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Isolation of a Wild Type Measles Virus Classified as Genotype H1 in Osaka City

Hideyuki Kubo*, Nobuhiro Iritani, Tsukasa Murakami and Kosuke Haruki

Department of Microbiology, Osaka City Institute of Public Health and Environmental Sciences,

Tojo-cho 8-34, Tennoji-ku, Osaka 543-0026

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Measles is one of the important infectious diseases in pediatrics (1). The World Health Organization (WHO) has recommended genotyping of wild isolates of the measles virus. Thus far, eight clades from A to H and a total of 20 genotypes have been classified (2). Because measles virus genotypes are considered to be associated with geographical location and chronological isolation, it has been considered that a genotype can reveal its own origin and transmission pathway (3). In August 2002, in Osaka City, we isolated a wild type measles virus classified as genotype H1 from a patient. Detailed are provided in this report.

The patient was a 4-month-old girl, a resident of Nishinari-

ku in Osaka City. The virus was transmitted to her from her mother. The virus was isolated in B95a cells from a blood specimen obtained on the sixth day of illness (12 August 2002). The isolated virus was designated MVi/Osaka C.JPN/32.02 according to the WHO nomenclature. For genotyping, a 650 bp fragment including the 3' terminus of the N gene was amplified by RT-PCR. About 550 bp in the PCR amplicon were sequenced directly using an ABI PRISM 310 DNA sequencer (Applied Biosystems, Foster City, Calif., USA), and the 3' terminal 456 nt sequence of the N gene was determined. We constructed a phylogenetic tree using the neighbor-joining method to confirm the genotype of the isolate, using the reference measles virus N gene sequences designated by WHO (the database is available from GenBank). We found that MVi/Osaka C.JPN/32.02 was assigned

*Corresponding author: Tel: +81-6-6771-3147, Fax: +81-6-6772-0676, E-mail: kubo@iphes.city.osaka.jp

genotype H1, represented by Hunan.CHN/93/7 (N gene accession No. AF045212) (Fig. 1). A BLAST2 search (<http://blast.genome.ad.jp/>) based on the 456 nt of the 3' terminal of the N gene revealed a 99.6% homology between our isolate and MVs/WA.AU/30.01. The amino acid sequence was 100% identical between the two. With MVs/Florida.USA/25.00, MVs/NSW.AU/52.00, and MVs/Toronto.CAN/8.01, it shared 98.9% homology, and one amino acid difference was observed.

We have been analyzing the genotypes of wild measles virus isolates as part of Infectious Disease Surveillance in Osaka City since 1997. Until 2001, all isolates were genotype

D3 or D5, which have been considered indigenous to Japan. No other genotypes were detected (4). Regarding isolations of genotype H1 wild type measles virus in Japan, isolates of this genotype were reported from Tokyo and Kawasaki City in 2001 (5). In Osaka City, the present case was the first detected. None of the family members of the infected 4-month-old baby had a history of travel abroad. This background data may suggest that the H1 wild type measles virus was circulating in Osaka City. Though the H1 genotype has been considered indigenous to China and Korea (2), MVi/Osaka C.JPN/32.02 had the highest homology to MVs/

