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ORIGINAL ARTICLE

Uniformity of rotavirus strain nomenclature proposed by the Rotavirus Classification Working Group (RCWG)

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Abstract In April 2008, a nucleotide-sequence-based, complete genome classification system was developed for group A rotaviruses (RVs). This system assigns a specific genotype to each of the 11 genome segments of a particular RV strain according to established nucleotide percent cutoff values. Using this approach, the genome of individual RV strains are given the complete descriptor of Gx-P[x]-Ix-Rx-Cx-Mx-Ax-Nx-Tx-Ex-Hx. The Rotavirus Classification Working Group (RCWG) was formed by scientists in the field to maintain, evaluate and develop the RV genotype classification system, in particular to aid in the designation of new genotypes. Since its conception, the group has ratified 51 new genotypes: as of April 2011, new genotypes for VP7 (G20-G27), VP4 (P[28]-P[35]), VP6 (I12-I16), VP1 (R5-R9), VP2 (C6-C9), VP3 (M7-M8), NSP1 (A15-A16), NSP2 (N6-N9), NSP3 (T8-T12), NSP4 (E12-E14) and NSP5/6 (H7-H11) have been defined for RV strains recovered from humans, cows, pigs, horses, mice, South American camelids (guanaco), chickens, turkeys, pheasants, bats and a sugar glider. With

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increasing numbers of complete RV genome sequences becoming available, a standardized RV strain nomenclature system is needed, and the RCWG proposes that individual RV strains are named as follows: RV group/species of origin/country of identification/common name/year of identification/G- and P-type. In collaboration with the National Center for Biotechnology Information (NCBI), the RCWG is also working on developing a RV-specific resource for the deposition of nucleotide sequences. This resource will provide useful information regarding RV strains, including, but not limited to, the individual gene genotypes and epidemiological and clinical information. Together, the proposed nomenclature system and the NCBI RV resource will offer highly useful tools for investigators to search for, retrieve, and analyze the ever-growing volume of RV genomic data.

Introduction

Rotaviruses (RVs) are members of the family *Reoviridae* and cause severe diarrheal illness in the young of various animal species [25]. In humans, RV infections lead to the death of more than 500,000 infants and young children each year, particularly in developing regions of the world [72]. RVs possess a genome consisting of 11 segments of double-stranded (ds) RNA [25]. Most segments encode a single polypeptide, allowing the virus to express six structural viral proteins (VPs) and five non-structural proteins (NSPs) [25]. However, in some group A RV strains, a second open reading frame (ORF) is detected in genome segment 11, leading to the expression of another protein product (NSP6) [35] in addition to NSP5. The viral particle has icosahedral symmetry and is composed of three concentric protein layers [25, 65]. VP7 and VP4 are the components of the outermost protein layer (outer capsid), and each carries neutralizing epitopes [25]. The middle protein layer (inner capsid) is composed of VP6 and surrounds the inner layer (the core shell), which is composed of VP2 [65]. Packaged within the core shell are the viral RNA-dependent RNA polymerase (VP1) and RNA capping enzyme (VP3), as well as the 11 dsRNA genome segments [25]. The RV NSPs have various functions in the replication and morphogenesis of RV progeny and in evasion of the host immune response [25]. Based on the antigenic properties of VP6, RVs have been subdivided into five serological species (A-E) and two additional tentative species (F and G) according to the International Committee on Taxonomy of Viruses (ICTV) [4, 79]. These "RV species" are commonly referred to as "RV groups". RVs belonging to species A, B and C (RVA, RVB and RVC, respectively) are known to infect humans and various animals, whereas RVs of species D, E, F and G (RVD, RVE, RVF and RVG, respectively) thus far have only been recovered from animals, mostly birds [4, 61]. Epidemiologically, RVA is the most important for human infection and disease and has been classified further using various approaches. Specifically, RVA strains have been categorized based on (i) the antigenic properties of VP6, VP7 and VP4 (subgroups, G-serotypes and P-serotypes, respectively); (ii) the migration pattern of the RNA genome segments when subjected to polyacrylamide gel electrophoresis (long, short, supershort or atypical electropherotypes); (iii) whole-genome RNA hybridization patterns (genogroups); and (iv) nucleotide sequence analysis (genotypes) [25, 57]. Due to the segmented nature of the RV genome, reassortment events can occur after co-infection with RV strains belonging to the same group/species both *in vitro* and *in vivo* [27, 34, 64]. Numerous examples of such gene exchanges are available in the

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literature for RVA strains [50, 61]. Recent data also suggest that reassortment involving the NSP1-encoding genome segment may have occurred between ancestral strains of avian RVA and RVD [92]. However, there is no evidence for reassortment among contemporary RVs that belong to different groups/species. Their inability to undergo segment exchange, even under experimental conditions, indicates that the RV groups can be thought of as unique viral species [4].

In April 2008, a nucleotide-sequence-based, complete genome classification system was developed for RVA strains [54]. This system assigns a specific genotype to each of the 11 RV genome segments according to established nucleotide percent cutoff values. The VP7-VP4-VP6-VP1-VP2-VP3-NSP1-NSP2-NSP3-NSP4-NSP5/6 genes of RV strains are described using the abbreviations Gx-P[x]-Ix-Rx-Cx-Mx-Ax-Nx-Tx-Ex-Hx (x = Arabic numbers starting from 1), respectively [54]. Full-genome analyses have increased our recognition of the relatedness between animal and human RV strains, and this highlights the relevance of a common nomenclature for both animal and public health. To maintain, evaluate, and develop this system, the Rotavirus Classification Working Group (RCWG) was formed [55], which includes researchers worldwide.

In this article, we report on the current status of genotype diversity for RVA strains that has been identified to date by the RCWG. Moreover, the RCWG is also working with researchers at the National Center for Biotechnology Information (NCBI) to develop a specific database for the deposition of RV sequence information. This RV resource will contain complete genome sequences that are annotated using VIGOR (VIral Genome ORF Reader) [99], as well as multiple types of metadata (epidemiological, clinical, etc.) to provide useful additional information to investigators. The new RV database will be very similar to the "Influenza Virus Resource", which is widely used to monitor influenza virus strains [10]. As part of the database development, the RCWG herein proposes a standardized nomenclature for RV strains, which is similar to that already established for influenza viruses. Universal adoption of this new system by the RV community will be crucial for the retrieval of relevant information from the RV resource.

Update from the RCWG

The task of the RCWG is to maintain, evaluate, and develop the RV genotype classification system. When the nucleotide sequence from a RVA strain of a potential new genotype is submitted to the RCWG, a thorough phylogenetic analysis is performed, and this analysis is reviewed by the members of the RCWG. When a consensus is reached, the submitter receives an e-mail with the novel genotype number(s) of the particular gene(s), which can then be used in publications. To facilitate the utilization of the RV genotype classification system, a regularly updated online automatic web application, RotaC (http://rotac.regatools.be/), was developed [47].

Since the establishment of the RCWG, its activities have been reviewed at annual face-to-face meetings, held in conjunction with major scientific virology meetings. The first three RCWG-meetings were held at (i) the 27th annual meeting of the American Society for Virology (ASV) (July 14th, 2008, Ithaca, New York), (ii) the 10th International Symposium on dsRNA Viruses (July 24th, 2009, Hamilton Island, Australia) and (iii) the 29th annual meeting of the ASV (July 19th, 2010, Bozeman, Montana). The fourth and fifth RCWG meetings are planned to take place during the 30th annual meeting of the ASV in Minneapolis, Minnesota (July 16th-20th, 2011) and the 11th International Symposium on dsRNA Viruses in San Juan, Puerto Rico (November 27th-December 1st, 2012), respectively.

Table 1 contains a list of RV strains possessing new genotypes that have been recognised by the RCWG since the introduction of the classification system in April 2008. The new genotypes were found for RVs identified in a variety of host species including humans, cows, pigs, horses, mice, chickens, turkeys, pheasants, South American camelids, bats and a sugar glider. Several of these new genotypes have been published [1, 19, 23, 30, 44, 58, 62, 85, 87, 91, 95]. Table 2 shows a large selection of RV strains of all recognised genotypes that are not represented in Table 1. Table 3 contains a list with representative RV strains and accession numbers for each of the 166 currently established genotypes divided over the 11 genome segments.

Although the RV classification system has so far been limited to that of RVA strains, the RCWG plans to develop similar systems for RV strains belonging to other RV groups/species once a critical number of complete genome sequences has become available. The complete genomes of four human RVB strains were recently sequenced and analyzed by Yamamoto and colleagues, bringing the total number of genomes to eight (seven human RVB strains and a single murine RVB strain) [70, 103]. So far, all of the fully analyzed human RVB strains were detected in China and South-East Asia (Bangladesh, India and Myanmar). Regarding RVC strains, the entire genome sequences have been determined for only eight strains: the porcine strain Cowden and seven human strains detected in the UK, Japan, China, Bangladesh and India [12, 15, 104]. The first complete genome sequence of a RVD strain (RVD/chicken-wt/DEU/05V0049/2005/GXP[X]) was published recently [92]. Furthermore, the complete genome sequences of two novel adult diarrhea rotavirus (NADRV) strains (RVX/Human-tc/CHN/NADRV-J19/1997/GXP[X] and

Table 1 RV strains possessing novel genotypes assigned by the RCWG since its formation in April 2008 [54, 55]

