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An Outbreak of Acute Gastroenteritis Caused by Human Group C Rotavirus in a Welfare Institution in Okayama Prefecture

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Rotaviruses are members of the *Reoviridae* family and are recognized as important causative agents of acute gastroenteritis. The genomes of rotaviruses consist of 11 segments

of double-stranded RNA (dsRNA) enclosed in double-shelled particles. Rotaviruses are classified into at least seven groups (groups A-G) on the basis of their dsRNA electropherotypes and a common group antigen on the inner capsid protein (1, 2). Three of these groups (A, B and C) are known to infect humans (1,2). Several outbreaks of acute gastroenteritis caused by human group C rotavirus (CHRV) have been reported in Japan (3-9). Most of these outbreaks occurred in school-aged people aged 6 to 18 years. Generally, an outbreak of CHRV

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gastroenteritis in adults is rather rare (10). Here we report an outbreak of CHR V infection in adults that occurred in a welfare institution.

On 25 December 2004, we received a report of an outbreak of gastroenteritis in a welfare institution located in the northern area of Okayama Prefecture. The outbreak was investigated immediately. Among 233 adults in the institution (149 residents and 84 employees), 24 people (16 residents and 8 employees) aged 34 to 67 years showed symptoms of gastroenteritis. The index case (a resident) developed the disease on December 22, and the outbreak then peaked on December 25 with 8 residents and 3 employees showing symptoms. Thereafter, small numbers of new patients continued to appear until December 31.

Fecal specimens were obtained from two patients on day 2 after the initial appearance of symptoms and were used for electron microscopic (EM) analysis and the detection of the norovirus genome by reverse transcriptase-polymerase chain reaction (RT-PCR) (11). Rotavirus-like particles were detected by EM in the specimen from case 2, but norovirus genome was not detected in either specimen (Table 1). Therefore, the specimens were further examined for the presence of group A rotavirus and CHR V by RT-PCR (9,12). As shown in Table 1, CHR V was detected in both patients but group A rotavirus was not detectable, indicating that this outbreak was caused

by CHR V. The route of the CHR V infection remains unknown because the number of fecal specimens from the patients was limited.

For further epidemiological analysis, the major outer capsid glycoprotein (VP7) genes of CHR V amplified by RT-PCR were directly sequenced. The nucleotide sequence data were analyzed by the GENETYX-MAC version 10 program (Genetyx, Tokyo, Japan), and phylogenetic analysis was performed using the Clustal W program employing the neighbor-joining method with bootstrapping 1,000 times. A comparison of the full-length VP7 genes of the CHR V isolates (AE52 and AE53) from the patients showed that both sequences were identical, suggesting that the outbreak was caused by a single CHR V strain. Phylogenetic analysis using published sequences of CHR V strains isolated in Okayama Prefecture showed that the isolate (AE53) was genetically closely related to the KW408 and OT99 strains (retrieved in 1998 and 1999, respectively) isolated from patients aged 4 and 11 years, respectively (Fig. 1). These results suggest that the present outbreak was caused by a CHR V strain circulating in Okayama Prefecture.

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Table 1. Clinical symptoms in patients with gastroenteritis and detection of viral agents in their fecal specimens

Case No.	Age (years)	Sex	Onset of disease	Clinical symptoms				Laboratory diagnosis for viral agents			
				AP	Diarrhea	N/V	Fever	EM	RT-PCR detection for		
									Norovirus	ARV	CHR V
1	53	F	Dec 27	+	+	+	-	-	-	-	+
2	53	M	Dec 27	+	+	-	-	Rotavirus	-	-	+

AP, abdominal pain; N/V, nausea or vomiting; EM, electron microscopy; ARV, group A rotavirus.

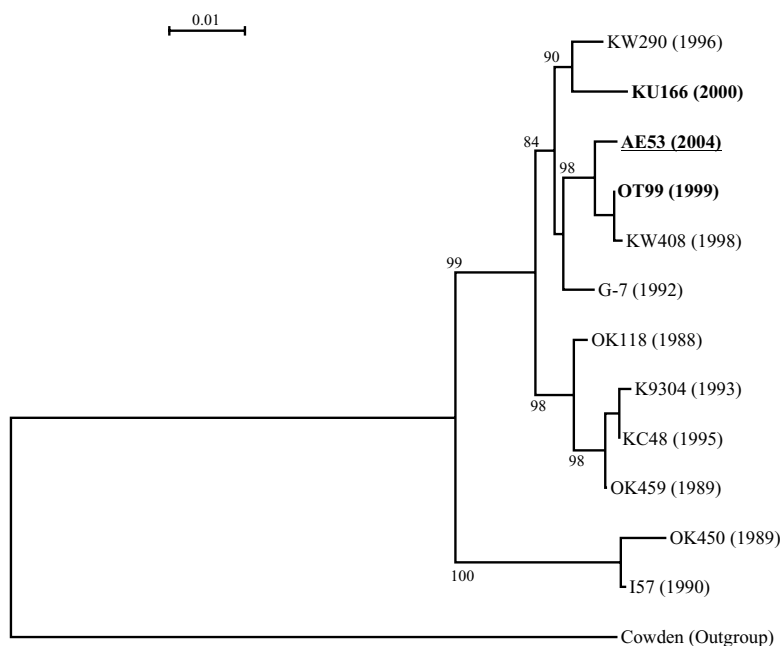


Fig. 1. Phylogenetic analysis of the nucleotide sequences of the VP7 gene of 12 CHR V specimens isolated in Okayama Prefecture (GeneBank accession numbers as follows: D87543, D87544, AB004250, AB086962-086969). The phylogenetic tree was constructed based on the neighbor-joining method with porcine group C rotavirus, Cowden strain (accession number, M61101) as an outgroup. The percentage of bootstrap values is shown at branch node. The scale bar represents a 1% nucleotide difference. The strains isolated from outbreak cases are indicated by boldface, and the isolate (AE53) from the present outbreak is underlined. The year in which each strain was isolated is indicated in parenthesis.

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