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First Detection of Measles Virus Genotype G3 in a Japanese Woman: an Imported Case

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Since 2007, the number of measles patients in Japan had continued to decrease because of regular and widespread measles immunization program (1). However, 450 cases of measles including the suspected cases were reported in 2010 (1). Epidemiological data suggests that most of these cases were imported into Japan, but domestic cases have also been reported (1). Recent molecular epidemiological studies reported the detection of measles virus (MV) genotypes D3, D4, D5, D9, and H1 in Japan (2–4). The D4 and D9 genotypes have usually been detected in imported cases, while the D3, D5, and H1 genotypes have been detected in domestic cases (2–4). Here, we describe the detection of another genotype, G3, in an imported case of measles in a Japanese woman. To the best of our knowledge, this is the first report on the detection of MV genotype G3 in Japan.

The patient was a 28-year-old Japanese woman who resided in Chiba Prefecture, Japan. She did not have a history of measles and had not been immunized against measles. She had visited Indonesia for 10 days (from January 31 to February 9, 2011) with six colleagues. On February 14, she developed common cold-like symptoms such as cough and shivering, and consulted a local physician, who made a diagnosis of common cold. On February 22, she developed clinical symptoms including high fever (39°C), cough, conjunctivitis, Koplik's spots, and rashes on the face and neck. She then consulted another physician at a general hospital. The physician suspected her to have contracted measles, and suggested that she get admitted to the hospital. Informed consent was obtained, and her whole blood sample was collected on the next day. Viral RNA was extracted from the blood sample using the High Pure Viral RNA Kit (Roche, Indianapolis, Ind., USA), and was suspended in DNase/RNase-free water. Thereafter, reverse transcriptase-polymerase chain reaction (RT-

PCR) and nested PCR were performed as previously described (2–4). Amplicons were purified using the High Pure PCR Product Purification Kit (Roche), and the nucleotide sequence was determined using direct se-

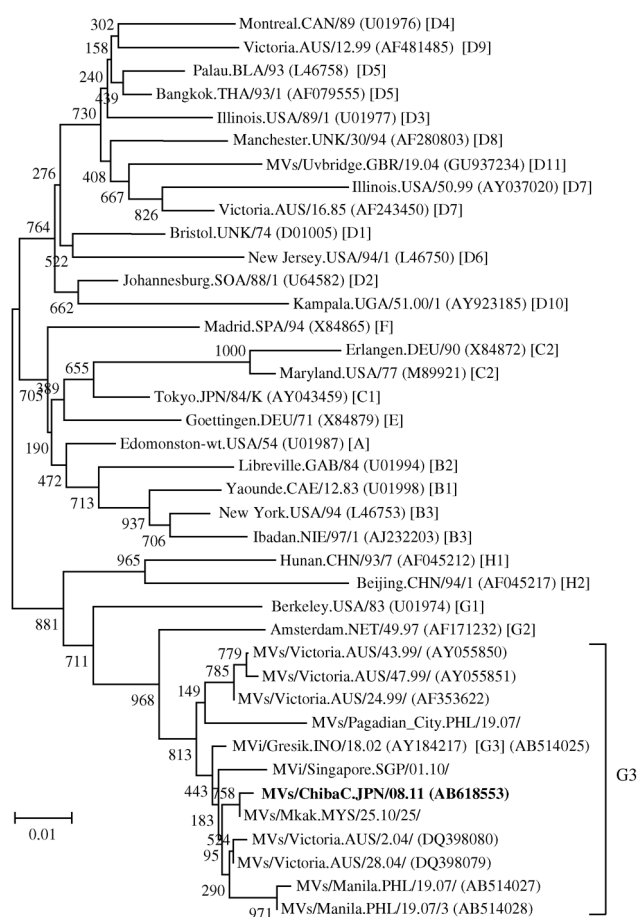


Fig. 1. Phylogenetic tree based on the nucleotide protein (N) gene sequences of various strains of the measles virus. The evolutionary distance was calculated using Kimura's two-parameter method, and the tree was plotted using the neighbor-joining method. Numbers at each branch indicate the bootstrap values of the clusters supported by that branch. Genbank accession numbers are given in parentheses. The present strain is represented in bold type.

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quencing method (4). The nucleotide sequence of the partial *N* gene (450 bp) of MVs was analyzed phylogenetically using Molecular Evolutionary Genetics Analysis (MEGA) software (version 4) (2–4). Evolutionary distances were estimated using Kimura’s two-parameter method and the phylogenetic tree was constructed using the neighbor-joining (NJ) method (2–4). Reliability of the phylogenetic tree was estimated by 1,000 bootstrap replications.

We constructed a phylogenetic tree based on the *N* gene of the detected MV strain and the reference strains (Fig. 1). The strain was genotyped as MV G3 in the phylogenetic tree. The homology between the reference strain (MVi/Gresik.INO/18.02 [G3], GenBank accession no. AY184217) and the present strain was 99.1% at the nucleotide level and 98.7% at the amino acid level. Epidemiological investigations have not reported occurrence of measles among the patient’s family and colleagues.

To the best of our knowledge, this is the first report on MV G3 detection in Japan. The genotype G3 was first detected in Australia and East Timor in 1999 (5). Infection with G3 has not been frequently reported in these countries after 1999. However, this may be attributed to the lack of aggressive MV surveillance in these countries. At present, a small number of the population in Chiba Prefecture may be susceptible to measles because of lack of immunization against the disease. However, as measles is highly contagious in humans (6), and spreads rapidly from one area to another, up-to-date information on the epidemiological status of this

disease in our country is needed.

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Conflict of interest None to declare.

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