Short Communication

Characterization of an Unusual DS-1-Like G8P[8] Rotavirus Strain from Japan in 2017: Evolution of Emerging DS-1-Like G8P[8] Strains through Reassortment

Hajime Kamiya¹, Ratana Tacharoenmuang^{2,3}, Tomihiko Ide², Manami Negoro⁴, Takaaki Tanaka⁵, Kazutoyo Asada⁶, Haruna Nakamura⁶, Katsumi Sugiura⁶, Masakazu Umemoto⁷, Haruo Kuroki⁸, Hiroaki Ito⁹, Shigeki Tanaka¹⁰, Mitsue Ito¹¹, Saori Fukuda², Riona Hatazawa², Yuya Hara², Ratigorn Guntapong³, Takayuki Murata², Kiyosu Taniguchi⁶, Shigeru Suga⁶, Takashi Nakano⁵, Koki Taniguchi², and Satoshi Komoto^{2*}

¹Infectious Disease Surveillance Center, National Institute of Infectious Diseases, Tokyo 162-8640;

²Department of Virology and Parasitology, Fujita Health University School of Medicine, Aichi 470-1192, Japan; ³National Institute of Health, Department of Medical Sciences, Nonthaburi, Thailand;

⁴Institute for Clinical Research and ⁶Department of Pediatrics, National Mie Hospital, Mie 514-0125;

⁵Department of Pediatrics, Kawasaki Medical School, Okayama 700-8505;

⁷Umemoto Children's Clinic, Mie 514-0004; ⁸Sotobo Children's Clinic, Chiba 299-4503;

⁹Department of Pediatrics, Kameda Medical Center, Chiba 296-8602;

¹⁰Department of Pediatrics, Mie Chuo Medical Center, Mie 514-1101; and ¹¹Department of Pediatrics, Japanese Red Cross Ise Hospital, Mie 516-8512, Japan

SUMMARY: The emergence of unusual DS-1-like intergenogroup reassortant rotaviruses with a bovine-like G8 genotype (DS-1-like G8P[8] strains) has been reported in several Asian countries. During the rotavirus surveillance program in Japan in 2017, a DS-1-like G8P[8] strain (RVA/Human-wt/JPN/SO1162/2017/G8P[8]) was identified in 43 rotavirus-positive stool samples. Strain SO1162 was shown to have a unique genotype constellation, including genes from both genogroup 1 and 2: G8-P[8]-I2-R2-C2-M2-A2-N2-T2-E2-H2. Phylogenetic analysis revealed that the VP1 gene of strain SO1162 appeared to have originated from DS-1-like G1P[8] strains from Thailand and Vietnam, while the remaining 10 genes were closely related to those of previously reported DS-1-like G8P[8] strains. Thus, SO1162 was suggested to be a reassortant strain that acquired the VP1 gene from Southeast Asian DS-1-like G1P[8] strains on the genetic background of co-circulating DS-1-like G8P[8] strains. Our findings provide important insights into the evolutionary dynamics of emerging DS-1-like G8P[8] strains.

Rotavirus A (RVA), a member of the genus *Rotavirus* and family *Reoviridae*, comprises an 11-segment RNA genome encoding 6 structural proteins (VP1–VP4, VP6, and VP7) and 6 non-structural proteins (NSP1–NSP6). Majority of the human RVAs have genes with sequences similar to those of the prototype human strain Wa (genogroup 1) or DS-1 (genogroup 2) gene. Wa-like strains are characterized by the non-G/P genotype I1-R1-C1-M1-A1-N1-T1-E1-H1 and tend to possess G/P genotypes G1P[8], G3P[8], G4P[8], G9P[8], and G12P[8]. In contrast, DS-1-like strains are characterized by the non-G/P genotype I2-R2-C2-M2-A2-N2-T2-E2-H2 and tend to have the G/P genotype G2P[4] (1). The rapid emergence and spread of novel intergenogroup reassortant strains have recently been reported in several countries (2). Of these, DS-1-like G8P[8] strains with bovine-like G8 genotypes have recently emerged as major strains in Thailand, Vietnam, and Japan in Asia (3–7).

