Laboratory and Epidemiology Communications

An Outbreak of Acute Respiratory Infections due to Human Respiratory Syncytial Virus in a Nursing Home for the Elderly in Ibaraki, Japan, 2014

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Communicated by Masayuki Saijo

(Accepted May 22, 2014)

Human respiratory syncytial virus (HRSV), a member of the family Paramyxoviridae and genus Pneumovirus, is a notable viral agent that causes acute respiratory infections (ARI) in humans (1). HRSV may also cause severe ARI such as pneumonia in infants (1). However, the epidemiology and pathogenicity of HRSV in elderly persons has not been elucidated. We encountered an outbreak of ARI due to HRSV in a nursing home for the elderly in Ibaraki, Japan during the winter of 2014. Here we report the molecular epidemiological analysis of the outbreak.

Epidemiological investigation suggested that 3 of the 99 residents showed symptoms, such as cough, sore throat, and acute wheezing in the middle of January 2014. They were also diagnosed with pneumonia by chest radiography. Within 9 days, 21 other residents presented with similar symptoms. During this outbreak, the prevalence of infection in the residents was approximately 24% (24/99), but the infection route could not be determined. Patients were aged from 68 to 97 years (81.5 ± 8.5 years; mean ± standard deviation [SD]). Clinical manifestations among the patients were as follows: fever (20/24 residents, 83.3%; 37.7 ± 0.8°C, mean ± SD), rhinorrhea (8/24, 33.3%), cough (21/24, 87.5%), sore throat (7/24, 29.1%), and wheezing (7/24, 29.1%). In total, 5 cases (20.8%) were diagnosed with pneumonia by chest radiography. No underlying conditions including cancer and/or immunosuppressive diseases were observed in all patients with pneumonia. The majority of the patients (21/24) resided on the second floor of the nursing home.

We collected 10 nasopharyngeal swab samples after obtaining verbal informed consent from the patients. We tried to detect and isolate HRSV, influenza A, B, and C viruses, human rhinovirus, enteroviruses, parainfluenza viruses (types 1–4), coronavirus, adenoviruses, Chlamydophila pneumoniae, Mycoplasma pneumoniae, Streptococcus pneumoniae, and Haemophilus influenzae using polymerase chain reaction (PCR), reverse transcription (RT)-PCR, or culture methods (2–4). Although HRSV was not isolated using cell culture methods, it was detected from samples by RT-PCR. No other viruses or bacteria were detected or iso-
Fig. 1. Phylogenetic tree constructed on the basis of partial sequences of the HRSV G gene. Distance was calculated using Kimura’s two-parameter method and the tree was plotted using the neighbor-joining method. Numbers above the branches represent the bootstrap probabilities (%). The present strains are shown in bold letters. Numbers in parentheses indicate GenBank accession numbers. The reference strains were as follows: Long (AY911262), A2 (M11486), MO02 (AF233910), NY CH09 93 (AF065254), SA97D1289 (AF348803), SA98V603 (AF348807), SA99V1239 (AF348808), LLC235-282 (AY114149), M055 (AF233915), DEL/609/03 (DQ248941), 18537 (M17213), AL19734-4 (AY114149), Long (AY751131), Ch10b (AF065250), Ch09 (AF065251), Ken/2/00 (AY524575), M035 (AF233911), M035 (AF233913), SA98D1656 (AF348826), SA98V192 (AF348828), SA98V1239 (AF348811), SA99V429 (AF348813), SA99V800 (AF348814), and SA99V1325 (AF348821).

Nucleic acids were extracted from the samples using the QIAamp MinElute Virus Spin Kit (Qiagen, Valencia, CA, USA) and suspended in DNase/RNase-free water. After DNA/RNA extraction, PCR or RT-PCR was performed as described previously (2–4). Amplicons were purified using the QIAquick PCR Purification Kit (Qiagen), and the nucleotide sequences were determined by direct sequencing (5). Next, we performed phylogenetic analysis on the basis of the HRSV G gene nucleotide sequences of HRSV (nucleotide positions: 670–969, 300 nucleotides for the genotype BA reference strain [BA4128B/99B]) using Molecular Evolutionary Genetics Analysis software version 4 (2). Evolutionary distances were estimated using Kimura’s two-parameter model, and a phylogenetic tree was constructed using the neighbor-joining method (6,7). The reliability of the tree was estimated using 1000 bootstrap replications.

The GenBank accession numbers of the nucleotide sequences obtained are AB918645 and AB918693 to AB918698.

HRSV alone was detected in 7 of the 10 samples collected, and no other pathogens were detected. The nucleotide identity of the analyzed regions (G gene) among the present strains was 100%. Phylogenetic analysis based on the HRSV G gene nucleotide sequences showed that the strains were HRSV subgroup B (HRSV-B) genotype BA (Fig. 1). In addition, the present strains genetically resembled other domestic HRSV-B genotype BA strains detected in nearby areas (within a 100-km radius) including in Gunma, Tochigi, and Kanagawa prefectures (93.2–99.9% nucleotide identity). All patients recovered without sequelae. Moreover, we carefully examined amino acid substitutions in the C-terminal hypervariable region among the present strains and
other domestic strains. As a result, 2 amino acid substitutions (T259I and T281A) were found. These substitutions might be unique, although further studies are warranted (2,5).

Primary HRSV infection mainly occurs in infants (1). Moreover, HRSV reinfections in the elderly may be associated with severe respiratory infection (pneumonia) or exacerbation of asthma and chronic obstructive pulmonary disease (8). However, the epidemiology of HRSV infection in adults including elderly people is not exactly known. In the present cases, HRSV was detected in 70% of the collected samples. In addition, phylogenetic analysis (Fig. 1) showed that the genotypes of the strains were identical (HRSV-B genotype BA), and the analyzed G gene nucleotide sequences completely matched each other. The present strains may be prevalent domestic strains and thus may be closely related genetically. Acute wheezing was observed in approximately 29% (7/24) of patients, and pneumonia was identified in approximately 21% (5/24) of patients. Among them, 4 of the 7 patients presented with pneumonia plus acute wheezing. All 4 of these patients were women, and no chronic pulmonary diseases such as asthma or chronic obstructive pulmonary disease were found. A previous report suggested that wheezing might occur in 6–35% of elderly patients with HRSV infection (8). Thus, constant acute wheezing as a complication of HRSV infection could be observed in the elderly as well as in infants with primary infection of the virus (8–10). In conclusion, HRSV should be considered a possible cause of outbreaks among elderly persons with ARI presenting with pneumonia and acute wheezing.


Acknowledgments We thank the staff of the nursing home for their cooperation during the epidemiological investigation. This work was supported in part by a Grant-in-Aid for Research on Emerging and Re-emerging Infectious Diseases (H25-Shinko-Ippan-015), Labour and Welfare Programs from the Ministry of Health, Labour and Welfare of Japan.

Conflict of interest None to declare.

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