Strain name	New genotypes											Ref.
	VP7	VP4	VP6	VP1	VP2	VP3	NSP1	NSP2	NSP3	NSP4	NSP5	
RVA/Human-wt/ECU/Ecu534/2006/G20P[28]	**G20**	**P[28]**	**I13**									[87]
RVA/Cow-wt/JPN/Azuk-1/2006/G21P[29]	**G21**	**P[29]**	I2	R2	C2	M2	A13	N2	**T9**	E2	H3	[1]
RVA/Guanaco-wt/ARG/Chubut/1999/G8P[14]	G8	P[14]	I2	**R5**	C2	M2	A3	N2	T6	**E12**	H3	[58]
RVA/Chicken-tc/DEU/02V0002G3/2002/G19P[30]	G19	**P[30]**	I11	**R6**	**C6**	**M7**	**A16**	**N6**	**T8**	E10	**H8**	[91]
RVA/Turkey-tc/DEU/03V0002E10/2003/G22P[35]	**G22**	**P[35]**	I4								H4	[85], NP
RVA/Chicken-tc/DEU/06V0661/2006/G19P[31]	G19	**P[31]**	I11								H8	[85]
RVA/Human-wt/NPL/KTM368/2004/G11P[25]	G11	P[25]	**I12**	R1	C1	M1	A1	N1	T1	E1	H1	[62]
RVA/Human-tc/ITA/260-97/1997/G3P[3]	G3	P[3]	I3	R3	C3	M3	**A15**	N2	T3	E3	H6	[63]
RVA/Horse-wt/ARG/E30/1993/G3P[12]	G3	P[12]	I6	R2	C2	M3	A10	N2	T3	E2	**H7**	NP
RVA/Pig-wt/IRL/61/07-ire/2007/G2P[32]	G2	**P[32]**	I5							E9		[19]
RVA/Pheasant-wt/HUN/Phea14246/2008/G23P[?]	**G23**											[95]
RVA/Pig-wt/CAN/CE-M-06-0003/2005/G2P[27]	G2	P[27]	**I14**									[44]
RVA/Cow-tc/JPN/Dai-10/2007/G24P[33]	**G24**	**P[33]**	I2	R2	C2	M2	A13	N2	T9	E2	H3	[1]
RVA/Mouse-tc/USA/ETD_822/XXXX/G16P[16]	G16	P[16]	I7	**R7**	**C7**	**M8**	A7	**N7**	**T10**	E7	**H9**	NP
RVA/Bat-wt/KEN/KE4852/07/2007/G25P[6]	**G25**	P[6]	**I15**	RY[a]	**C8**			**N8**	**T11**	E2	**H10**	[23]
RVA/Pig-wt/JPN/FGP51/2009/G4P[34]	G4	**P[34]**										NP
RVA/Human-tc/KEN/B10/1987/G3P[2]	G3	P[2]	**I16**	**R8**	C5	M5	A5	N5	T5	**E13**	H5	[30]
RVA/Pig-wt/JPN/TJ4-1/2010/G26P[?]	**G26**											NP
RVA/Horse-tc/GBR/L338/1991/G13P[18]	G13	P[18]	I6	**R9**	**C9**	M6	A6	**N9**	**T12**	**E14**	**H11**	NP
RVA/SugarGlider-wt/JPN/SG33/2010/G27P[X]	**G27**											NP

The strain name, available genotype constellation and publication are shown. Novel assigned genotypes are in bold

An open space means the genotype is not known because sequencing has not been performed

An "X" in the name of a strain indicates that this information is missing

NP not published

[a] Partial sequences of this gene segment have been determined, but it could not be assigned to any of the established genotypes. It may be the representatives of a new genotype, but the entire ORF needs to be determined, as stated in the guidelines from the RCWG [55], before this can be confirmed

RVX/Human-wt/BAN/NADRV-B219/2002/GXP[X]), causing diarrhea in adults, have been determined [39, 70, 105]. These NADRV strains have not yet been assigned to an RV group/species by the ICTV. Recently, VP6 sequence information was obtained for avian RVF and RVG strains [40]. In the future, analysis of these sequence data should allow the calculation of sequence-based thresholds to define (new) RV groups/species and genotypes within groups/species. A detailed overview of the current classification for non-RVA strains was published recently [61].

Proposed nomenclature of RV strains

Currently, no guidelines exist for the naming of RV strains. The lack of a standardized nomenclature system has lead to discrepancies in the literature where researchers have developed their own naming systems. With increasing numbers of complete RV genome sequences becoming available, and with the development of specific resources to retrieve and analyze these sequences, a more uniform nomenclature is clearly needed. The RCWG has discussed this issue, and we propose the following nomenclature for individual strains:

RV group/species of origin/country of identification/common name/year of identification/G- and P-type

A) Guidelines for *wild-type* RV strains

These guidelines apply to any wild-type RV strain or naturally occurring reassortant RV strain recovered from human or animal populations that have been sequenced directly from clinical specimens (such as stool, blood or tissue samples) or environmental samples. Guidelines for nomenclature of i) tissue-culture-adapted RV strains, ii) RV vaccine strains, iii) RV strains that have been generated in the laboratory by reassortment or iv) RV strains engineered in the laboratory by reverse genetics or equivalent mechanisms are provided further below in sections B), C), D), and E).

Table 2 List of RV strains representing all of the currently established genotypes except for those represented in Table 1

Strain name	Genotypes											Ref.
	VP7	VP4	VP6	VP1	VP2	VP3	NSP1	NSP2	NSP3	NSP4	NSP5	
RVA/Human-tc/USA/Wa/1974/G1P1A[8]	G1	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[54]
RVA/Human-wt/BGD/Dhaka16-03/2003/G1P[8]	G1	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[76]
RVA/Human-wt/USA/LB2719/2006/G1P[8]	G1	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[7]
RVA/Human-wt/IND/06361/2006/G1P[8]	G1	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[2]
RVA/Human-wt/IND/0613158/2006/G1P[8]	G1	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[2]
RVA/Human-wt/IND/061060/2006/G1P[8]	G1	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[2]
RVA/Human-wt/IND/NIV929893/1992/G1P[19]	G1	P[19]	I1							E1		[16]
RVA/Pig-wt/SVN/P21-5/2004/G1P[27]	G1	P[27]								E9		[88]
RVA/Human-tc/USA/DS-1/1976/G2P1B[4]	G2	P[4]	I2	R2	C2	M2	A2	N2	T2	E2	H2	[54]
RVA/Human-wt/CHN/TB-Chen/1996/G2P[4]	G2	P[4]	I2	R2	C2	M2	A2	N2	T2	E2	H2	[13]
RVA/Human-wt/USA/LB2744/2006/G2P[4]	G2	P[4]	I2	R2	C2	M2	A2	N2	T2	E2	H2	[7]
RVA/Human-wt/BGD/MMC6/2005/G2P[4]	G2	P[4]	I2	R2	C2	M2	A2	N2	T2	E2	H2	[33]
RVA/Human-wt/BGD/MMC88/2005/G2P[4]	G2	P[4]	I2	R2	C2	M2	A2	N2	T2	E2	H2	[33]
RVA/Pig-wt/ESP/34461-4/2003/G2P[23]	G2	P[23]	I5							E1	H1	[42]
RVA/Pig-wt/THA/CMP034/2000/G2P[27]	G2	P[27]	I5							E9	H1	[42]
RVA/Simian-tc/ZAF/SA11-H96/1958/G3P5B[2]	G3	P[2]	I2	R2	C5	M5	A5	N5	T5	E2	H5	[86]
RVA/Simian-tc/USA/RRV/1975/G3P[3]	G3	P[3]	I2	R2	C3	M3	A9	N2	T3	E3	H6	[59]
RVA/Human-tc/USA/HCR3A/1984/G3P[3]	G3	P[3]	I3	R3	C2	M3	A9	N2	T3	E3	H6	[93]
RVA/Cat-tc/AUS/Cat97/1984/G3P[3]	G3	P[3]	I3	R3	C2	M3	A9	N2	T3	E3	H6	[93]
RVA/Dog-tc/USA/CU-1/1982/G3P[3]	G3	P[3]	I3	R3	C2	M3	A9	N2	T3	E3	H6	[93]
RVA/Human-wt/THA/CMH222/2001/G3P[3]	G3	P[3]	I8							E3		[41]
RVA/Human-tc/AUS/RV3/1977/G3P2A[6]	G3	P[6]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[82]
RVA/Cow-lab/GBR/PP-1/1976/G3P[7]	G3	P[7]					A3			E8		[22]
RVA/Pig-tc/VEN/A131/1988/G3P9[7]	G3	P[7]	I5	R1	C2	M1	A1	N1	T1	E1	H1	[54]
RVA/Human-tc/USA/P/1974/G3P1A[8]	G3	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[54]
RVA/Human-wt/USA/DC5544-Bethesda/1991/G3P[8]	G3	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[66]
RVA/Cat-wt/ITA/BA222/2005/G3P[9]	G3	P[9]	I2	R2	C2	M2	A3	N1	T3	E2	H3	[51]
RVA/Human-wt/ITA/PAH136/1996/G3P[9]	G3	P[9]	I2	R2	C2	M2	A3	N1	T6	E2	H3	[20]
RVA/Human-wt/ITA/PAI58/1996/G3P[9]	G3	P[9]	I2	R2	C2	M2	A3	N2	T6	E2	H3	[20]
RVA/Cat-tc/AUS/Cat2/1984/G3P[9]	G3	P[9]	I3	R3	C2	M3	A3	N1	T6	E3	H3	[93]
RVA/Human-tc/JPN/AU-1/1982/G3P3[9]	G3	P[9]	I3	R3	C3	M3	A3	N3	T3	E3	H3	[54]
RVA/Human-wt/BEL/B4106/2000/G3P[14]	G3	P[14]	I2	R2	C2	M3	A9	N2	T6	E5	H3	[52]
RVA/Rabbit-tc/ITA/30/96/1996/G3P[14]	G3	P[14]	I2	R2	C2	M3	A9	N2	T6	E5	H3	[52]
RVA/Rabbit-wt/ITA/229/01/2001/G3P[22][a]	G3	P[22]								E5		[48]
RVA/Rhesus-tc/USA/TUCH/2002/G3P[24]	G3	P[24]	I9	R3	C3	M3	A9	N1	T3	E3	H6	[59]
RVA/Human-wt/IND/mani-253/2007/G4P[4]	G4	P[4]	I1	R1	C1	M2	A8	N1	T1	E1	H1	[69]
RVA/Human-wt/IND/mani-362/2007/G4P[6]	G4	P[6]	I1	R1	C1	M1	A8	N1	T1	E1	H1	[69]
RVA/Human-tc/GBR/ST3/1975/G4P2A[6]	G4	P[6]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[54]
RVA/Pig-tc/USA/Gottfried/1983/G4P[6]	G4	P[6]	I1	R1	C1	M1	A8	N1	T1	E1	H1	[62]
RVA/Human-tc/CHN/R479/2004/G4P[6]	G4	P[6]	I5	R1	C1	M1	A1	N1	T7	E1	H1	[100]
RVA/Pig-tc/USA/OSU/1977/G5P9[7]	G5	P[7]	I5	R1	C1	M1	A1	N1	T1	E1	H1	[62]
RVA/Human-tc/BRA/IAL28/1992/G5P[8]	G5	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[54]
RVA/Pig-tc/VEN/A34/1985/G5P[23]	G5	P[23]								E1		[45]
RVA/Pig-wt/ITA/134/04-15/2003/G5P[26]	G5	P[26]	I5							E1		[49]
RVA/Cow-tc/VEN/BRV033/1990/G6P6[1]	G6	P[1]	I2	R2	C2	M2	A3	N2	T6	E2	H3	[54]
RVA/Cow-tc/FRA/RF/1982/G6P[1]	G6	P[1]	I2	R2	C2	M2	A3	N2	T6	E2	H3	[18]
RVA/Goat-tc/BGD/GO34/1999/G6P[1]	G6	P[1]	I2	R2	C2	M2	A11	N2	T6	E2	H3	[29]