The first DS-1-like G8P[8] strains were identified in children with severe diarrhea in Thailand in 2013 (3,6,7), with others subsequently detected in Vietnam and Hokkaido Prefecture, the main northern island of Japan, in 2014 (4,5). Furthermore, in 2017 we identified a DS-1-like G8P[8] strain (RVA/Human-wt/JPN/SO1162/2017/G8P[8]) in Chiba Prefecture, Japan. To the best of our knowledge, strain SO1162 is one of the first DS-1-like G8P[8] strains to have emerged on the main island of Japan.

Here, we report the full genome of strain SO1162 isolated from a 32-month-old diarrheic child during an epidemiological study carried out in Chiba, Mie, and Okayama Prefectures of Japan in 2017, in which a total of 43 RVA-positive stool samples were examined. In the 43 samples, G9P[8] ($n = 24$), G2P[4] ($n = 6$), G3P[8] ($n = 5$), G2P[8] ($n = 4$), G1P[8] ($n = 3$), and G8P[8] ($n = 1$) genotypes were identified. The diarrheic child had been admitted to Sotobo Children's Clinic in Chiba Prefecture for severe acute gastroenteritis characterized by watery or loose non-bloody diarrhea and vomiting, and had received the RV5 vaccination. This study was approved by the review boards of National Mie Hospital [28–33] and Fujita Health University (HM18-019). Viral RNA extraction, cDNA library building, and Illumina MiSeq sequencing were performed as reported previously (2,8). Briefly, a 200 bp fragment library ligated with bar-coded adapters was constructed using a

Received November 20, 2018. Accepted February 4, 2019.

J-STAGE Advance Publication February 28, 2019.

DOI: 10.7883/yoken.JJID.2018.484

*Corresponding author: Mailing address: Department of Virology and Parasitology, Fujita Health University School of Medicine, Aichi 470-1192, Japan. Tel: +81-562-93-2486, Fax: +81-562-93-2649, E-mail: satoshik@fujita-hu.ac.jp

Evolution of DS-1-Like G8P[8] Rotaviruses in Japan

Table 1. Genotypes of the 11 gene segments of a Japanese DS-1-like G8P[8] strain SO1162 compared with those of selected human and animal strains with known genomic constellations

