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Imported Cases of Measles in Niigata, Japan in 2011

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In Japan, the measles surveillance system was changed in January 2008, from sentinel surveillance of children and adults to nationwide case-based reporting on the basis of experience from a large measles outbreak, and to achieve measles elimination by 2012, according to an agreement reached among Western Pacific Region member states. All medical practitioners were required to report every clinical or laboratory-confirmed measles case to a local public health center (1).

According to the new surveillance-reporting system, we have performed laboratory diagnoses of suspected measles cases in Niigata Prefecture. From 2008 to 2011, a total of 42 clinical specimens (throat swab, blood, and/or urine samples) were collected from 18 individuals with suspected measles. These collected samples were tested by measles virus (MV)-specific reverse transcription-nested polymerase chain reaction (2). We detected 4 hemagglutinin (*H*) and 3 nucleoprotein (*N*) genes of MV from 3 patients who had returned from abroad. This report summarizes these 3 imported cases of measles in Niigata, Japan in 2011.

Patient 1 was a 7-month-old Malaysian boy who had stayed in Malaysia for about 5 months after the 2011 Great East Japan Earthquake disaster with his brother apart from their mother. Their mother, who resided in Niigata, had visited Malaysia on August 15 and brought back her children to Japan on September 1. On August 29, Patient 1 developed a fever (over 39°C), which was followed by a rash on September 2. In fact, in mid-August, his brother had been hospitalized with the same symptoms in Malaysia. Throat swab, blood, and urine samples of Patient 1 were collected on September 8: *H* and *N* genes of MV were detected only from the throat swab.

Patient 2 was an 11-month-old boy who resided in Niigata. He had not been immunized against measles. Patient 3 was his mother, a 33-year-old Japanese woman who had been immunized against measles once. They had visited New Zealand for 10 days (from September 17 to 26). On October 4, Patient 2 developed a fever (38.8°C), which was followed by a rash on October 8. His throat swab, blood, and urine samples were collected on October 13; *H* and *N* genes of MV were detected from the throat swab, and the *H* gene alone was detected from the urine sample. On October 12, 8 days after onset of the illness in Patient 2, Patient 3 developed a fever (38.9°C), which was followed by a rash on October 13. Her throat swab and blood samples were harvested on October 12; *H* and *N* genes of MV were detected only from the throat swab.

Patients 1 and 2 were reported to a local public health center as measles cases and Patient 3 was classified as having modified measles, due to her measles vaccination history and atypical symptoms, such as a shorter period of rash.

For genetic analysis, partial nucleotide sequences of the *N* gene (456 bp) of the MV strains were determined by the direct sequencing method (2). These sequences were analyzed phylogenetically using Molecular Evolutionary Genetics Analysis (MEGA) software (version 5). Evolutionary distances were estimated using the maximum composite likelihood method and the phylogenetic tree was constructed using the neighbor-joining (NJ) method. The reliability of the phylogenetic tree was estimated by 1,000 bootstrap replications.

The 3 sequences from Patients 1, 2, and 3 were designated MVs/Niigata.JPN/38.11, MVs/Niigata.JPN/42.11/1, and MVs/Niigata.JPN/42.11/2, respectively, according to the World Health Organization nomenclature, and deposited in the DNA Data Bank of Japan with the accession numbers AB675481, AB678710, and AB678711, respectively.

Phylogenetic analysis revealed that MVs/Niigata.JPN/38.11 belonged to genotype D9, represented by MVs/Victoria.AUS/12.99, and MVs/Niigata.JPN/42.11/1 and MVs/Niigata.JPN/42.11/2, which were identical, belonged to genotype D4, represented by MVi/Montreal.CAN/89 (Fig. 1). The sequence homologies between MVs/Victoria.AUS/12.99 and MVs/Niigata.JPN/38.11, and between MVs/KLumpur.MYS/21.11 and MVs/Niigata.JPN/38.11 were 97.8% and 99.3%, respectively. Similarly, those between MVi/Montreal.CAN/89 and MVs/Niigata.JPN/42.11/1, and between MVs/Auckland.NZL/23.11 and MVs/Niigata.JPN/42.11/1 were 97.5% and 100%, respectively. The D9 genotype of MV was reported from Australia, Hong Kong (China), Japan, Malaysia, New Zealand, Philippines, Republic of Korea, and Singapore in 2011. On the other hand, the D4 genotype of MV was reported from Australia, Japan, New Zealand, and Singapore and caused outbreaks in Europe, Africa, and the

