Short Communication

Monitoring of Influenza Viruses in the Aftermath of the Great East Japan Earthquake

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SUMMARY: Influenza has a significant impact on public health when a natural disaster occurs during the influenza season. However, the epidemiological characteristics of influenza following natural disasters have not been well documented due to the difficulty of implementing laboratory-based influenza surveillance in such situations. The Great East Japan Earthquake occurred on March 11, 2011, when influenza was already circulating. Since routine influenza surveillance was not performed in Miyagi Prefecture, we initiated an ad hoc laboratory-based monitoring system immediately after the earthquake. From March 15 to May 19, we tested 277 samples for influenza virus collected around Sendai City and from evacuation centers in Miyagi Prefecture. Influenza A (H3N2) was detected in 112 cases, influenza A (H1N1) 2009 in one case, and influenza B in 92 cases. The H3N2 virus was dominant until the 14th week. However, a sudden increase in the number of influenza B cases occurred after schools were reopened. According to phylogenetic analysis, a major clade switch of the H3N2 virus took place after the earthquake. The Yamagata lineage of influenza B was detected in one patient from western Japan, indicating the importing of viruses into the affected area.

Outbreaks of infectious diseases often become a public health concern after major natural disasters. The risk of outbreaks can increase due to poor hygiene, stress, malnutrition, inadequate and densely populated shelters housing many vulnerable people, and lack of access to healthcare services in affected areas. Among respiratory infections, influenza can have a significant public health impact if a natural disaster occurs during the influenza season. However, the epidemiological characteristics of influenza following natural disasters have not been well-documented.

The Great East Japan Earthquake occurred on March 11, 2011. This earthquake and the subsequent tsunami caused devastating damage in the Tohoku region (in northeast Japan). Due to earthquake-related events, more than 300,000 people were housed in evacuation centers. Sendai City is located in Miyagi Prefecture, the area most severely affected by the tsunami. In Sendai City, the influenza A virus (A) (H3N2) became predominant in the first week of March, and the earthquake occurred during the influenza season. The National Institute of Infectious Diseases (NIID) conducted a rapid risk assessment of infectious disease immediately after the earthquake, and influenza was considered a "high risk" communicable disease in the assessment.

After the earthquake in Sendai City and the surrounding areas, routine influenza surveillance was not carried out because of the damage caused to health facilities and the lack of transportation. Therefore, we established an ad hoc laboratory-based monitoring system immediately after the earthquake in order to bridge this gap to some extent.

This ad hoc monitoring system was established to monitor circulating influenza viruses in Sendai City and the surrounding areas from March 15 (11th week) to May 19 (20th week). We obtained 277 samples, including 76 nasopharyngeal or throat swabs and 201 residues from point-of-care (POC) tests during the 2-month observation period from temporary clinics in 5 evacuation centers (3 in Yamamoto town, 1 in Iwanuma city, and 1 in Ishinomaki city), the Tohoku University Hospital emergency room (ER), Sendai Emergency Medical Care Center, and 7 private outpatient clinics. Samples were collected from patients with suspected influenza infection in each sentinel. As it was difficult to distribute viral transport medium (VTM) for virus isolation to all sentinels after the earthquake, mainly POC test kit samples were collected instead of VTM swabs. During the first 4 weeks, we collected samples from evacuation centers during site visits for risk assessment of communicable diseases and from the Tohoku University Hospital ER. Most patients were residents of the affected area, but there were also non-residents from other parts of Japan.

From March 17, we commenced viral detection using reverse transcription PCR (RT-PCR) and/or real-time RT-PCR, and influenza virus was detected in 36% (27/76) of swabs and 89% (178/201) of POC test residues. Types A (H3N2), A (H1N1) 2009, and B were found in 112, 1, and 92 cases, respectively. A (H3N2)
Fig. 1. Phylogenetic tree of partial HA1 gene of A (H3N2) (781 nt) (A) and B (208 nt) (B). The trees were constructed by the Neighbor-Joining method. The bootstrap values (1,000 replicates) are shown next to the branches. ● and ○ show the samples collected after and before the earthquake, respectively. In (A), the samples collected from patients in evacuation centers in Yamamoto town are surrounded by line boxes. In (B), the samples collected from elementary schools around Kita-Sendai area are surrounded by line boxes, and samples collected from patients who visited Sendai from outside are surrounded by dashed line boxes.

was dominant until the 14th week, and detected until the 18th week. The prevalence of B increased in the 15th week. In the 16th and 17th weeks, we observed a sudden increase in the number of B cases from pediatric clinics in the Kita-Sendai area, with most originating in elementary schools. Only one case of A (H1N1) 2009 was detected in the 11th week in Sendai Emergency Medical Care Center.