Strain	Genotype										
	VP7	VP4	VP6	VP1	VP2	VP3	NSP1	NSP2	NSP3	NSP4	NSP5
RVA/Human-wt/JPN/SO1162/2017/G8P[8]	G8	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/THA/PCB-79/2013/G8P[8]</i>	G8	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/THA/CMH-S016-13/2013/G8P[8]</i>	G8	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/THA/NP-130/2014/G8P[8]</i>	G8	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/VNM/RVN1149/2014/G8P[8]</i>	G8	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/JPN/To14-0/2014/G8P[8]</i>	G8	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/JPN/HC12016/2012/G1P[8]*</i>	G1	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/JPN/NT004/2012/G1P[8]*</i>	G1	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/VNM/SP071/2012/G1P[8]*</i>	G1	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/PHL/TGO12-016/2012/G1P[8]*</i>	G1	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/MWI/BID1KS/2013/G1P[8]*</i>	G1	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/THA/SKT-109/2013/G1P[8]*</i>	G1	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/VNM/16020_92/2014/G1P[8]*</i>	G1	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/THA/LS-04/2013/G2P[8]*</i>	G2	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/AUS/D388/2013/G3P[8]*</i>	G3	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/THA/SKT-281/2013/G3P[8]*</i>	G3	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/JPN/15R429/2015/G3P[8]*</i>	G3	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/USA/3000390639/2015/G3P[8]*</i>	G3	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/HUN/ERN8263/2015/G3P[8]*</i>	G3	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/JPN/IS1078/2015/G3P[8]*</i>	G3	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/IDN/SOEP003/2015/G3P[8]*</i>	G3	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/ESP/SS98244047/2015/G3P[8]*</i>	G3	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/BRA/AM-16-31/2016/G3P[8]*</i>	G3	P[8]	I2	R2	C2	M2	A2	N1	T2	E2	H2
<i>RVA/Human-wt/DEU/GER34-16/2016/G3P[8]*</i>	G3	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/JPN/IS1090/2016/G3P[8]*</i>	G3	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-tc/JPN/KU/1974/G1P[8]</i>	G1	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1
<i>RVA/Human-tc/USA/Wa/1974/G1P[8]</i>	G1	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1
<i>RVA/Human-wt/THA/CU956-KK/2011/G1P[8]</i>	G1	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1
<i>RVA/Human-wt/THA/CU957-KK/2011/G1P[8]</i>	G1	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1
<i>RVA/Human-wt/THA/PCB-118/2013/G1P[8]</i>	G1	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1
<i>RVA/Human-wt/THA/SKT-98/2013/G1P[8]</i>	G1	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1
<i>RVA/Human-tc/USA/DS-1/1976/G2P[4]</i>	G2	P[4]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/AUS/CK20055/2010/G2P[4]</i>	G2	P[4]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/AUS/CK20048/2011/G2P[4]</i>	G2	P[4]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/THA/BD-20/2013/G2P[4]</i>	G2	P[4]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/THA/NP-M51/2013/G2P[4]</i>	G2	P[4]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/THA/SKT-138/2013/G2P[4]</i>	G2	P[4]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/HUN/ERN5523/2012/G3P[4]</i>	G3	P[4]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/JPN/S13-30/2013/G3P[4]</i>	G3	P[4]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-wt/JPN/S13-45/2013/G3P[4]</i>	G3	P[4]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-tc/USA/P/1974/G3P[8]</i>	G3	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1
<i>RVA/Human-tc/USA/DC23/1976/G3P[8]</i>	G3	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1
<i>RVA/Human-tc/JPN/YO/1977/G3P[8]</i>	G3	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1
<i>RVA/Human-wt/CHN/R1604/2011/G3P[8]</i>	G3	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1
<i>RVA/Cow-tc/USA/NCDV/1967/G6P[1]</i>	G6	P[1]	I2	R2	C2	M2	A3	N2	T6	E2	H3
<i>RVA/Cow-tc/GBR/UK/1973/G6P[5]</i>	G6	P[5]	I2	R2	C2	M2	A3	N2	T7	E2	H3
<i>RVA/Cow-tc/USA/WC3/1981/G6P[5]</i>	G6	P[5]	I2	R2	C2	M2	A3	N2	T6	E2	H3
<i>RVA/Cow-wt/ZAF/1604/2007/G8P[1]</i>	G8	P[1]	I2	R2	C2	M2	A3	N2	T6	E2	H3
<i>RVA/Human-tc/JPN/AU109/1994/G8P[4]</i>	G8	P[4]	I2	R2	C2	M2	A2	N2	T2	E2	H3
<i>RVA/Human-wt/GHA/GH018/2008/G8P[6]</i>	G8	P[6]	I2	R2	C2	M2	A2	N2	T2	E2	H3
<i>RVA/Human-tc/JPN/AU109/1994/G8P[4]</i>	G8	P[4]	I2	R2	C2	M2	A2	N2	T2	E2	H3
<i>RVA/Human-wt/COD/DRC88/2003/G8P[8]</i>	G8	P[6]	I2	R2	C2	M2	A2	N2	T2	E2	H2
<i>RVA/Human-tc/IDN/69M/1980/G8P[10]</i>	G8	P[10]	I2	R2	C2	M2	A2	N2	T2	E2	H2

Strain SO1162 is shown in bold, while the other DS-1-like G8P[8] strains are shown in italic.

Asterisk indicate other DS-1-like intergenogroup reassortant strains.