Table 2 continued

Strain name	Genotypes											Ref.
	VP7	VP4	VP6	VP1	VP2	VP3	NSP1	NSP2	NSP3	NSP4	NSP5	
RVA/Cow-tc/USA/WC3/1981/G6P[5]	G6	P[5]	I2	R2	C2	M2	A3	N2	T6	E2	H3	[54]
RVA/Cow-tc/GBR/UK/1973/G6P7[5]	G6	P[5]	I2	R2	C2	M2	A3	N2	T7	E2	H3	[21]
RVA/Human-wt/BEL/B1711/2002/G6P[6]	G6	P[6]	I2	R2	C2	M2	A2	N2	T2	E2	H2	[56]
RVA/Human-wt/IND/HP140/1987/G6P[13]	G6	P[13]	I2	R1	C1	M1				E1	H1	[97]
RVA/Human-wt/BEL/B10925-97/1997/G6P[14]	G6	P[14]	I2	R2	C2	M2	A3	N2	T6	E2	H3	[58]
RVA/Human-wt/HUN/Hun5/1997/G6P[14]	G6	P[14]	I2	R2	C2	M2	A11	N2	T6	E2	H3	[58]
RVA/Human-wt/HUN/BP1879/2003/G6P[14]	G6	P[14]	I2	R2	C2	M2	A11	N2	T6	E2	H3	[6]
RVA/Turkey-tc/IRL/Ty-3/1979/G7P[17]	G7	P[17]	I4							E11		[68]
RVA/Guanaco-wt/ARG/Rio_Negro/1998/G8P[1]	G8	P[1]	I2	R5	C2	M2	A13	N2	T6	E12	H3	[58]
RVA/Macaque-tc/USA/PTRV/1990/G8P[1]	G8	P[1]	I2	R2	C2	M2	A3	N2	T6	E2	H3	[59]
RVA/Human-wt/NIC/NIC522/2008/G8P[1]	G8	P[1]	I2	R2	C2	M2	A13	N2	T6[c]	E2	H3	[5]
RVA/Human-tc/KEN/B12/1987/G8P[1]	G8	P[1]	I2	R2	C2	M	A3	N2	T6	E2	H3	[32]
RVA/Cow-tc/THA/A5-13/1988/G8P[1]	G8	P[1]					A14					[71]
RVA/Human-wt/DEU/GER1H-09/2009/G8P[4]	G8	P[4]	I2	R2	C2	M2	A2	N2	T2	E2	H2	[73]
RVA/Human-wt/COD/DRC86/2003/G8P[6]	G8	P[6]	I2	R2	C2	M2	A2	N2	T2	E2	H2	[53]
RVA/Human-wt/COD/DRC88/2003/G8P[8]	G8	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2	[53]
RVA/Human-tc/IDN/69M/1980/G8P4[10]	G8	P[10]	I2	R2	C2	M2	A2	N2	T2	E2	H2	[54]
RVA/Human-wt/HUN/BP1062/2004/G8P[14]	G8	P[14]	I2	R2	C2	M2	A11	N2	T6	E2	H3	[9]
RVA/Sheep-tc/ESP/OVR762/2002/G8P[14]	G8	P[14]	I2	R2	C2	M2	A11	N2	T6	E2	H3	[58]
RVA/Human-wt/BEL/B3458/2003/G9P[8]	G9	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[54]
RVA/Human-tc/USA/WI61/1983/G9P1A[8]	G9	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[54]
RVA/Human-wt/USA/OM46/1998/G9P[8]	G9	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[67]
RVA/Human-wt/USA/OM473/2000/G9P[8]	G9	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[67]
RVA/Human-tc/IND/116E/1985/G9P[11]	G9	P[11]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[82]
RVA/Human-wt/IND/RMC321/1990/G9P[19]	G9	P[19]	I5	R1	C1	M1	A1	N1	T1	E1	H1	[96]
RVA/Human-wt/IND/mani-97/2006/G9P[19]	G9	P[19]	I5	R1	C1	M1	A8	N1	T1	E1	H1	[69]
RVA/Human-wt/IND/mani-265/2007/G10P[6]	G10	P[6]	I2	R2	C2	M2	A3	N2	T2	E2	H2	[69]
RVA/Human-wt/NGA/6717ARN/2002/G10P[8]	G10	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[24]
RVA/Human-wt/CIV/6755ARN/2002/G10P[8]	G10	P[8]	I2	R1	C1	M1	A1	N1	T1	E1	H1	[24]
RVA/Human-wt/IND/N155/2003/G10P[11]	G10	P[11]	I2	R2	C2	M2	A1	N1	T1	E2	H3	[77]
RVA/Cow-tc/CHN/DQ-75/2008/G10P[11]	G10	P[11]	I2	R2	C2	M2	A3	N2	T6	E2	H3	[102]
RVA/Sheep-tc/CHN/Lamb-NT/XXXX/G10P[15]	G10	P[15]	I10	R2	C2	M2	A11	N2	T6	E2	H3	[14]
RVA/Human-wt/ECU/EC2184/2005/G11P[6]	G11	P[6]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[8]
RVA/Pig-tc/MEX/YM/1983/G11P9[7]	G11	P[7]	I5	R1	C1	M1	A8	N1	T1	E1	H1	[62]
RVA/Pig-tc/VEN/A253/1988/G11P9[7]	G11	P[7]	I5	R1	C2	M1	A1	N1	T1	E1	H1	[54]
RVA/Human-wt/BGD/Matlab36-02/2002/G11P[8]	G11	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[62]
RVA/Human-wt/BGD/Dhaka6/2001/G11P[25]	G11	P[25]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[62]
RVA/Human-wt/NPL/KTM368/2004/G11P[25]	G11	P[25]	I12	R1	C1	M1	A1	N1	T1	E1	H1	[62]
RVA/Human-tc/PHL/L26/1987/G12P[4]	G12	P[4]	I2	R2	C2	M1	A2	N1	T2	E2	H1	[75]
RVA/Human-wt/BGD/Dhaka12-03/2003/G12P[6]	G12	P[6]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[75]
RVA/Human-wt/BGD/Matlab13/2003/G12P[6]	G12	P[6]	I1	R1	C1	M1	A1	N1	T2	E1	H1	[75]
RVA/Human-wt/BGD/RV161/2000/G12P[6]	G12	P[6]	I2	R2	C2	M2	A2	N2	T2	E1	H2	[75]
RVA/Human-wt/BGD/RV176-00/2000/G12P[6]	G12	P[6]	I2	R2	C2	M2	A2	N2	T2	E6	H2	[75]
RVA/Human-tc/KOR/CAU195/200X/G12P[6]	G12	P[6]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[89]
RVA/Human-tc/KOR/CAU214/200X/G12P[6]	G12	P[6]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[89]
RVA/Pig-wt/IND/RU172/2002/G12P[7]	G12	P[7]	I5	R1	C1	M1	A1	N1	T1	E1	H1	[31]
RVA/Human-wt/BEL/B4633/2003/G12P[8]	G12	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[75]

Table 2 continued

Strain name	Genotypes											Ref.
	VP7	VP4	VP6	VP1	VP2	VP3	NSP1	NSP2	NSP3	NSP4	NSP5	
RVA/Human-wt/BGD/Dhaka25-02/2002/G12P[8]	G12	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	[75]
RVA/Human-tc/THA/T152/1998/G12P[9]	G12	P[9]	I3	R3	C3	M3	A12	N3	T3	E3	H6	[75]
RVA/Horse-wt/ARG/E403/2006/G14P[12]	G14	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	NP
RVA/Cow-wt/ARG/B383/1998/G15P[11]	G15	P[11]	I2	R5	C2	M2	A13	N2	T6	E12	H3	[58]
RVA/Cow-tc/IND/Hg18/XXXX/G15P[21]	G15	P[21]								E2		[80]
RVA/Mouse-tc/BRA/EHP/1981/G16P[20]	G16	P[20]					A7			E7		[26]
RVA/Turkey-tc/IRL/Ty-1/1979/G17P[17]	G17	P[17]	I4					N4		E4		[68]
RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]	G18	P[17]	I4	R4	C4	M4	A4	N4	T4	E4	H4	[38]
RVB/Rat-tc/USA/IDIR/1984/G1P[X][b]	G1[b]											[98]
RVB/Human-wt/CHN/WH-1/2002/G2P[X][b]	G2[b]											[106]
RVB/Human-wt/BGD/Bang117/2003/G2P[X][b]	G2[b]											[103]
RVB/Cow-wt/IND/DB176/2001/G3P[X][b]	G3[b]											[11]
RVC/Pig-tc/USA/Cowden/1982/G1P[1][b]	G1[b]	P[1][b]										[74]
RVC/Cow-tc/JPN/Shintoku/1991/G2P[3][b]	G2[b]	P[3][b]										[94]
RVC/Human-tc/GBR/Bristol/1998/G4P[2][b]	G4[b]	P[2][b]										[37]
RVC/Human-wt/BGD/BS347/2005/G4P[2][b]	G4[b]	P[2][b]										[104]
RVD/chicken-wt/DEU/05V0049/2005/GXP[X]												[92]

