Genotypes of the circulating rotavirus strains in the seven prevaccine seasons from September 2000 to August 2007 in South Korea

H. S. Jeong[1], K. B. Lee[1], A.-Y. Jeong[1], M. Y. Jo[1], S. Y. Jung[1], J. H. Ahn[1], Y. Jee[1], J. Kim[2] and D.-S. Cheon[1]

1) *Division of Enteric and Hepatitis Viruses, Center for Infectious Diseases, National Institute of Health, Korea Centers for Disease Control and Prevention, Seoul*, 2) *Department of Pediatrics, College of Medicine, Catholic University of Korea, St Vincent Hospital, Suwon, South Korea*

Abstract

A Korean nationwide surveillance on circulating rotavirus strains was conducted from September 2000 to August 2007 aiming to obtain prevaccine data for predicting vaccine effectiveness. The predominant strains among the 2779 strains analyzed varied annually and only approximately 50% had either a G or a P antigen present in both RotaTeq (Merck & Co. Inc., Whitehouse Station, NJ, USA) and Rotarix (GlaxoSmithKline, Brentford, UK).

Keywords: Gastroenteritis, genotype, group A rotavirus, surveillance, vaccination

Original Submission: 15 January 2010; **Revised Submission:** 23 March 2010; **Accepted:** 27 March 2010
Editor: J.-M. Pawlotsky
Article published online: 2 April 2010
Clin Microbiol Infect 2011; **17**: 232–235
10.1111/j.1469-0691.2010.03232.x

Corresponding author: D.-S. Cheon, Division of Enteric and Hepatitis Viruses, Center for Infectious Diseases, National Institute of Health, 5 Nokbun-dong, Eunpyung-gu, Seoul 122-701, South Korea
E-mail: cheonds@hanmail.net

Group A rotaviruses (RV-A) are the leading cause of severe acute gastroenteritis among infants and young children. In developing countries, severe diarrhoea caused by human RV-A results in an estimated 600 000 childhood deaths annually; worldwide, this disease results in 2 million hospitalizations [1–3]. Although the RV-A infection-associated mortality is relatively low in industrialized countries, RV-A diarrhoea remains a major reason for visits to paediatric clinics and emergency departments, as well as inpatient hospitalizations.

Two new RV-A vaccines, Rotarix (GlaxoSmithKline, Brentford, UK) and RotaTeq (Merck & Co. Inc., Whitehouse Station, NJ, USA), have been licensed in approximately 100 countries worldwide and are already part of the national vaccination schedules of several countries [4,5]. RotaTeq, introduced in South Korea (hereafter referred to as Korea) in September 2007, is a pentavalent vaccine constructed by introducing common human RV-A serotype antigen genes (G1–G4, P[8]) into a bovine RV-A parent strain to create five different reassortant strains [4]. Rotarix is a monovalent vaccine based on an attenuated genotype G1P[8] strain that is designed to provide serotype-specific and heterotypic protection against common RV-A serotypes; it was launched in July 2008 in Korea.

RV-A belong to the family *Reoviridae*. Viral particles are nonenveloped, and triple-layered protein capsids enclose the genome of 11 dsRNA segments. The outer layer of the viral capsid is composed of two structural proteins: VP4, a protease-cleaved or P protein, and VP7, a glycoprotein or G protein [1]. These proteins carry the major antigenic determinants, which elicit neutralization antibodies, form the basis for the dual molecular classification scheme that indicates the viral G and P serotypes, and play key roles in the development of protective immunity [1]. Because VP4 and VP7 genes reassort independently from one another during mixed infection, the G and P genotypes are monitored during surveillance studies. Such surveillance studies help to identify the most important strains in circulation before the introduction of RV-A vaccines and to evaluate the effectiveness of the vaccines against the common genotypes.

The Korea Centers for Disease Control and Prevention, in collaboration with 16 laboratories of local public health institutes and participants ($n > 100$) in a sentinel hospital, initiated an agent surveillance system for acute gastroenteritis in 1999.