Gray shading indicates the gene segments with genotypes identical to those of strain SO1162.

NEBNext Ultra RNA Library Prep Kit for Illumina v1.2 (New England Biolabs, Ipswich, MA, USA) according to the manufacturer's instructions. Library purification was performed using Agencourt AMPure XP magnetic beads (Beckman Coulter, Brea, CA, USA). After assessing the quality and quantity of the purified cDNA library, nucleotide sequencing was performed with an Illumina MiSeq sequencer (Illumina) using a MiSeq Reagent Kit v2 (Illumina) to generate 151 paired-end reads. Data analysis was performed using CLC Genomics Workbench v8.0.1 (CLC Bio, Aarhus, Denmark) and contigs were assembled from the obtained sequence reads by de novo assembly. The contigs included RVA sequences and other sequences, such as human and bacterial sequences. Using the assembled contigs as query sequences, the Basic Local Alignment Search Tool (BLAST) non-redundant nucleotide database was searched to determine the nucleotide sequence of each gene segment of strain SO1162. Complete or nearly complete nucleotide sequences of all the genes from strain SO1162 were obtained (Table 1). Because strain SO1162 was sequenced at low coverage using MiSeq, presumably due to a low viral load in the original stool sample, the obtained sequence information for all 11 gene segments of strain SO1162 was confirmed by Sanger sequencing of the RT-PCR products using specific primers (9). Sanger sequencing found that strain SO1162 possessed the MiSeq-determined nucleotide sequences (data not shown). The nucleotide sequence data for strain SO1162 were deposited in the DDBJ and EMBL/GenBank data libraries. The accession numbers for the nucleotide sequences of the VP1-VP4, VP6, VP7, and NSP1-NSP5 genes of strain SO1162 are LC386065-LC386075.

The genotype of each gene of strain SO1162 was determined using the RotaC v2.0 automated genotyping tool (10). The 11 genes of strain SO1162 were found to be G8-P[8]-I2-R2-C2-M2-A2-N2-T2-E2-H2 (Table 1). Except for the G genotype, strain SO1162 exhibited a unique genotype constellation (P[8]-I2-R2-C2-M2-A2-N2-T2-E2-H2), which is commonly found in DS-1-like intergenogroup reassortant strains (2,4–6) (Table 1).

Strain SO1162 was further characterized by constructing phylogenetic trees. Multiple sequence

alignment of each segment was performed using ClustalW, and maximum-likelihood phylogenetic trees were constructed using the Jukes-Cantor substitution model in MEGA7.0.26 (11). The best substitution models for the 11 genes were selected based on the corrected Akaike information criterion value as implemented in MEGA7.0.26. The reliability of the branching order was estimated from 1,000 bootstrap replicates. The nucleotide sequence identities between each gene segment of strain SO1162 and close strain(s) are shown in Table 2. The VP1 gene of strain SO1162 exhibited the highest nucleotide sequence identity (99.7%) with the Vietnamese DS-1-like G1P[8] strain 16020_92 (12) (Table 2), and comparable identity (99.5%–99.6%) with the Thai DS-1-like G1P[8] strains (PCB-180, SKT-109, and SSKT-41) (13) and Vietnamese DS-1-like G1P[8] strains (16020_72 and 16020_80) (12) (data not shown). On the other hand, the VP1 gene of strain SO1162 showed somewhat lower identity (99.0%–99.4%) with DS-1-like G1/3P[8] strains from Hungary, Japan, Spain, and the United States (data not shown). Phylogenetically, the VP1 gene of strain SO1162 was found to be closely related with the above-mentioned DS-1-like G1P[8] strains from Thailand and Vietnam, Southeast Asia, and further from the cluster comprising the other DS-1-like G8P[8] strains (Fig. 1), while the remaining 10 genes were closely related to those of previously reported DS-1-like G8P[8] strains (data not shown).