An open space means the (1) genotype not known because sequencing has not been performed or (2) genotypes have not yet been established for non-group-A RVs. An "X" in the name of a strain indicates that this information is missing. Accession numbers for representative strains of all the different genotypes can be found in Table 3

NP not published

[a] Only the partial VP8* coding region of the VP4 sequence of P[22] strains is currently available

[b] Genotypes are provisional. Guidelines about the classification of RV strains belonging to RVB and RVC will be determined in the near future by the RCWG

[c] Due to a typographic error, the NSP3 genotype of strain NIC522 was previously misidentified as T2 [5]

- *RV group/species*: RVA, RVB, RVC, RVD, RVE, RVF or RVG. RVX should be used in cases where a strain has not yet been assigned to an established or new RV group/species.
- *Species of origin*: The "species of origin" field contains two components. The first component is human, pig, cow, dog, cat, rhesus, simian, horse, rabbit, mouse, goat, sheep, guanaco, bat, turkey, chicken, pheasant, sugar glider or other, as appropriate. In cases in which the sample was obtained from the environment (i.e., sewage, soil, river, lake, ocean or similar), "Env" should be used. If the species of origin is unknown, "X" should be used. The second component is "-wt" (for wild-type) to distinguish from tissue-culture-adapted (-tc) and laboratory-generated or -engineered (-lab) RV strains. If a tissue-culture-adapted or laboratory-generated strain is introduced into the population (e.g., a vaccine strain) and later recovered from a human or animal, the species from which the sample was recovered should be used, followed by "-wt". The researcher should be able to give a name to a strain *without the need to perform any analyses*. If subsequent analyses reveal that a strain is wholly or partially derived from a vaccine strain, this information can be added in the metadata of the record in GenBank or any other database.
- *Country of identification*: A unique 3-letter abbreviation code is used for each country as listed on the website https://www.cia.gov/library/publications/the-world-factbook/appendix/appendix-d.html. If the country of identification is unknown, "XXX" should be used. If a tissue-culture-adapted or laboratory-generated RV strain is introduced into the population and later recovered from a human or animal, the country from which the sample was recovered should be used (further details, e.g., of city/site of identification, can be added in the common name or the metadata; see below).
- *Common name*: This is a short name given by investigators, preferentially not using forward slashes ("/") or backslashes ("\") to avoid confusion and computer-processing problems. If appropriate, the common name can contain geographically/clinically

Table 3 Reference strains and accession numbers representing the 166 currently established genotypes

Geno-type	Reference Strain	Accession number	Geno-type	Reference Strain	Accession number
VP7			P[17]	RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]	AB009632
G1	RVA/Human-tc/USA/Wa/1974/G1P1A[8]	K02033	P[18]	RVA/Horse-tc/GBR/L338/1991/G13P[18]	JF712558
G2	RVA/Human-tc/USA/DS-1/1976/G2P1B[4]	AB118023	P[19]	RVA/Human-wt/IND/RMC321/1990/G9P[19]	AF523677
G3	RVA/Human-tc/JPN/AU-1/1982/G3P3[9]	D86271	P[20]	RVA/Mouse-tc/XXX/EHP/1981/G16P[20]	U08424
G4	RVA/Human-tc/GBR/ST3/1975/G4P2A[6]	X13603	P[21]	RVA/Cow-tc/IND/Hg18/1995/G15P[21]	AF237665
G5	RVA/Pig-tc/USA/OSU/1977/G5P9[7]	X04613	P[22]	RVA/Rabbit-wt/ITA/160-01/2001/G3P[22]	AF526374
G6	RVA/Cow-tc/FRA/RF/1982/G6P[1]	X65940	P[23]	RVA/Pig-tc/VEN/A34/1985/G5P[23]	AY174094
G7	RVA/Turkey-tc/IRL/Ty-3/1979/G7P[17]	AB080737	P[24]	RVA/Rhesus-tc/USA/TUCH/2002/G3P[24]	AY596189
G8	RVA/Human-tc/IND/69M/1980/G8P4[10]	EF672560	P[25]	RVA/Human-wt/BGD/Dhaka6/2001/G11P[25]	GU199520
G9	RVA/Human-tc/USA/WI61/1983/G9P1A[8]	AB180969	P[26]	RVA/Pig-wt/ITA/134-04-15/2003/G5P[26]	DQ061053
G10	RVA/Human-tc/GBR/A64/1987/G10P11[14]	A01321	P[27]	RVA/Pig-wt/THA/CMP034/2000/G2P[27]	DQ534016
G11	RVA/Pig-tc/MEX/YM/1983/G11P9[7]	M23194	P[28]	RVA/Human-wt/ECU/Ecu534/2006/G20P[28]	EU805773
G12	RVA/Human-tc/PHL/L26/1987/G12P[4]	M58290	P[29]	RVA/Cow-wt/JPN/Azuk-1/2006/G21P[29]	AB454420
G13	RVA/Horse-tc/GBR/L338/1991/G13P[18]	JF712560	P[30]	RVA/Chicken-tc/DEU/02V0002G3/2002/G19P[30]	EU486956
G14	RVA/Horse-wt/ARG/E403/2006/G14P[12]	JF712582	P[31]	RVA/Chicken-tc/DEU/06V0661/2006/G19P[31]	EU486962
G15	RVA/Cow-wt/ARG/B383/1998/G15P[11]	FJ347116	P[32]	RVA/Pig-wt/IRL/61-07-ire/2007/G2P[32]	FJ492835
G16	RVA/Mouse-tc/USA/ETD_822/XXXX/G16P[16]	GQ479955	P[33]	RVA/Cow-tc/JPN/Dai-10/2007/G24P[33]	AB513836
G17	RVA/Turkey-tc/IRL/Ty-1/1979/G17P[17]	S58166	P[34]	RVA/Pig-wt/JPN/FGP51/2009/G4P[34]	AB571047
G18	RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]	D82979	P[35]	RVA/Turkey-tc/DEU/03V0002E10/2003/G22P[35]	EU486958
G19	RVA/Chicken-tc/DEU/02V0002G3/2002/G19P[30]	FJ169861	**VP6**		
G20	RVA/Human-wt/ECU/Ecu534/2006/G20P[28]	EU805773	I1	RVA/Human-tc/USA/Wa/1974/G1P1A[8]	K02086
G21	RVA/Cow-wt/JPN/Azuk-1/2006/G21P[29]	AB454421	I2	RVA/Human-tc/USA/DS-1/1976/G2P1B[4]	DQ870507
G22	RVA/Turkey-tc/DEU/03V0002E10/2003/G22P[35]	EU486973	I3	RVA/Human-tc/JPN/AU-1/1982/G3P3[9]	DQ490538
G23	RVA/Pheasant-wt/HUN/Phea14246/2008/G23P[?]	FN393054	I4	RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]	D16329
G24	RVA/Cow-tc/JPN/Dai-10/2007/G24P[33]	AB513837	I5	RVA/Pig-tc/MEX/YM/1983/G11P9[7]	X69487
G25	RVA/Bat-wt/KEN/KE4852/07/2007/G25P[6]	GU983676	I6	RVA/Horse-tc/GBR/L338/1991/G13P[18]	JF712559
G26	RVA/Pig-wt/JPN/TJ4-1/2010/G26P[?]	AB605258	I7	RVA/Mouse-tc/USA/ETD_822/XXXX/G16P[16]	GQ479952
G27	RVA/SugarGlider-wt/JPN/ SG33/2010/G27P[X]	AB621363	I8	RVA/Human-wt/THA/CMH222/2001/G3P[3]	ABC41660
VP4			I9	RVA/Rhesus-tc/USA/TUCH/2002/G3P[24]	AY594670
P[1]	RVA/Cow-tc/FRA/RF/1982/G6P[1]	U65924	I10	RVA/Sheep-tc/CHN/Lamb-NT/XXXX/G10P[15]	FJ032028
P[2]	RVA/Simian-tc/ZAF/SA11-H96/1958/G3P5B[2]	DQ841262	I11	RVA/Chicken-tc/DEU/02V0002G3/2002/G19P[30]	DQ096805
P[3]	RVA/Dog-tc/AUS/K9/1981/G3P[3]	D14725	I12	RVA/Human-wt/NPL/KTM368/2004/G11P[25]	GU199496
P[4]	RVA/Human-tc/USA/DS-1/1976/G2P1B[4]	AJ540227	I13	RVA/Human-wt/ECU/Ecu534/2006/G20P[28]	EU805774
P[5]	RVA/Cow-tc/GBR/UK/1973/G6P7[5]	M22306	I14	RVA/Pig-wt/CAN/CE-M-06-0003/2006/G2P[27]	GU183245
P[6]	RVA/Human-tc/GBR/ST3/1975/G4P2A[6]	L33895	I15	RVA/Bat-wt/KEN/KE4852/07/2007/G25P[6]	GU983675
P[7]	RVA/Pig-tc/USA/OSU/1976/G5P9[7]	M33516	I16	RVA/Human-tc/KEN/B10/1987/G3P[2]	HM627557
P[8]	RVA/Human-tc/USA/Wa/1974/G1P1A[8]	L34161	**VP1**		
P[9]	RVA/Human-tc/JPN/AU-1/1982/G3P3[9]	D10970	R1	RVA/Human-tc/USA/Wa/1974/G1P1A[8]	DQ490539
P[10]	RVA/Human-tc/IND/69M/1980/G8P4[10]	M60600	R2	RVA/Human-tc/USA/DS-1/1976/G2P1B[4]	DQ870505
P[11]	RVA/Human-tc/IND/116E/1985/G9P[11]	L07934	R3	RVA/Human-tc/JPN/AU-1/1982/G3P3[9]	DQ490533
P[12]	RVA/Horse-wt/ARG/E30/1993/G3P[12]	JF712575	R4	RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]	AB009629
P[13]	RVA/Human-wt/IND/HP140/1987/G6P[13]	DQ003291	R5	RVA/Guanaco-wt/ARG/Chubut/1999/G8P[14]	FJ347100
P[14]	RVA/Human-tc/GBR/A64/1987/G10P11[14]	EF672563	R6	RVA/Chicken-tc/DEU/02V0002G3/2002/G19P[30]	FJ169853
P[15]	RVA/Sheep-tc/CHN/Lamb-NT/XXXX/G10P[15]	FJ031027	R7	RVA/Mouse-tc/USA/ETD_822/XXXX/G16P[16]	GQ479947
P[16]	RVA/Mouse-tc/USA/ETD_822/XXXX/G16P[16]	GQ479950	R8	RVA/Human-tc/KEN/B10/1987/G3P[2]	HM627553

important information or specific (engineered) mutations, as long as the number of characters is less than or equal to 15.