Faecal samples testing positive for the group A RV-A antigen by antigen-capturing ELISA (IDEIA Rotavirus; Dako Diagnostics, Ely, UK) were collected for genotyping using reverse transcription-PCR, as described previously [6]. From September 2000 until August 2007, faecal samples from 164 081 patients with acute gastroenteritis were analyzed. Of these samples, 19 845 (12%, range 9.1%–15%; 2000–2001 to 2006–2007) were positive for RV-A by ELISA. The peak seasons of RV-A infection were winter and spring, from December to May (Fig. 1). During the first two seasons, the highest number of RV-A infections was detected in April, whereas the peak was in February, and a marked number of infections was detected in May, from the 2002–2003 season onward.

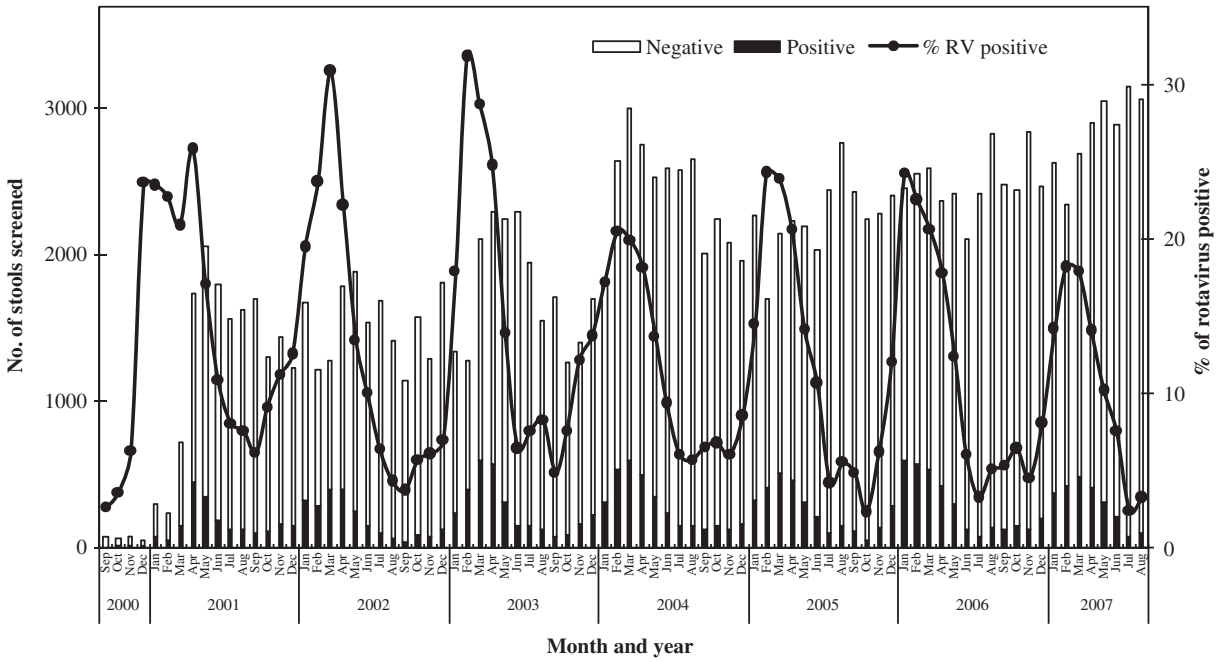

FIG. 1. Temporal distribution of rotavirus infections from September 2000 to August 2007 in South Korea.

Using RT-PCR, we determined the G and P genotypes of 2779 RV-A strains received from around the country. Overall, 23.0% of the strains from the period 2000–2007 were G1P[8], 18.8% were G3P[8], 18.3% were G2P[4] and 15.9% were G4P[6] as the neonatal strain (Table 1); these four strains represented 80.1% of all the strains analyzed. There was considerable genotype diversity among strains, and the incidence of predominant strains fluctuated annually.

