

Brief Communication



Outbreak associated with Rotavirus G11,P[25] in Korea in 2018

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Conflict of Interest

No conflicts of interest.

ABSTRACT

We here report the first outbreak caused by rotavirus G11,P[25] in Korea in 2018, representing a case of re-assortment with pig-derived rotavirus. The genotype constellation was identical to the virus identified in Korea in 2012 as G11-P[25]-I12-R1-C1-M1-A1-N1-T1-E1-H1. The infection source was not known exactly but it must be considered infection from swine.

Keywords: Rotavirus G11,P[25]; Pig-derived rotavirus; Genotype constellation; Infection source

Rotavirus is a major pathogen of pediatric diarrhea and causes infections mainly in children under 5 years of age. Sometimes, rotaviruses from pigs and cows were known to cause human infection. In particular, G11 type derived from pig was known to cause recombination with P[6], P[8], and P[25] [1]. Recently, there has been an outbreak caused by rotavirus G11, P[25] recombined with pig-derived rotavirus in Korea. In this study, we investigated the molecular epidemiologic characteristics of outbreak of rotavirus G11, P[25].

Outbreak occurred in junior high school students who completed training at a training center in Geoje-si, Gyeongnam Province, Korea. The number of students was 575 from middle schools located in Gyeongnam Province and Busan Metropolitan City. The training process was carried out 3 days, and clinical symptom were observed 3 days after the training. The main symptoms were diarrhea, vomiting and fever. Cases were defined as cases with diarrhea symptoms more than 3 times a day. According to case definition, the incidence of clinical symptoms was 111 patients (19.3%) of a total of 575 exposed people. The residences in the training center varied from 7 to 20 people, and drinking water was used for chlorinated groundwater. The water tank was able to accommodate 50 tons and was operated by installing one chlorine dispenser, but no additional control was made after installation two years ago. Most of the food was cooked and some unheated foods were provided by the training center (Table 1).

To identify causative pathogens, fecal specimens were collected from the 111 patients and groundwater and preserved foods were collected to keep track of contamination sources. Case-related samples were obtained and analyzed according to the law of infectious disease prevention and management. Therefore, there was no additional IRB review. The pathogens

Author Contributions

Conceptualization: DYL. Writing - Original Draft: SJC. Investigation: SJC, SJ, SRC. Writing - Review & Editing: WC.

Table 1. List of foods consumed by patients during the training

Day	1st	2nd	3rd
Breakfast		Rice	Rice
		Beef Soup	Sea Mustard Soup
		Egg Roll	Fried Pork with kimchi
		Seasoned Laver	Seasoned dried-Laver
		Fried ham and vegetable	Stir-fried Fish Cake
		Kimchi	Kimchi
Lunch		Rice	Rice
		Seafood miso stew	Soybean Paste Soup with Dried Radish Leaves
		Pork Cutlet	Sweet and Sour Pork
		Stir-fried Rice cake	Seasoned Bean Sprouts
		Buttercup herb	Salad with Vegetable and razor-clam Meat
		Kimchi	Kimchi
Dinner	Rice	Rice	
	Tuna Kimchi Stew	Fish Cake Soup	
	Fried vegetables	Stir-fried Anchovies	
	Stir-fried Pork	Chicken Stew	
	Stewed Potatoes	Shredded Daikon	
	Kimchi	Kimchi	

Foods using porks as ingredients are marked in bolded letter.

to be tested were 10 species of bacteria and 5 species of virus, and they were inspected by the local health and environment research institutes in accordance with the “Practical Guidelines for Diagnosis of Waterborne Foodborne Diseases” [2]. Rotavirus was identified by EIA and norovirus was by real-time RT-PCR. In human specimens, 15 cases of rotavirus and 1 case of norovirus were detected, but no pathogen was detected in groundwater and preserved food tests. Rotavirus was confirmed to be non - rotavirus by one sample in the genetic test, and the final 14 cases were determined as positive. Genotyping tests were performed according to the World Health Organization recommended protocol on human specimens confirmed to be rotavirus. All 14 samples were identified as G11, P[25] [3].