- *Year of identification*: This is given using the "yyyy" format. If the year of identification is unknown, "XXXX" should be used. If a tissue-culture-adapted or laboratory-generated strain is introduced into a population and later recovered from a human or animal, the year in which the sample was recovered should be used.
- *G-type*: This is given using the form Gx, where x is the established G genotype/serotype number. If the G-type is unknown, GX should be used.
- *P-type*: This is given using the form Py[z], where y is the established P *sero*type number and z [in square brackets] is the established P *geno*type number. If the P-serotype is unknown, P[z] should be used, and if the P-genotype is unknown, Py[X] or P[X] should be used.

Table 3 continued

Geno-type	Reference Strain	Accession number
VP1 continued		
R9	RVA/Horse-tc/GBR/L338/1991/G13P[18]	JF712555
VP2		
C1	RVA/Human-tc/USA/Wa/1974/G1P1A[8]	X14942
C2	RVA/Human-tc/USA/DS-1/1976/G2P1B[4]	DQ870506
C3	RVA/Human-tc/JPN/AU-1/1982/G3P3[9]	DQ490536
C4	RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]	AB009630
C5	RVA/Simian-tc/ZAF/SA11-H96/1958/G3P5B[2]	DQ838635
C6	RVA/Chicken-tc/DEU/02V0002G3/2002/G19P[30]	FJ169854
C7	RVA/Mouse-tc/USA/ETD_822/XXXX/G16P[16]	GQ479948
C8	RVA/Bat-wt/KEN/KE4852/07/2007/G25P[6]	GU983673
C9	RVA/Horse-tc/GBR/L338/1991/G13P[18]	JF712556
VP3		
M1	RVA/Human-tc/USA/Wa/1974/G1P1A[8]	AY267335
M2	RVA/Human-tc/USA/DS-1/1976/G2P1B[4]	AY277914
M3	RVA/Human-tc/JPN/AU-1/1982/G3P3[9]	DQ490537
M4	RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]	AB009631
M5	RVA/Simian-tc/ZAF/SA11-H96/1958/G3P5B[2]	DQ838645
M6	RVA/Horse-tc/GBR/L338/1991/G13P[18]	JF712557
M7	RVA/Chicken-tc/DEU/02V0002G3/2002/G19P[30]	FJ169855
M8	RVA/Mouse-tc/USA/ETD_822/XXXX/G16P[16]	GQ479949
NSP1		
A1	RVA/Human-tc/USA/Wa/1974/G1P1A[8]	L18943
A2	RVA/Human-tc/USA/DS-1/1976/G2P1B[4]	L18945
A3	RVA/Human-tc/JPN/AU-1/1982/G3P3[9]	D45244
A4	RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]	AB009633
A5	RVA/Simian-tc/ZAF/SA11-H96/1958/G3P5B[2]	DQ838599
A6	RVA/Horse-tc/GBR/L338/1991/G13P[18]	JF712561
A7	RVA/Mouse-tc/USA/ETD_822/XXXX/G16P[16]	GQ479951
A8	RVA/Pig-tc/MEX/YM/1983/G11P9[7]	BAA20545
A9	RVA/Human-wt/BEL/B4106/2000/G3P[14]	AY740735
A10	RVA/Horse-wt/ARG/E30/1993/G3P[12]	JF712572
A11	RVA/Human-wt/HUN/Hun5/1997/G6P[14]	EF554110
A12	RVA/Human-tc/THA/T152/1998/G12P[9]	AB097459
A13	RVA/Cow-wt/ARG/B383/1998/G15P[11]	FJ347117
A14	RVA/Cow-tc/THA/A5-13/XXXX/G8P[1]	D38148
A15	RVA/Human-tc/ITA/PA260-97/1997/G3P[3]	HQ661118
A16	RVA/Chicken-tc/DEU/02V0002G3/2002/G19P[30]	FJ169857
NSP2		
N1	RVA/Human-tc/USA/Wa/1974/G1P1A[8]	L04534
N2	RVA/Human-tc/USA/DS-1/1976/G2P1B[4]	L04529
N3	RVA/Human-tc/JPN/AU-1/1982/G3P3[9]	DQ490534
N4	RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]	AB009625
N5	RVA/Simian-tc/ZAF/SA11-H96/1958/G3P5B[2]	DQ838615
N6	RVA/Chicken-tc/DEU/02V0002G3/2002/G19P[30]	FJ169860
N7	RVA/Mouse-tc/USA/ETD_822/XXXX/G16P[16]	GQ479954
N8	RVA/Bat-wt/KEN/KE4852/07/2007/G25P[6]	GU983677
N9	RVA/Horse-tc/GBR/L338/1991/G13P[18]	JF712562
NSP3		
T1	RVA/Human-tc/USA/Wa/1974/G1P1A[8]	X81434
T2	RVA/Human-tc/USA/DS-1/1976/G2P1B[4]	EF136660
T3	RVA/Human-tc/JPN/AU-1/1982/G3P3[9]	DQ490535
T4	RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]	AB009626
T5	RVA/Simian-tc/ZAF/SA11-H96/1958/G3P5B[2]	DQ838610
T6	RVA/Cow-tc/USA/WC3/1981/G6P[5]	EF990701
T7	RVA/Cow-tc/GBR/UK/1973/G6P7[5]	K02170
T8	RVA/Chicken-tc/DEU/02V0002G3/2002/G19P[30]	FJ169859
T9	RVA/Cow-wt/JPN/Azuk-1/2006/G21P[29]	AB513838
T10	RVA/Mouse-tc/USA/ETD_822/XXXX/G16P[16]	GQ479953
T11	RVA/Bat-wt/KEN/KE4852/07/2007/G25P[6]	GU983678
T12	RVA/Horse-tc/GBR/L338/1991/G13P[18]	JF712563
NSP4		
E1	RVA/Human-tc/USA/Wa/1974/G1P1A[8]	K02032
E2	RVA/Human-tc/USA/DS-1/1976/G2P1B[4]	AF174305
E3	RVA/Human-tc/JPN/AU-1/1982/G3P3[9]	D89873
E4	RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]	AB009627
E5	RVA/Human-wt/BEL/B4106/2000/G3P[14]	AY740732
E6	RVA/Human-wt/BGD/N26/2000/G12P[6]	DQ146691
E7	RVA/Mouse-tc/USA/ETD_822/XXXX/G16P[16]	GQ479956
E8	RVA/Cow-lab/GBR/PP-1/1976/G3P[7]	AF427521
E9	RVA/Pig-wt/THA/CMP034/2000/G2P[27]	AF427521
E10	RVA/Chicken-tc/DEU/02V0002G3/2002/G19P[30]	FJ169862
E11	RVA/Turkey-tc/IRL/Ty-3/1979/G7P[17]	AB065286
E12	RVA/Guanaco-wt/ARG/Chubut/1999/G8P[14]	FJ347109
E13	RVA/Human-tc/KEN/B10/1987/G3P[2]	HM627562
E14	RVA/Horse-tc/GBR/L338/1991/G13P[18]	JF712564
NSP5		
H1	RVA/Human-tc/USA/Wa/1974/G1P1A[8]	AF306494
H2	RVA/Human-tc/USA/DS-1/1976/G2P1B[4]	M33608
H3	RVA/Human-tc/JPN/AU-1/1982/G3P3[9]	AB008656
H4	RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]	AB009628
H5	RVA/Simian-tc/ZAF/SA11-H96/1958/G3P5B[2]	DQ838630
H6	RVA/Human-tc/THA/T152/1998/G12P[9]	DQ146706
H7	RVA/Horse-wt/ARG/E30/1993/G3P[12]	JF712575
H8	RVA/Chicken-tc/DEU/02V0002G3/2002/G19P[30]	FJ169863
H9	RVA/Mouse-tc/USA/ETD_822/XXXX/G16P[16]	GQ479957
H10	RVA/Bat-wt/KEN/KE4852/07/2007/G25P[6]	GU983680
H11	RVA/Horse-tc/GBR/L338/1991/G13P[18]	JF712565

An "X" in the name of a strain indicates that this information is missing

Examples of strain names using this nomenclature system can be found in Tables 1 and 2.

B) Guidelines for *tissue culture-adapted* RV strains or RV strain passaged *in vivo* in their homologous host species

These guidelines apply to any non-vaccine RV strain that has been adapted in tissue culture or passaged *in vivo* in a homologous animal model without the intention to introduce specific changes in the genome sequence. Specific details about the number of passages and the cell lines or animal used should be provided in the metadata. Guidelines for nomenclature of i) RV vaccine strains, ii) RV strains that have been generated in the laboratory by reassortment and iii) RV strains engineered in the laboratory by reverse genetics or equivalent mechanisms are provided below in sections C), D) and E).