In summary, all 11 genes of strain SO1162 clustered with the genes of DS-1-like intergenogroup reassortant strains. However, the VP1 gene of strain SO1162 differed significantly from that of other previously described DS-1-like G8P[8] strains which form a distant cluster from most of the DS-1-like G1/3P[8] strains. This suggests that Southeast Asian DS-1-like G1P[8] strains may have donated their VP1 gene to co-circulating DS-1-like G8P[8] strains, resulting in the generation of a novel DS-1-like G8P[8] strain, SO1162. Conversely, the other 10 genes showed significant genetic identity ($\geq 99.4\%$) with those of the previously detected DS-1-like G8P[8] strains, indicating that these DS-1-like G8P[8] strains derived from a common ancestor. Regarding DS-1-like G8P[8] strains, it has been

Table 2. Nucleotide sequence identity between strain SO1162 and close strain(s) in each gene segment

Gene	Strains which exhibit close nucleotide sequence identities in the BLAST database	% identity	Reference
VP7	RVA/Human-wt/VNM/RVN1149/2014/G8P[8]	99.7	(4)
VP4	RVA/Human-wt/THA/SKT-109/2013/G1P[8]	99.5	(12)
VP6	RVA/Human-wt/VNM/RVN1149/2014/G8P[8]	99.4	(4)
VP1	RVA/Human-wt/VNM/16020_92/2014/G1P[8]	99.7	(13)
VP2	RVA/Human-wt/THA/PCB-79/2013/G8P[8]	99.5	(6)
VP3	RVA/Human-wt/THA/NP-130/2014/G8P[8]	99.6	(6)
	RVA/Human-wt/JPN/To14-0/2014/G8P[8]	99.6	(5)
NSP1	RVA/Human-wt/THA/PCB-79/2013/G8P[8]	99.8	(6)
NSP2	RVA/Human-wt/VNM/RVN1149/2014/G8P[8]	99.8	(4)
NSP3	RVA/Human-wt/VNM/RVN1149/2014/G8P[8]	99.7	(4)
NSP4	RVA/Human-wt/THA/NP-130/2014/G8P[8]	99.7	(6)
NSP5	RVA/Human-wt/JPN/NT004/2012/G1P[8]	99.7	(14)

Evolution of DS-1-Like G8P[8] Rotaviruses in Japan

Fig. 1. Phylogenetic tree constructed from the nucleotide sequences of the R2-VP1 genes of strain SO1162 and representative RVA strains. The position of strain SO1162 is shown by filled circle, while those of the other DS-1-like G8P[8] strains are shown by open circle. Asterisks indicate other DS-1-like intergenogroup reassortant strains. Bootstrap values of < 75% are not shown. Scale bar: 0.05 substitutions per nucleotide.

suggested that the reassortment event that generated these strains occurred in Asia before their import into Japan because the bovine-like VP7 genes of DS-1-like G8P[8] strains have a close relationship with Asian, not Japanese, bovine and bovine-like human strains (5,6). Thus, the suspected ancestral DS-1-like G8P[8] strain of strain SO1162 might also have been imported into Japan from areas of Asia such as Thailand and Vietnam. It should be noted that an outbreak of G8P[8] strains in central Japan in 2017 was reported by Shizuoka Prefecture very recently (15). Although a full genomic analysis was not performed in this study, 3 genes from the outbreak strains (VP7, VP4, and VP6) exhibited the genotype constellation G8-P[8]-I2, indicating the possibility of a common origin with strain SO1162.

Acknowledgments Space limitations preclude the inclusion as authors of the following members of the Rotavirus Epidemiology Study Group: Drs. Toshiaki Ihara and Takao Fujisawa, and Ms. Maiko Kinoshita (National Mie Hospital), Dr. Masaru Ido (Mie Chuo Medical Center), and Drs. Masamune Higashikawa, Takashi Fujiwara, and Ryoji Ichimi (Japanese Red Cross Ise Hospital). This study was supported in part by the Research on Regulatory Science of Pharmaceuticals and Medical Devices from the Japan Agency for Medical Research and Development (17fk0108215h0002), AMED (SK).