Sequence analysis was performed from April 12 for the partial HA1 (781 nt), NA (1455 nt), and M2 transmembrane domain (M2-TM) (339 nt) regions of A (H3N2) and the HA1 region of B (208 nt) to observe the phylogenetic relationship and drug resistance of the circulating viruses. The sequences of 39 and 48 samples were obtained from the 112 A (H3N2) and 92 B cases, respectively (GenBank accession nos. AB679525–AB679621). Neighbor-joining trees for A (H3N2) and B were constructed using MEGA 5 software after the monitoring period to summarize the phylogenetic relationship of the samples (6) (Fig. 1). Ten A (H3N2) samples, which were detected before the earthquake during the 2010/2011 season, were also included in the tree (Fig. 1A).

A (H3N2) viruses were classified into 2 clades: A/Perth/16/2009 and A/Victoria/208/2009. The major clade switched from A/Victoria/208/2009 to A/Perth/16/2009 after the earthquake. Within the A/Victoria/208/2009 clade, all viruses detected before the earthquake and most detected after the earthquake belonged to subclade 5. All viruses in the A/Perth/16/2009 clade belonged to subclade 1. All samples collected from evacuation centers in Yamamoto town belonged to the A/Perth/16/2009 clade, and shared high homology (Fig. 1A). All samples possessed the S31N mutation in the M2-TM region, indicating amantadine resistance, but there was no known mutation in the neuraminidase (NA) gene, which is associated with NA inhibitors (E119V, R292K) (7).

For type B, all but one virus, of the Yamagata lineage, belonged to the Victoria lineage (Fig. 1B). The viruses detected in the elementary schools in the Kita-Sendai area were highly homologous, which indicated influenza outbreaks in schools. There was a sharp increase in the number of B-positive cases in the 15th week when the affected areas shifted from the early response phase to the reconstruction phase, which suggests the importance of re-strengthening communicable disease monitoring when social activity normalizes during the
The recovery phase. On the other hand, viruses detected from patients in other areas, especially outside Sendai City, were genetically distinct from those detected in the Kita-Sendai area. One Yamagata lineage virus was detected in a patient who visited Sendai City for volunteer activity from the western part of Japan, where sporadic cases of Yamagata lineage B viruses have been reported (8). Fortunately, this virus did not spread widely, and the number of isolates of this lineage detected was limited even at the national level. However, this finding indicates how population flow leads to the importing of viruses into the affected area. At the same time, this finding also highlights that proper preventive measures, including necessary vaccinations, should be implemented for volunteers and support staff to minimize the introduction of infectious diseases into affected areas.

From March 24, when cell maintenance became possible in the laboratory, isolation of influenza virus was performed using the Madin-Darby canine kidney (MDCK) cell line. We isolated 7 A (H3N2) and 9 B (Victoria lineage) types from 40 swab samples. From April 27, hemagglutination inhibition tests were performed on A (H3N2) and B (Victoria lineage) viruses, determining no significant difference in antigenicity compared with the vaccine strains present during the 2010/2011 season (A/Victoria/210/2009 and B/Brisbane/60/2008, respectively).

After the earthquake, information on influenza was limited and discrete, and it was therefore difficult to assess influenza activity and risks. By establishing this ad hoc monitoring system, we were able to monitor influenza activity in Sendai City and the surrounding areas. Using this system, we rapidly circulated a situation report on influenza with laboratory confirmation by March 21, within 10 days of the earthquake, providing information about the risk of influenza in the affected areas (9). Due to difficulties with sample collection and transportation during this period, we used POC test samples as the template for genetic analysis, an alternative method of virus isolation. Moreover, we performed genetic analysis to investigate genetic mutations, antiviral resistance, and transmission patterns during the post-disaster phase within the first few weeks after the earthquake. This analysis allows us to understand the trend of circulating viruses, which is crucial for early response to and control of the spread of influenza in such a large-scale natural disaster. This study had a limitation in that due to asymmetrical monitoring methods, the number of cases might not reflect the magnitude of viral transmission. However, our findings contribute to the evidence base regarding public health during natural disasters.

In conclusion, we were able to document influenza activity in the area affected by the earthquake through our ad hoc monitoring system. This study sheds light on the importance of such monitoring systems for the control of outbreaks of infectious disease following natural disasters.

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Conflict of interest None to declare.

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