- *RV group/species*: See section A) above.
- *Species of origin*: The "species of origin" field contains two components. The first component is human, pig,

cow, dog, cat, rhesus, simian, horse, rabbit, mouse, goat, sheep, bat, guanaco, turkey, chicken, pheasant, sugar glider or other, as appropriate. If the sample was obtained from the environment (i.e., sewage, soil, river, lake, ocean or similar), "Env" should be used. If the species of origin is unknown, "X" should be used. The second component is "-tc" (for tissue cultured) or "-hhp" (homologous host passaged) to distinguish from wild-type (-wt) and laboratory-generated or engineered (-lab) RV strains. If a tissue-culture-adapted or *in vivo*-passaged RV strain is introduced into the population (e.g., a vaccine strain) and later recovered from a human or animal, the species from which the sample was recovered should be used followed by "-wt".

- *Country of identification*: A unique 3-letter abbreviation code is used for each country as listed on the website https://www.cia.gov/library/publications/the-world-factbook/appendix/appendix-d.html. If the country of identification is unknown, "XXX" should be used. If a tissue-culture-adapted RV strain is introduced into the population and later recovered from a human or animal, the country from which the sample was recovered should be used (further details, e.g., of city/site of identification, can be added to the common name or the metadata, see below).
- *Common name*: See section A) above
- *Year of identification*: This is given using the "yyyy" format. If the year of identification is unknown, "XXXX" should be used. If a tissue-cultured strain is introduced into a population and later recovered from a human or animal, the year in which the sample was recovered should be used.
- *G-type*: See section A) above.
- *P-type*: See section A) above.

Examples of strain names using this nomenclature system can be found in Tables 1 and 2.

C) Guidelines for RV strains *generated in a laboratory* for which a host species can be assigned unambiguously

These guidelines apply to any RV strain in which small deliberate changes have been introduced (examples: chemically mutagenised RV strains, moderately modified RV strains using reverse genetics techniques, etc.) or RV strains that were passaged in a heterologous animal model and for which there is no ambiguity about the original host species. Specific details about the introduced changes and the methods used should be provided in the metadata. Guidelines for nomenclature for i) RV vaccine strains, ii) RV strains that have been generated in the laboratory by reassortment, iii) RV strains with a designed synthetic sequence generated using reverse genetics or iv) RV strains in which large modifications have been applied using reverse genetics or equivalent mechanisms are provided below in sections D) and E).

- *RV group/species*: See section A) above.
- *Species of origin*: The "species of origin" field contains two components. The first component is human, pig, cow, dog, cat, rhesus, simian, horse, rabbit, mouse, goat, sheep, bat, guanaco, turkey, chicken, pheasant, sugar glider or other, as appropriate. If the sample was obtained from the environment (i.e., sewage, soil, river, lake, ocean or similar), "Env" should be used. If the species of origin is unknown, "X" should be used. The second component is "-lab" (lab engineered) to distinguish from wild-type (-wt) and tissue-culture (-tc)-adapted RV strains. If a laboratory-generated strain is introduced into the population (e.g., a vaccine strain) and later recovered from a human or animal, the species from which the sample was recovered should be used followed by "-wt".
- *Country of identification*: A unique 3-letter abbreviation code is used for each country as listed on the website https://www.cia.gov/library/publications/the-world-factbook/appendix/appendix-d.html. If the country of identification is unknown, "XXX" should be used. If a laboratory-generated strain is introduced into the population and later recovered from a human or animal, the country from which the sample was recovered should be used (further details, e.g., of city/site of identification, can be added to the common name or the metadata, see below).
- *Common name*: See section A) above.
- *Year of identification*: This is given using the "yyyy" format. If the year of identification is unknown, "XXXX" should be used. If a laboratory-engineered strain is introduced into a population and later recovered from a human or animal, the year in which the sample was recovered should be used.
- *G-type*: See section A) above.
- *P-type*: See section A) above.

Examples of strain names using this nomenclature system can be found in Table 2.

D) Guidelines for RV strains *generated in a laboratory* for which a host species cannot be assigned unambiguously

These guidelines for nomenclature apply to RV strains that have been generated in the laboratory by reassortment (except for vaccine strains), strains with a designed synthetic sequence generated using reverse genetics, strains in which large modifications have been applied using reverse genetics or RV strains generated by combinations of the above procedures. Specific details about the changes

Table 4 Hypothetical examples of nomenclature for RV vaccine strains and laboratory-generated/engineered strains

Strain name	Genotypes											Ref.
	VP7	VP4	VP6	VP1	VP2	VP3	NSP1	NSP2	NSP3	NSP4	NSP5	
RVA/Env/CHE/River-Swiss/1998/G3P[X][a]	G1											[3]
RVA/Simian-lab/USA/SA11-tsE-1400/1982/G3P[2][b]	G3	P[2]	I2	R2	C5	M5	A5	N2	T5	E2	H5	[78]
RVA/Cow-lab/GBR/PP-1/1976/G3P[7][c]	G3	P[7]					A3			E8		[22]
RVA/Labstr/USA/RRV-E4/1996/G3P[20][d]	G3	P[20]	I2	R2	C3	M3	A9	N2	T3	E3	H6	[46]
RVA/Labstr/USA/SA11-huN2/2010/G3P[2][e]	G3	P[2]	I2	R2	C5	M5	A5	N2	T5	E2	H5	[90]
RVA/Vaccine/USA/RotaTeq-WI79-9/1992/G1P7[5][f]	G1	P7[5]	I2	R2	C2	M1	A3	N2	T6	E2	H3	[60]
RVA/Vaccine/USA/RotaTeq-SC2-9/1992/G2P7[5][f]	G2	P7[5]	I2	R2	C2	M1	A3	N2	T6	E2	H3	[60]
RVA/Vaccine/USA/RotaTeq-WI78-8/1992/G3P7[5][f]	G3	P7[5]	I2	R2	C2	M2	A3	N2	T6	E2	H3	[60]
RVA/Vaccine/USA/RotaTeq-BrB-9/1996/G4P7[5][f]	G4	P7[5]	I2	R2	C2	M2	A3	N2	T6	E2	H3	[60]
RVA/Vaccine/USA/RotaTeq-WI79-4/1992/G6P1A[8][f]	G6	P1A[8]	I2	R2	C2	M2	A3	N2	T6	E2	H3	[60]
RVA/Vaccine/USA/Rotarix-RIX4414/1988/G1P1A[8][g]	G1	P1A[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	NP

An open space means that the genotype has not been established/determined

[a] Hypothetical name of an RV strain identified in a river in Switzerland [3]

[b] Strain SA11-tsE is a temperature-sensitive RV strain (SA11) generated using chemical mutagenesis [78]

[c] Strain PP-1 is a bovine RV strain that has been passaged several times in the heterologous pig model [22]

[d] Hypothetical name of a RV strain generated using *in vitro* reassortment in cell culture, possessing an RRV-like gene background with the VP4 gene (genotype P[20]) of the murine RV strain EHP [46]

[e] Hypothetical name of a RV strain generated using reverse genetic techniques, possessing an SA11-like gene background with the NSP2 gene (genotype N2) of the human RV strain DS-1 [90]

[f] Hypothetical names of the 5 reassortant RV strains present in the RotaTeq vaccine [60]

[g] Hypothetical name of the RV strain present in the Rotarix vaccine

introduced and the methods used should be provided in the metadata.

- *RV group/species*: See section A) above.
- *Species of origin*: "LabStr". More specific details about the procedure used to create the virus should be provided in the metadata.
- *Country of identification*: The country in which the RV strain was generated should be provided according to the unique 3-letter abbreviation code for each country: https://www.cia.gov/library/publications/the-world-factbook/appendix/appendix-d.html.
- *Common name*: This is a short name given by investigators, preferentially without the use of forward slashes ("/") or backslashes ("\") to avoid confusion. If appropriate, the common name can contain specific information about the laboratory strain, such as the procedure used to generate it, as long as the number of characters is less than or equal to 15.
- *Year of identification*: The year in which the RV strain was generated should be provided using the "yyyy" format.
- *G-type*: See section A) above.
- *P-type*: See section A) above.

Examples using this nomenclature system for naming laboratory strains can be found in Table 4.

E) Guidelines for RV *vaccine* strains

Due to the increasing use of live-attenuated RV vaccine, it will be important to distinguish vaccine strains from naturally-occurring wild-type strains. Therefore, a specific notation for vaccine strains was developed and should be used if the strain is the sole component or part of a multi-component live vaccine. Only the sequences obtained from virus production lots or batches are officially recognized as vaccine strains and should have "vaccine" in their strain name. Other "pre-vaccine" strains or sequences of strains that were used in laboratories and were not generated by sequencing the actual vaccine production lots of a given manufacturer should use the normal guidelines to name their strains. Additional information such as the "pre-vaccine" status of a strain could be added in the "common name" section or in the metadata of the record.

- *RV group/species*: See section A) above.
- *Species of origin*: "Vaccine". Further specific details about the generation of the vaccine strain should be provided in the metadata.
- *Country of identification*: The country in which the vaccine strain was recovered (in the case of a vaccine containing a tissue-culture-adapted strain) or developed (in the case of a vaccine developed using reassortment or *in vitro* engineering) should be provided according to

the unique 3-letter abbreviation code for each country: https://www.cia.gov/library/publications/the-world-factbook/appendix/appendix-d.html.

- *Common name*: This is a short name given by investigators, preferentially without the use of forward slashes ("/") or backslashes ("\") to avoid confusion. It is recommended that the commercial name of the vaccine is included in the common name. The number of characters should be less than or equal to 15.
- *Year of identification*: The year in which the RV strain was recovered (in the case of a vaccine containing a tissue-culture-adapted strain) or developed (in the case of a vaccine developed using reassortment or *in vitro* engineering) should be provided using the "yyyy" format.
- *G-type*: See section A) above.
- *P-type*: See section A) above.