The genotypes of eleven gene segments were confirmed by re-extracting nucleic acid from 14 specimens identified as rotavirus G11, P[25]. Genes were amplified for each segment, and the genotype was confirmed by the Rota C v1.0 that web based rotavirus classification tool (<http://rotac.regatools.be>) [4]. The relationship between rotavirus was analyzed by Clustal W using the MEGA v6.0 software (<http://megasoftware.net>). The genotype constellation of rotavirus detected in the outbreak was finally determined as G11-P[25] -I12-R1-C1-M1-A1-N1-T1-E1-H1 (**Table 2**). Above all, VP6 has been identified as genotype I12, similar to other virus identified in Korea in 2012 [5]. However, all the patients reported in the two regions formed the same cluster, but the difference between the cases confirmed in domestic (Hu / CAU12-2, [5]) and the reference gene (Hu / KTM368, [6]) in the relational analysis (**Fig. 1**).

Table 2. Comparison of genomic constellation of human rotavirus, porcine rotavirus and outbreak cases

Strains	VP7	VP4	VP6	VP1	VP2	VP3	NSP1	NSP2	NSP3	NSP4	NSP5	References	
Hu/Wa	G1	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[6]	
Hu/KTM368	G11	P[25]	I12	R1	C1	M1	A1	N1	T1	E1	H1		
Hu/Dhaka6	G11	P[25]	I1	R1	C1	M1	A1	N1	T1	E1	H1		
Hu/Matlab36-02	G11	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1		
Po/YM	G11	P[7]	I5	R1	C1	M1	A8	N1	T1	E1	H1		
Po/Gottfried	G4	P[6]	I1	R1	C1	M1	A8	N1	T1	E1	H1		
Po/OSU	G5	P[7]	I5	R1	C1	M1	A1	N1	T1	E1	H1		
Hu/CAU12-2	G11	P[25]	I12	R1	C1	M1	A1	N1	T1	E1	H1		[5]
BS-18-04-0004	G11	P[25]	I12	R1	C1	M1	A1	N1	T1	E1	H1		In this study

