of the related Heartland virus in 2012 in the United States [14], which is closely related to SFTSV, supports this hypothesis. The determination of the common lineage will provide more details on the timeline of the spread between China and Japan and may offer a glimpse into the possible determinants of virus spread. This retrospective study demonstrates the value of reevaluating past unknown cases to answer current questions and better define the extent of public health threats. It is an important publication that will bring more attention to this newly emerging virus and highlight the importance of effective surveillance and detection to public health.

Overall, this study further supports improved monitoring and detection to discover viruses, like SFTSV, that may have gone unnoticed not so long ago. The number of undiscovered viruses was recently estimated at 320 000 [15]; today's technologies and surveillance protocols are actively identifying some of these viruses. The scientific community and public health systems may have reached a point where they are now identifying and characterizing previously unknown pathogens from fewer cases, owing to enhanced detection methods. Better surveillance and detection systems are widely recognized as a critical aspect of better preparedness and response to public health events involving the spread of infectious agents. Very few countries have active surveillance systems, which can detect unknown pathogens via algorithms. The detection of new viruses following systematic processes is a rapidly growing yet young scientific field. Interestingly, the present work by Takahashi et al stems from a retrospective study of a single initial case and was not facilitated by a centralized clinical database. These results bode well for the future and suggest that more important findings of the sort are to come, possibly at an accelerated pace, in the mostly unexplored world of unknown pathogens.

Note

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