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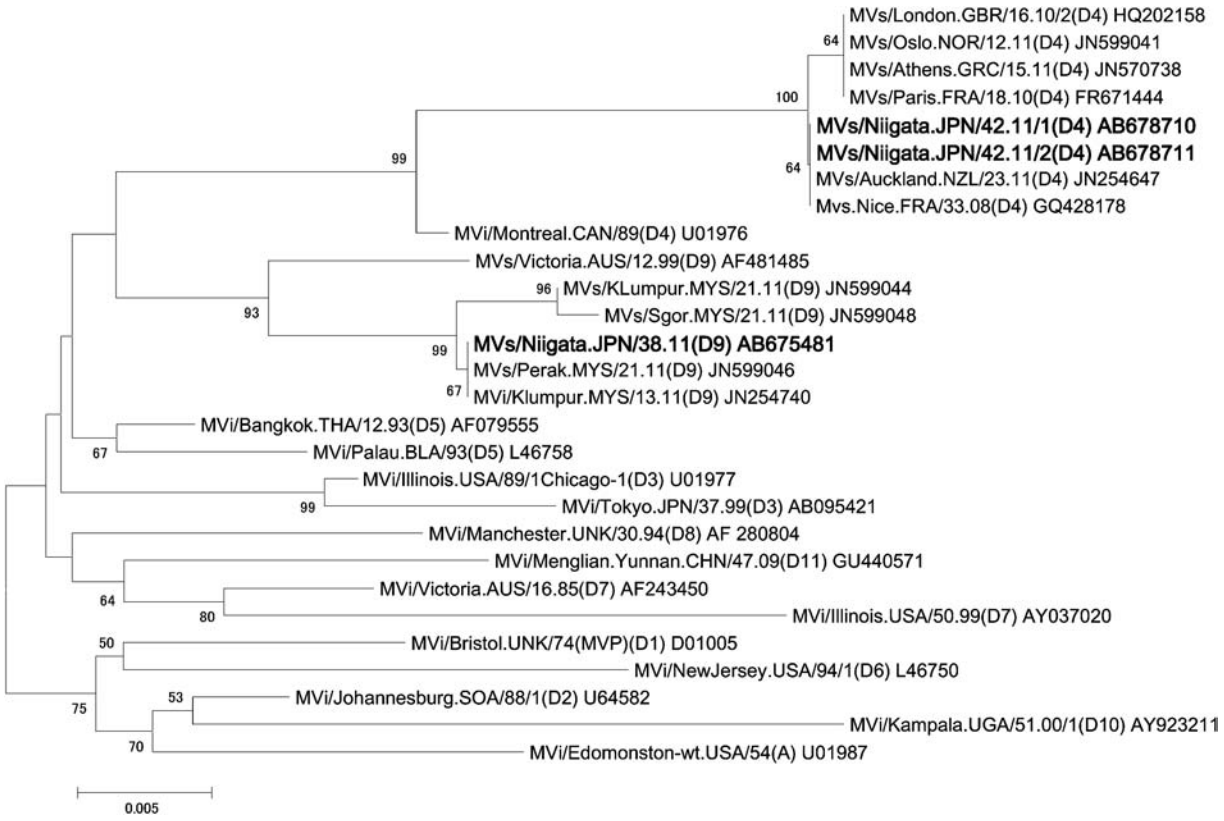

Fig. 1. Phylogenetic tree based on the nucleoprotein gene sequences (456 bp) of genotype A and D reference strains of the measles virus. The evolutionary distance was calculated using the maximum composite likelihood method, and the tree was plotted using the neighbor-joining method. Numbers at each branch indicate the bootstrap values of the clusters supported by that branch. The scale indicates 0.5% nucleotide differences. DDBJ/EMBL/GenBank accession numbers are given in parentheses. The present strains are represented in bold type.

Americas in 2011 (3–5). From our laboratory data along with epidemiological information, these 3 patients were considered infected with MVs circulating in the countries they had each visited, and finally confirmed as cases of imported measles or import-related measles.

In the United States, in addition to vaccinating infants aged 6–11 months, it is recommended that people who have insufficient measles immunity be administered the measles vaccine prior to travel abroad (6). People should recognize the risk of exposure to measles during a stay abroad, regardless of whether a stay is long or short, and receive the measles vaccine as needed in advance, in order to protect themselves as well as to avoid bringing back measles into Japan. Fortunately, no outbreak has been reported around the cases described here.

Only 2 measles cases in 2010 and 3 imported or import-related cases in 2011 were reported in Niigata Prefecture, which has a population of 2.4 million. Consequently, Niigata Prefecture has achieved the measles elimination target (under 1 case per million population, excluding imported cases) (7). Moreover, the measles vaccination rate in the 2010 fiscal year was 97%, 97%, 95%, and 91% for the 1st (at 1 year of age), 2nd (at 5–6 years), 3rd (at 12–13 years), and 4th (at 17–18 years) vaccinations (8), respectively, and 95% of the population over 2 years of age were seropositive for measles in 2010 (9). Therefore, measles is no longer considered to be endemically transmitted in Niigata Prefecture. In addition, some of the other prefectures in Japan have also achieved the measles elimination target (7) and endemic measles transmission might have ceased in these prefectures. However, resurgence of measles transmission by MV from abroad or from endemic prefectures is easily conceivable, because MV is highly contagious. Therefore, maintenance of high-level immunity against measles and an appropriate surveillance system are required to prevent the resurgence of measles in Niigata.

Conflict of interest None to declare.

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