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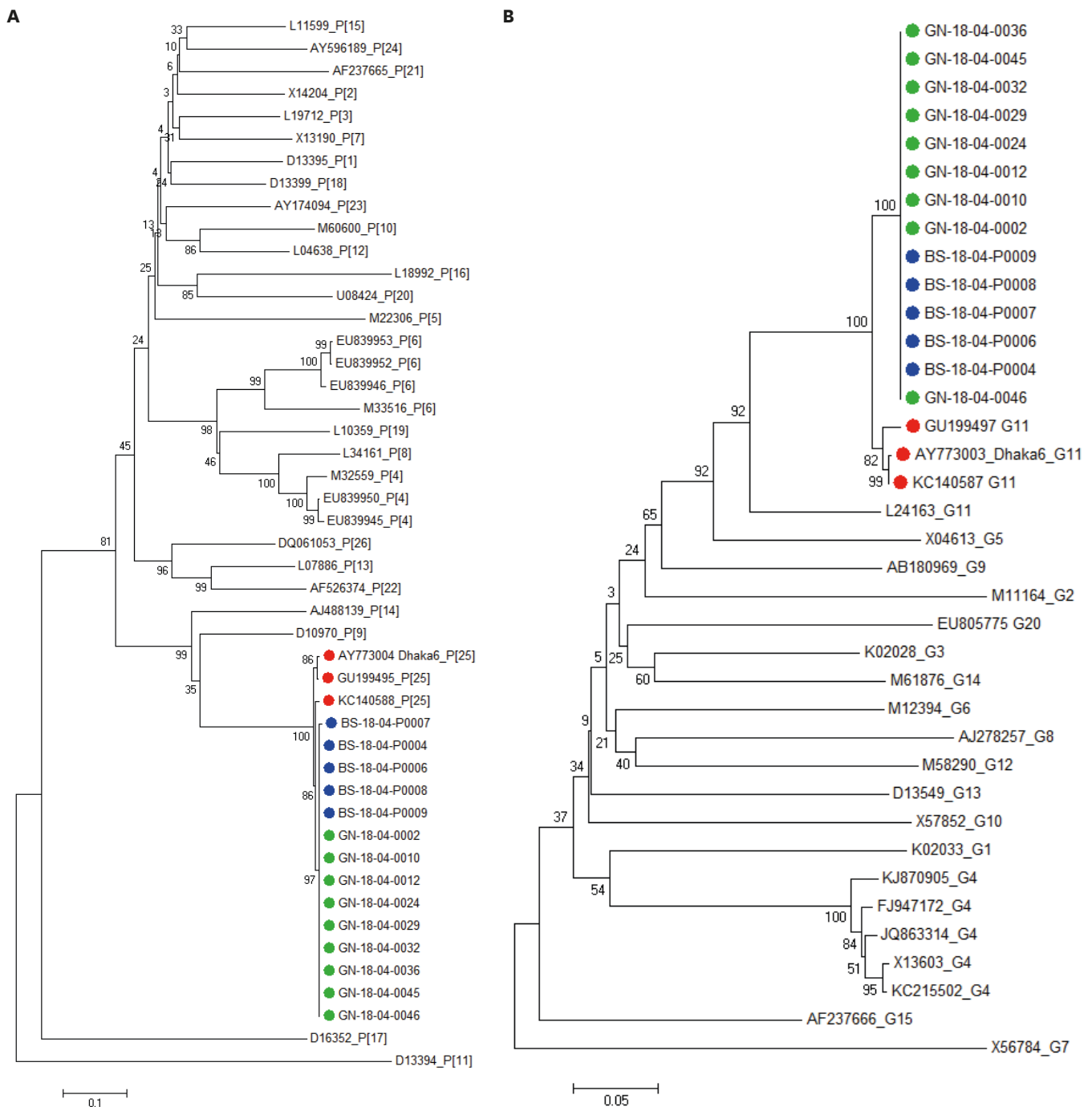


Figure 1. Phylogenetic Analysis of Patients with Rotavirus. Rotaviruses reported in the two regions formed the same cluster, but differ from the reference genes. (A) Phylogenetic tree of VP4, (B) Phylogenetic tree of VP7. Green circle (●), the samples of Gyoungnam region; blue circle (●), the samples of Busan region; Red circle (●), reference genes. KC140588 / KC140587 (2012, Korea), AY773004 / AY773003_Dhaka6 (2001, Dhaka, Bangladesh), GU199495 / GU199497 (2004, Kathmandu, Nepal).

This is the first outbreak case associated with rotavirus G11, P[25] infection, which have been reported only as individual cases. The infection of rotavirus G11, P[25] was first confirmed in a 21-year-old adolescent youth in Dhaka, Bangladesh [7], followed in Nepal [8] and India [9, 10]. In Korea, there was a first case report in the Gwangju region during the acute diarrheal

laboratory surveillance (EnterNet-Korea) [11], and thereafter another case report [5]. There was no report of other infections caused by pig-derived rotavirus other than infection by G11, P[4], which is known to be the same pig-derived rotavirus [1]. All of these were single infected cases.

In the course of the investigation, the possibility of food-borne propagation was considered to be extremely low for most of the food was cooked. However, even though laboratory tests did not detect rotavirus, it is unlikely that the infection caused by pork could be ruled out. Because there were 4 kinds of foods that used pork as a material out of 36 kinds of food that was offered 6 times in total for 3 days. We could not directly prove that the rotavirus was derived from pigs in this study. However, the results of genetic analysis suggest that swine-derived virus such as rotavirus G11,P[25] are likely to be in constant circulation.

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