Examples using this nomenclature system for naming vaccine strains can be found in Table 4.

RV resource under development at NCBI

Due to the rapid increase in the number of complete RV genome sequences available, the RCWG is working with NCBI to develop an advanced RV resource, which will include a value-added database and a suite of tools for the analysis of RV sequences. When new sequence records are submitted to GenBank, their contents will be added to the RV database through an automated process. A web-based interface will allow researchers to search the RV database using a variety of genetic, epidemiological and clinical criteria, retrieve relevant sequences and analyze them. With this in mind, the RCWG proposes that the following list of biological descriptors (if available and relevant) should be included with sequence records submitted to GenBank. This list of metadata was agreed upon by members of the RCWG but is by no means exclusive, as additional metadata can also be added.

Strain-specific features

- a) Wild-type primary strain
  b) Cell-culture-adapted strain
  c) *In vitro*-generated reassortant strain
  d) Strain engineered by reverse genetics procedures
  e) *In vitro*-generated reassortant RV strain or RV strain engineered by reverse genetics that was recovered in nature from any host (e.g., a vaccine strain recovered in a human infant)
  f) *In vivo*-generated strain resulting from reassortment of a laboratory-generated strain and a wild-type strain (e.g., a strain recovered from a vaccinated infant that is the result of a reassortment event of the vaccine stain and a wild-type strain).
- In cases b, c and d, more details should be provided to account for any engineered changes. It is important to note that natural reassortant RVs should be categorized as "wild-type strains".
- Genotypes of the remaining 9 RNA segments according to RCWG guidelines [55].
- Species/group (RVA, RVB, RVC, RVD, RVE, RVF, RVG or RVX)
- For RVA: subgroup (SG, I, II, I+II, non-I/non-II) specificity
- Electropherotype: long, short, super-short or atypical
- Banding pattern (example: 4:2:3:2 for RVA, 4:2:2:3 for RVB, 4:3:2:2 for RVC, etc.)
- Region of identification: country, state, province, city/village
- Latitude / longitude (LAT/LON) coordinates: a Google Earth-like application might be incorporated where the location can be pinpointed on a map, and the coordinates will be added automatically.
- Collection date: time of sample collection (year, month, and day).

Host-specific features

- Host species: both the "common English name" and the scientific Latin name
- Host date of birth
- Host age at infection (or date of sample collection)
- Host gender
- Vaccination status of host
- Name of administered vaccine, number of administered doses and vaccination dates
- For animal RV vaccines: adjuvant used (oil or aqueous) and RV genotypes and/or other microbes included in the vaccine.

Disease-related and clinical features

- Symptomatic or asymptomatic infection
- Clinical symptoms of host: diarrhea, vomiting, fever, other
- Clinical severity: mild, moderate, severe, using established clinical gastroenteritis severity scoring systems (Vesikari, Clark, other) [17, 28, 83, 84] or World Health Organization (WHO) reference schemes
- Clinical outcome: dehydration (using WHO or Gorelick reference schemes) [36, 101], emergency room or its equivalent (outpatient), hospitalization and/or death

- Sample type: stool, serum, nasal swabs or other systemic tissues (lung, brain, etc.)
- Other co-infecting agents detected
- For RVs detected in domestic animals (calves, foals, piglets, etc.): indicate if the animal received electrolyte solutions, antibiotic, anti-diarrheic or other nonspecific treatment before and/or after sample collection
- Sample derived from a single case of diarrhea or an outbreak. In the case of an outbreak, what were the morbidity and mortality rates?
- For animals indicate type of exploitation (dairy or beef herds; extensive or intensive production; thoroughbred or standard-bred horses, etc.).

Analysis-specific information

- Was sequencing performed on stool, rectal swabs, intestinal contents, other types of samples from the patient, environmental samples or cell-culture-adapted virus?
- Cell type (e.g., Vero) and number of times the virus was passaged in cell culture before sequencing
- Sequencing method: Sanger sequencing, pyrosequencing, other
- Termini: were the 5'- and 3'-terminal sequences primer-derived or sequenced de novo?

Conclusions

The quickly evolving sequencing capabilities of research laboratories and commercial organizations around the world have resulted in a rapid growth of sequence data for RVs, and dealing with these data has become a major challenge. In an attempt to introduce a systematic method of naming RV strains, the RCWG proposes the following nomenclature: RV group/species of origin/country of identification/common name/year of identification/G- and P-type. In this nomenclature, specific guidelines were developed for wild-type RV strains, tissue-culture-adapted strains, RV vaccine strains and RV strains that have been generated or engineered in a laboratory using reassortment or reverse genetics procedures. The current proposal only leaves room for 15 explanatory characters in the "common name" section of the complete strain name. For all of the other sections (RV group, species of isolation, country of isolation, year of isolation and G/P-genotype), the guidelines are very rigorous. The reason for allowing the freedom of choosing 15 characters in the "common name" section is to provide authors an opportunity to highlight specific or important information. Examples of information that could be added include: i) the city or state of strain identification, ii) clinical outcomes or viral phenotypic characteristics and iii) mutations or engineered changes in the viral genome. However, we think that it is impossible to include all relevant information about a strain in the actual name. Instead, such information should be added in the metadata linked to each record in GenBank or any other database.

The RCWG is fully aware that it is impossible to define rules for each real-life or hypothetical situation, especially when a strain has undergone several types of manipulations (e.g., a combination of cell culture adaptation, passaging in a homologous host animal and the introduction of reverse-genetic engineered mutations). Therefore, we encourage researchers to choose a strain name that appears to be most appropriate or to contact the RCWG for guidance. While it is not necessary to include in the actual strain name, detailed information about manipulations should be added to the metadata of a record.

This standardized naming procedure is reminiscent of the nomenclature guidelines for influenza viruses and will be very useful for future analysis. However, this system will only succeed if the entire research community supports and adheres to the proposed guidelines. Regarding the use of this new nomenclature in scientific articles, the RCWG suggests that authors use the full strain name the first time it is mentioned in the text and then subsequently use the "common name" (i.e., a suitable abbreviation). In addition, authors should consider using the full strain name in phylogenetic trees, tables and figures if it enhances the interpretation or presentation of the data. However, depending on the individual characteristics of a manuscript, authors have the flexibility to use alternative strategies.

Towards utilizing the large amount of RV nucleotide sequence data, an RV-specific database is being developed by the NCBI, which is expected to be launched in the second half of 2011. This resource will be similar to the NCBI Virus Variation resources developed for influenza and dengue viruses [10, 81] and the resources developed at the Los Alamos National Laboratory for hepatitis C virus (HCV) [43] and for human immunodeficiency virus (HIV) (http://www.hiv.lanl.gov./content/). RV nucleotide sequence data, as well as metadata describing the biological and epidemiological context of associated sequences, will be stored in specially designed relational databases. A new, user-friendly web interface will allow investigators to construct and explore resource queries based on a variety of criteria. Additionally, novel web-based tools and displays will allow users to compare retrieved nucleotide and protein sequences on the basis of chronology, geography and biological significance. In order to fully exploit the possibilities of such a resource for the study of viral epidemiology, seasonality, geographical spread, links between specific strains and clinical manifestations, possible

vaccine escape-mutants, etc., it is imperative that nucleotide sequence submissions include relevant metadata. In addition, the RCWG strongly encourages researchers to retrospectively update the names of their RV sequences in GenBank and add relevant metadata to the files. This process is straightforward and will greatly enhance the scientific potential of individual sequence records. From Table 1, it is obvious that close monitoring, updating and genotype assignment activities of the RCWG as practiced during the past three years are absolutely necessary to sustain and develop the new RV genotype-based classification and nomenclature system. With the increasing number of sequence data becoming available for non-RVA strains, the activities of the RCWG will probably be expanded in the near future.

