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Epidemic of Hand, Foot and Mouth Disease in Kawasaki City, Japan

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Hand, Foot and Mouth Disease (HFMD) is caused by enteroviruses. Group A coxsackievirus type 16 (CA16) and enterovirus type 71 are the most commonly isolated from HFMD cases. In general, epidemic of HFMD occurs in summer. However, an outbreak of this illness was identified for a short period (February and March) over the winter of 2005 in Kawasaki City. This report describes a minor epidemic of HFMD in the Saiwai Ward in Kawasaki City (total area: 10.09 km^2).

According to the National Epidemiological Surveillance of Infectious Diseases of Kawasaki City, the number of patients increased in this area in the 7th week (February 14 - 20 Sentinel), with a subsequent peak in the 12th week (March 21 - 27: 3.25 per sentinel). The epidemic of HFMD ended in the 14th week (April 4 - 10). In total, 41 patients were reported in these 2 months. The age of patients ranged from 0 to 7 years old. The highest incidence was in the group of 3-year-olds (29%; 12 of 41), followed by th group of 2-year-olds (22%; 9 of 41). This was suspected as the outbreak of nursery school. But HFMD patients were spotted in this area.

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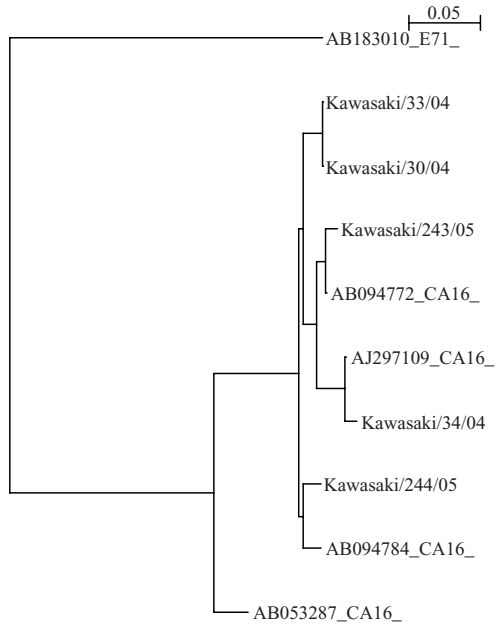

Fig. 1. Phylogenetic of group A coxsackievirus type 16 by neighbor-joining analysis. Kawasaki/243/05, Isolation from a 7-year-old male patient on March 25; Kawasaki/244/05, Isolation from a 2-year-old female patient on March 29; Kawasaki/30/04, Kawasaki/33/04 and Kawasaki/34/04, Isolation on 2004; AB183010_E71_, AB094772_ CA16_, AJ297109_ CA16_, AB094784_CA16_ and AB053287_ CA16_ (accession numbers), They were obtained from DDBJ (DNA Data Bank of Japan).

Throat swabs were collected from a 7-year-old male patient (No. 243) on March 25, and a 2-year-old female patient (No. 244) on March 29. These specimens were propagated on CaCo-2 and Vero cells producing extensive CPE. A neutralization test was performed by a specific antiserum, but serotype was not identified. Therefore, RT-PCR was used to determine their serotypes by sequencing its VP4 region (207 bp). As a result, two viruses were serotyped as CA16. Two viruses differed from 10 nucleotides. The homology of VP4 was 95.2% (Fig. 1).

In conclusion, more than one strain of CA16 was involved in this outbreak.

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