Short Communication

Distribution of Rotavirus Genotypes from the 2008/2009 to the 2015/2016 Season in Nara Prefecture, Japan

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SUMMARY: This study was conducted to investigate the distribution of rotavirus genotypes in Nara Prefecture, Japan before and after the introduction of rotavirus vaccination in 2011. Since the 2011/2012 season, DS-1-like G1P[8] strains have been detected in Nara Prefecture, accounting for about half of all strains in the 2014/2015 season. During the 2015/2016 season, no DS-1-like G1P[8] strains were detected; G2P[4] was the predominant genotype.

Group A rotavirus (RVA), a major cause of severe gastroenteritis in infants and young children, poses an important public health issue in Japan. Molecular surveillance of RVA infections has been conducted in Nara Prefecture, Japan since 1999.

Two licensed oral live vaccines have become commercially available in Japan: Rotarix (GlaxoSmithKline Vaccines, Rixensart, Belgium) since 2011, and RotaTeq (Merck and Co. Inc., Whitehouse Station, NJ, USA) since 2012. Although the 2 vaccines have been highly efficacious (1), changes in the distribution of RVA genotypes after introduction of the vaccines have been observed in several countries (2–4). In Japan, DS-1-like G1P[8] strains, regarded as new reassortant strains, have been detected since January 2012 (5,6). Therefore, we investigated the distribution of G and P genotypes of RVA and examined the presence of DS-1-like G1P[8] strains.

Between September 2008 and August 2016, stool samples were collected from patients with acute non-bacterial sporadic gastroenteritis at 13 hospitals in Nara Prefecture. Samples were screened for RVA using a commercial kit (RapidTesta Rota Adeno, Sekisui Medical Co., Ltd., Tokyo, Japan). Genetic analysis was conducted on 449 RVA-positive samples (Table 1).

Viral RNA was extracted, as previously reported (7), and tested for the presence of the VP7 gene using reverse transcription-polymerase chain reaction (RT-PCR; PrimeScript One Step RT-PCR Kit Version 2; Takara Bio Inc., Shiga, Japan) with primers, as previously reported (8). VP7 gene-positive strains were classified into G and P genotypes using a multiplex PCR method, as described in an earlier report (8,9). Strains that were classified as G1P[8] were tested to determine whether they were Wa-like strains or DS-1-like strains. According to the manual of rotavirus detection published by the National Institute of Infectious Diseases of Japan (NIID), after reverse transcription reaction, PCR was performed with a forward primer, NSP5F (5’-GGCTTTTAAAGCGCTACAGT-3’) and a reverse primer, NSP5R (5’-GGTCACAAAAACGGAGTGAGGA-3’) (10), under the following thermal cycling conditions: 35 cycles of 10 s at 98°C, 15 s at 55°C, 45 s at 68°C, and 3 min at 68°C. The genotype of the NSP5 gene was determined according to the size of the PCR product (Fig. 1). The VP6 genes of some strains classified as DS-1-like G1P[8] were assigned to genotype I2 by sequencing. PCR was performed using the primer pair VP6F and VP6R (10), and PCR amplicons were separated by 1.5% agarose gel electrophoresis and purified using the NucleoSpin Extract II Kit (Takara Bio Inc.). The purified amplicons were used as templates for direct sequencing. Sequencing of the purified amplicons was performed using the BigDye Terminator Cycle Sequencing Kit and 310 Genetic Analyzer System (Applied Biosystems, Foster City, CA, USA).

The distributions of genotypes for 8 seasons are shown in Table 2. Since the 2011/2012 epidemiological season, DS-1-like G1P[8] strains were detected in Nara Prefecture, accounting for about half of all strains in the 2014/2015 season. During the 2015/2016 season, no DS-1-like G1P[8] strains were detected; G2P[4] was the predominant genotype.

Fig. 1. PCR typing of NSP5 genes. Lanes 1. molecular weight markers; 2, 3. Wa like strains (H1:663 bp); 4, 5. DS-1 like strains (H2: 816 bp).
Prefecture. These accounted for about half of all strains in the 2014/2015 season. During the 2015/2016 season, no DS-1-like G1P[8] strains were detected; G2P[4] was the predominant genotype (96.1%).

We investigated the diversity of G and P genotypes of RVAs detected from the 2008/2009 to the 2015/2016 season in Nara Prefecture and detected DS-1-like G1P[8] strains. Since 5 DS-1-like G1P[8] strains were first detected during the 2011/2012 season, DS-1-like G1P[8] strains were detected every season. During the 2014/2015 season, the DS-1-like G1P[8] strain became the predominant genotype. During the 2015/2016 season, the predominant genotype was G2P[4], which is the DS-1-like genotype constellation (11). In Nara Prefecture, 2015/2016 was the first season during which G2P[4] was the predominant genotype since 1999 (data not shown).

Incidentally, the number of samples is dependent on the epidemic prevalence rate of rotavirus infection and interest level of pediatricians. There was a temporary decline in rotavirus-positive samples in the 2013/14 season.

In high-income countries, both rotavirus vaccines have shown high effectiveness (1). Nevertheless, the constellation of G/P genotypes reportedly changed after the introduction of RVA vaccines in Brazil, Belgium, and Australia (2–4). In Japan, after introduction of the monovalent vaccine in 2011, emergence of DS-1-like G1P[8] strains, regarded as new reassortant strains, was a concern among many pediatricians. A possibility exists of continuous detection of predominantly G2P[4] over the next few years in Japan, which has occurred in Brazil and Belgium. Further studies must be undertaken to survey the emergence of such unusual RVA strains and changes in the distribution of RVA genotypes.

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Conflict of interest None to declare.

REFERENCES