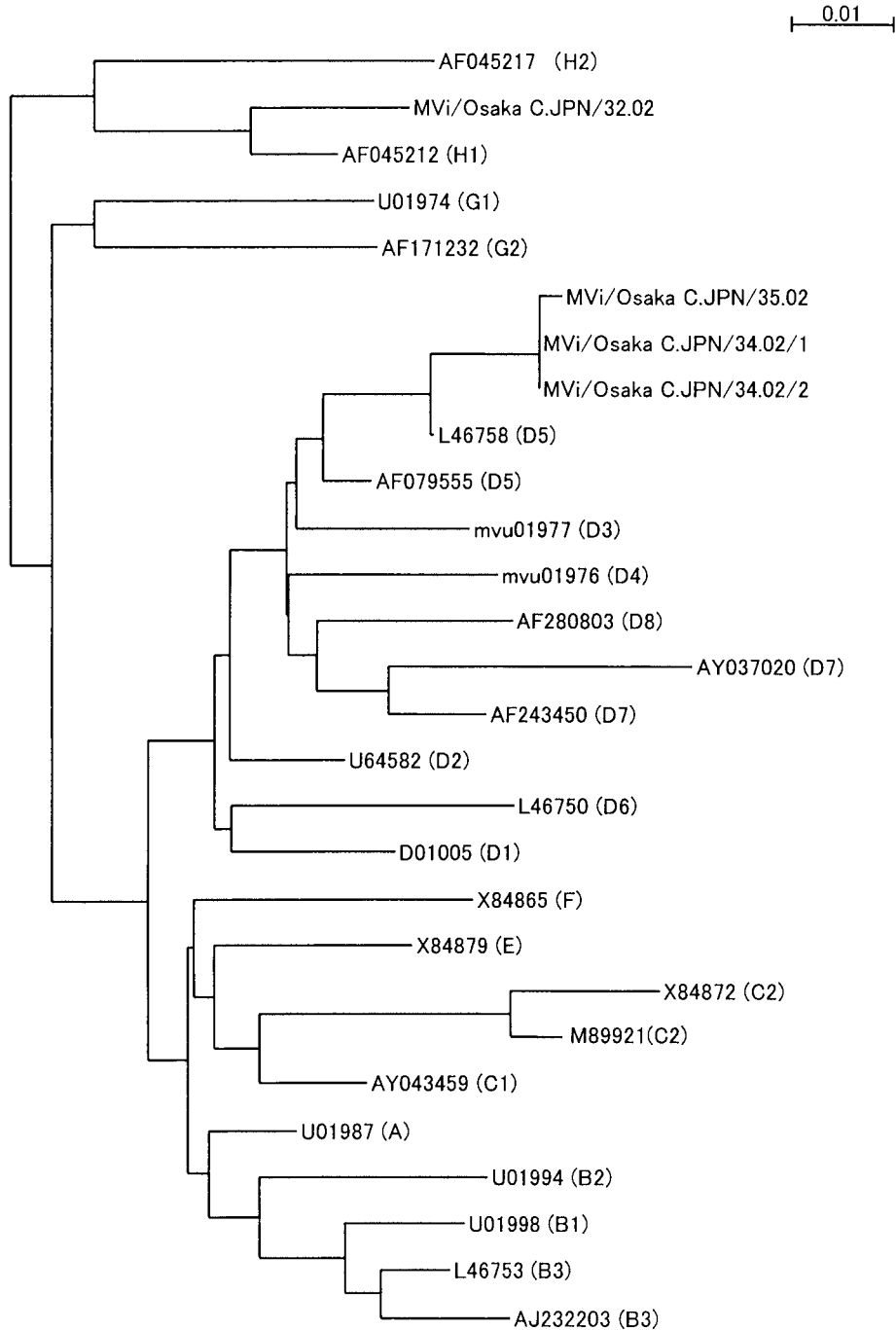


Fig. 1. Phylogenetic analysis of measles viruses based on the nucleotide sequence in the 3' terminal 456 nt of the N gene. Reference strains designated by WHO are indicated by accession number to GenBank. The genotypes are shown in parentheses. In addition to the isolate MVi/Osaka C.JPN/32.02 reported herein, three other strains isolated in Osaka City in 2002, of genotype D5, are also shown.

WA.AU/30.01, a strain detected in Australia in 2001. The next highest homology was to strains identified in the USA and Australia in 2000 and in Canada in 2001. Analyses of the transmission pathway of these measles viruses to such countries and the comparison of sequences among measles viruses, including H1 viruses isolated recently in indigenous countries and MVi/Osaka C.JPN/32.02, will reveal the transmission pathway of the genotype H1 wild type measles virus to Osaka City.

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