Conflict of interest TN received honoraria from Daiichi Sankyo Co., Sanofi K.K., Mitsubishi Tanabe Pharma Corporation, and Astellas Pharma Inc.

REFERENCES

- Matthijnssens J, Ciarlet M, Heiman E, et al. Full genome-based classification of rotaviruses reveals a common origin between human Wa-like and porcine rotavirus strains and human DS-1-like and bovine rotavirus strains. *J Virol*. 2008;82:3204-19.
- Komoto S, Ide T, Negoro M, et al. Characterization of unusual DS-1-like G3P[8] rotavirus strains in children with diarrhea in Japan. *J Med Virol*. 2018;90:890-8.
- Guntapong R, Tacharoenmuang R, Singchai P, et al. Predominant prevalence of human rotaviruses with the G1P[8] and G8P[8] genotypes with a short RNA profile in 2013 and 2014 in Sukhothai and Phetchaboon provinces, Thailand. *J Med Virol*. 2017;89:615-20.
- Hoa-Tran TN, Nakagomi T, Vu HM, et al. Abrupt emergence and predominance in Vietnam of rotavirus A strains possessing a bovine-like G8 on a DS-1-like background. *Arch Virol*. 2016;161:479-82.
- Kondo K, Tsugawa T, Ono M, et al. Clinical and molecular characteristics of human rotavirus G8P[8] outbreak strain, Japan, 2014. *Emerg Infect Dis*. 2017;23:968-72.
- Tacharoenmuang R, Komoto S, Guntapong R, et al. Full genome characterization of novel DS-1-like G8P[8] rotavirus strains that have emerged in Thailand: reassortment of bovine and human rotavirus gene segments in emerging DS-1-like intergenogroup reassortant strains. *PLoS One*. 2016;11:e0165826.
- Yodmeeklin A, Khamrin P, Kumthip K, et al. Increasing predominance of G8P[8] species A rotaviruses in children admitted to hospital with acute gastroenteritis in Thailand, 2010–2013. *Arch Virol*. 2018;163:2165-78.
- Dennis FE, Fujii Y, Haga K, et al. Identification of novel Ghanaian G8P[6] human-bovine reassortant rotavirus strain by next generation sequencing. *PLoS One*. 2014;9:e100699.
- Komoto S, Wandera Apondi E, Shah M, et al. Whole genomic analysis of human G12P[6] and G12P[8] rotavirus strains that have emerged in Kenya: identification of porcine-like NSP4 genes. *Infect Genet Evol*. 2014;27:277-93.
- Maes P, Matthijnssens J, Rahman M, et al. RotaC: a web-based tool for the complete genome classification of group A rotaviruses. *BMC Microbiol*. 2009;9:238.
- Kumar S, Stecher G, Tamura K. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Mol Biol Evol*. 2016;33:1870-4.
- Phan MVT, Anh PH, Cuong NV, et al. Unbiased whole-genome deep sequencing of human and porcine stool samples reveals circulation of multiple groups of rotaviruses and a putative zoonotic infection. *Virus Evol*. 2016;2:vew027.
- Komoto S, Tacharoenmuang R, Guntapong R, et al. Emergence and characterization of unusual DS-1-like G1P[8] rotavirus strains in children with diarrhea in Thailand. *PLoS One*. 2015;10:e0141739.
- Fujii Y, Nakagomi T, Nishimura N, et al. Spread and predominance in Japan of novel G1P[8] double-reassortant rotavirus strains possessing a DS-1-like genotype constellation typical of G2P[4] strains. *Infect Genet Evol*. 2014;28:426-33.
- Hoque SA, Kobayashi M, Takanashi S, et al. Role of rotavirus vaccination on an emerging G8P[8] rotavirus strain causing an outbreak in central Japan. *Vaccine*. 2018;36:43-9.