In brief, the most common strains were G2P[4] during the first two seasons, G3P[8] from 2002–2003 until

TABLE 1. Distribution of rotavirus genotypes in seven consecutive seasons of rotavirus infection from 2000 to 2007 in South Korea

Strain group, genotype	Number (%) of strains by season of rotavirus infection							
	2000–01 (*n* = 318)	2001–02 (*n* = 463)	2002–03 (*n* = 433)	2003–04 (*n* = 332)	2004–05 (*n* = 399)	2005–06 (*n* = 280)	2006–07 (*n* = 554)	Total (*n* = 2779)
Common human strains	222 (69.81)	316 (68.25)	309 (71.36)	262 (78.92)	274 (68.67)	188 (67.14)	359 (64.80)	1,930 (69.45)
G1P[8]	104 (32.70)	**143 (30.89)**	**79 (18.24)**	39 (11.75)	**52 (13.03)**	**72 (25.71)**	**289 (52.17)**	778 (28.00)
G2P[4]	110 (34.59)	**145 (31.32)**	**54 (12.47)**	62 (18.67)	90 (22.56)	**37 (13.21)**	**11 (1.99)**	509 (18.32)
G3P[8]	6 (1.89)	**13 (2.81)**	**124 (28.64)**	**155 (46.69)**	**108 (27.07)**	71 (25.36)	45 (8.12)	522 (18.78)
G4P[8]	2 (0.63)	11 (2.37)	10 (2.31)	0 (0)	6 (1.50)	1 (0.36)	5 (0.90)	35 (1.26)
G9P[8]	0 (0)	4 (0.86)	**42 (9.70)**	**6 (1.81)**	18 (4.51)	7 (2.50)	9 (1.62)	86 (3.09)
Reassortants common human strains	14 (4.40)	4 (0.86)	1 (0.23)	6 (1.81)	28 (7.02)	9 (3.21)	22 (3.97)	84 (3.02)
G1P[4]	7 (2.20)	2 (0.43)	1 (0.23)	0 (0)	3 (0.75)	3 (1.07)	8 (1.44)	24 (0.86)
G2P[8]	6 (1.89)	1 (0.22)	0 (0)	1 (0.30)	5 (1.25)	1 (0.36)	12 (2.17)	26 (0.94)
G3P[4]	0 (0)	0 (0)	0 (0)	2 (0.60)	10 (2.51)	2 (0.71)	0 (0)	14 (0.50)
G4P[4]	1 (0.31)	1 (0.22)	0 (0)	3 (0.90)	10 (2.51)	3 (1.07)	1 (0.18)	19 (0.68)
G9P[4]	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (0.18)	1 (0.04)
Zoonotic	53 (16.67)	109 (23.54)	108 (24.94)	55 (16.57)	71 (17.79)	55 (19.64)	69 (12.45)	520 (18.71)
G1P[6]	**21 (6.60)**	**6 (1.30)**	3 (0.69)	5 (1.51)	0 (0)	3 (1.07)	1 (0.18)	39 (1.40)
G2P[6]	2 (0.63)	3 (0.65)	2 (0.46)	**0 (0)**	**8 (2.01)**	1 (0.36)	0 (0)	16 (0.58)
G2P[9]	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (0.18)	1 (0.04)
G3P[6]	1 (0.31)	4 (0.86)	2 (0.46)	0 (0)	0 (0)	1 (0.36)	0 (0)	8 (0.29)
G3P[10]	0 (0)	1 (0.22)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (0.04)
G4P[6]	**29 (9.12)**	**86 (18.57)**	**98 (22.63)**	**50 (15.06)**	62 (15.54)	49 (17.50)	67 (12.09)	441 (15.87)
G9P[6]	0 (0)	9 (1.94)	3 (0.69)	0 (0)	0 (0)	1 (0.36)	0 (0)	13 (0.47)
G10P[6]	0 (0)	0 (0)	0 (0)	0 (0)	1 (0.25)	0 (0)	0 (0)	1 (0.04)
Partially typed strains	8 (2.52)	13 (2.80)	2 (0.46)	0 (0)	0 (0)	7 (2.50)	49 (8.84)	79 (2.84)
Mixed types	21 (6.60)	21 (4.54)	13 (3.00)	9 (2.71)	26 (6.52)	21 (7.50)	55 (9.93)	166 (5.97)

Bold indicates a significant ($p < 0.001$) change in the genotype distribution from one year to the next.