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References

1. Abe M, Ito N, Masatani T, Nakagawa K, Yamaoka S, Kanamaru Y, Suzuki H, Shibano K, Arashi Y, Sugiyama M (2011) Whole genome characterization of new bovine rotavirus G21P[29] and G24P[33] strains provides evidence for interspecies transmission. J Gen Virol 92:952–960
2. Arora R, Chitambar SD (2011) Full genomic analysis of Indian G1P[8] rotavirus strains. Infect Genet Evol 11(2):504–511
3. Baggi F, Peduzzi R (2000) Genotyping of rotaviruses in environmental water and stool samples in Southern Switzerland by nucleotide sequence analysis of 189 base pairs at the 5' end of the VP7 gene. J Clin Microbiol 38:3681–3685
4. Ball LA (2005) The universal taxonomy of viruses in theory and practice. In: Fauquet CM, Mayo MA, Maniloff J, Desselberger U, Ball LA (eds) Virus taxonomy: eight report of the international committee on taxonomy of viruses. Elsevier/Academic Press, Amsterdam/Holland, pp 3–8
5. Banyai K, Esona MD, Mijatovic S, Kerin TK, Pedreira C, Mercado J, Balmaseda A, Perez MC, Patel MM, Gentsch JR (2009) Zoonotic bovine rotavirus strain in a diarrheic child, Nicaragua. J Clin Virol 46:391–393
6. Bányai K, Martella V, Molnár P, Mihály I, Van Ranst M, Matthijnssens J (2009) Genetic heterogeneity in human G6P[14] rotavirus strains detected in Hungary suggests independent zoonotic origin. J Infect 59(3):213–215
7. Banyai K, Mijatovic-Rustempasic S, Hull JJ, Esona MD, Freeman MM, Frace AM, Bowen MD, Gentsch JR (2011) Sequencing and phylogenetic analysis of the coding region of six common rotavirus strains: Evidence for intragenogroup reassortment among co-circulating G1P[8] and G2P[4] strains from the United States. J Med Virol 83:532–539
8. Bányai K, Esona MD, Kerin TK, Hull JJ, Mijatovic S, Vásconez N, Torres C, de Filippis AM, Foytich KR, Gentsch JR (2009) Molecular characterization of a rare, human-porcine reassortant rotavirus strain, G11P[6], from Ecuador. Arch Virol 154(11):1823–1829
9. Bányai K, Papp H, Dandar E, Molnar P, Mihaly I, Van Ranst M, Martella V, Matthijnssens J (2010) Whole genome sequencing and phylogenetic analysis of a zoonotic human G8P[14] rotavirus strain. Infect Genet Evol 10:1140–1144
10. Bao Y, Bolotov P, Dernovoy D, Kiryutin B, Zaslavsky L, Tatusova T, Ostell J, Lipman D (2008) The influenza virus resource at the National Center for Biotechnology Information. J Virol 82:596–601
11. Barman P, Ghosh S, Das S, Varghese V, Chaudhuri S, Sarkar S, Krishnan T, Bhattacharya SK, Chakrabarti A, Kobayashi N, Naik TN (2004) Sequencing and sequence analysis of VP7 and NSP5 genes reveal emergence of a new genotype of bovine group B rotaviruses in India. J Clin Microbiol 42:2816–2818
12. Bremont M, Juste-Lesage P, Chabanne-Vautherot D, Charpilienne A, Cohen J (1992) Sequences of the four larger proteins of a porcine group C rotavirus and comparison with the equivalent group A rotavirus proteins. Virology 186:684–692
13. Chen Y, Wen Y, Liu X, Xiong X, Cao Z, Zhao Q, Yu Y, Yin X, Li C, Fan Y (2008) Full genomic analysis of human rotavirus strain TB-Chen isolated in China. Virology 375:361–373
14. Chen Y, Zhu W, Sui S, Yin Y, Hu S, Zhang X (2009) Whole genome sequencing of lamb rotavirus and comparative analysis with other mammalian rotaviruses. Virus Genes 38:302–310
15. Chen Z, Lambden PR, Lau J, Caul EO, Clarke IN (2002) Human group C rotavirus: completion of the genome sequence and gene coding assignments of a non-cultivatable rotavirus. Virus Res 83:179–187
16. Chitambar SD, Arora R, Chhabra P (2009) Molecular characterization of a rare G1P[19] rotavirus strain from India: evidence of reassortment between human and porcine rotavirus strains. J Med Microbiol 58:1611–1615
17. Clark HF, Borian FE, Bell LM, Modesto K, Gouvea V, Plotkin SA (1988) Protective effect of WC3 vaccine against rotavirus diarrhea in infants during a predominantly serotype 1 rotavirus season. J Infect Dis 158:570–587
18. Cohen J, Lefevre F, Estes MK, Bremont M (1984) Cloning of bovine rotavirus (RF strain): nucleotide sequence of the gene coding for the major capsid protein. Virology 138:178–182
19. Collins PJ, Martella V, Buonavoglia C, O'Shea H (2010) Identification of a G2-like porcine rotavirus bearing a novel VP4 type, P[32]. Vet Res 41:73
20. De Grazia S, Giammanco GM, Potgieter CA, Matthijnssens J, Bányai K, Platia MA, Colomba C, Martella V (2010) Unusual assortment of segments in 2 rare human rotavirus genomes. Emerg Infect Dis 16:859–862
21. Dyall-Smith ML, Elleman TC, Hoyne PA, Holmes IH, Azad AA (1983) Cloning and sequence of UK bovine rotavirus gene segment 7: marked sequence homology with simian rotavirus gene segment 8. Nucleic Acids Res 11:3351–3362
22. El-Attar L, Dhaliwal W, Howard CR, Bridger JC (2001) Rotavirus cross-species pathogenicity: molecular characterization of a bovine rotavirus pathogenic for pigs. Virology 291:172–182
23. Esona MD, Mijatovic-Rustempasic S, Conrardy C, Tong S, Kuzmin IV, Agwanda B, Breiman RF, Bányai K, Niezgoda M, Rupprecht CE, Gentsch JR, Bowen MD (2010) Reassortant Group A rotavirus from straw-colored fruit bat (*Eidolon helvum*). Emerg Infect Dis 16:1844–1852

24. Esona MD, Banyai K, Foytich K, Freeman M, Mijatovic-Rustempasic S, Hull J, Kerin T, Steele AD, Armah GE, Geyer A, Page N, Agbaya VA, Forbi JC, Aminu M, Gautam R, Seheri LM, Nyangao J, Glass R, Bowen MD, Gentsch JR (2011) Genomic characterization of human rotavirus G10 strains from the African Rotavirus Network: relationship to animal rotaviruses. Infect Genet Evol 11:237–241
25. Estes M, Kapikian A (2007) Rotaviruses. In: Knipe DM, Howley PM, Griffin DE, Lamb RA, Martin MA, Roizman B, Straus SE (eds) Fields Virology, 4th edn. Kluwer/Lippincott Williams and Wilkins, Philadelphia, pp 1917–1974
26. Feng N, Sen A, Nguyen H, Vo P, Hoshino Y, Deal EM, Greenberg HB (2009) Variation in antagonism of the interferon response to rotavirus NSP1 results in differential infectivity in mouse embryonic fibroblasts. J Virol 83:6987–6994
27. Garbarg-Chenon A, Bricout F, Nicolas JC (1986) Serological characterization of human reassortant rotaviruses. J Virol 59:510–513
28. Georges-Courbot MC, Monges J, Siopathis MR, Roungou JB, Gresenguet G, Bellec L, Bouquety JC, Lanckriet C, Cadoz M, Hessel L et al (1991) Evaluation of the efficacy of a low-passage bovine rotavirus (strain WC3) vaccine in children in Central Africa. Res Virol 142:405–411
29. Ghosh S, Alam MM, Ahmed MU, Talukdar RI, Paul SK, Kobayashi N (2010) Complete genome constellation of a caprine group A rotavirus strain reveals common evolution with ruminant and human rotavirus strains. J Gen Virol 91:2367–2373
30. Ghosh S, Gatheru Z, Nyangao J, Adachi N, Urushibara N, Kobayashi N (2010) Full genomic analysis of a simian SA11-like G3P[2] rotavirus strain isolated from an asymptomatic infant: Identification of novel VP1, VP6 and NSP4 genotypes. Infect Genet Evol 11:57–63
31. Ghosh S, Kobayashi N, Nagashima S, Chawla-Sarkar M, Krishnan T, Ganesh B, Naik TN (2010) Full genomic analysis and possible origin of a porcine G12 rotavirus strain RU172. Virus Genes 40:382–388
32. Ghosh S, Gatheru Z, Nyangao J, Adachi N, Urushibara N, Kobayashi N (2011) Full genomic analysis of a G8P[1] rotavirus strain isolated from an asymptomatic infant in Kenya provides evidence for an artiodactyl-to-human interspecies transmission event. J Med Virol 83:367–376
33. Ghosh S, Paul SK, Hossain MA, Alam MM, Ahmed MU, Kobayashi N (2011) Full genomic analyses of two human G2P[4] rotavirus strains detected in 2005: identification of a caprine-like VP3 gene. J Gen Virol 92:1222–1227
34. Gombold JL, Ramig RF (1986) Analysis of reassortment of genome segments in mice mixedly infected with rotaviruses SA11 and RRV. J Virol 57:110–116
35. Gonzalez RA, Torres-Vega MA, Lopez S, Arias CF (1998) In vivo interactions among rotavirus nonstructural proteins. Arch Virol 143:981–996
36. Gorelick MH, Shaw KN, Murphy KO (1997) Validity and reliability of clinical signs in the diagnosis of dehydration in children. Pediatrics 99:E6
37. Grice AS, Lambden PR, Caul EO, Clarke IN (1994) Sequence conservation of the major outer capsid glycoprotein of human group C rotaviruses. J Med Virol 44:166–171
38. Ito H, Sugiyama M, Masubuchi K, Mori Y, Minamoto N (2001) Complete nucleotide sequence of a group A avian rotavirus genome and a comparison with its counterparts of mammalian rotaviruses. Virus Res 75:123–138
39. Jiang S, Ji S, Tang Q, Cui X, Yang H, Kan B, Gao S (2008) Molecular characterization of a novel adult diarrhoea rotavirus strain J19 isolated in China and its significance for the evolution and origin of group B rotaviruses. J Gen Virol 89:2622–2629
40. Johne R, Otto P, Roth B, Löhren U, Belnap D, Reetz J, Trojnar E (2011) Sequence analysis of the VP6-encoding genome segment of avian group F and G rotaviruses. Virology 412(2):384–391
41. Khamrin P, Maneekarn N, Peerakome S, Yagyu F, Okitsu S, Ushijima H (2006) Molecular characterization of a rare G3P[3] human rotavirus reassortant strain reveals evidence for multiple human-animal interspecies transmissions. J Med Virol 78:986–994
42. Khamrin P, Maneekarn N, Peerakome S, Chan-it W, Yagyu F, Okitsu S, Ushijima H (2007) Novel porcine rotavirus of genotype P[27] shares new phylogenetic lineage with G2 porcine rotavirus strain. Virology 361:243–252
43. Kuiken C, Hraber P, Thurmond J, Yusim K (2008) The hepatitis C sequence database in Los Alamos. Nucleic Acids Res 36:D512–D516
44. Lamhoujeb S, Cook A, Pollari F, Bidawid S, Farber J, Mattison K (2010) Rotaviruses from Canadian farm samples. Arch Virol 155:1127–1137
45. Liprandi F, Gerder M, Bastidas Z, Lopez JA, Pujol FH, Ludert JE, Joelsson DB, Ciarlet M (2003) A novel type of VP4 carried by a porcine rotavirus strain. Virology 315:373–380
46. Ludert JE, Feng N, Yu JH, Broome RL, Hoshino Y, Greenberg HB (1996) Genetic mapping indicates that VP4 is the rotavirus cell attachment protein in vitro and in vivo. J Virol 70:487–493
47. Maes P, Matthijnssens J, Rahman M, Van Ranst M (2009) RotaC: a web-based tool for the complete genome classification of group A rotaviruses. BMC Microbiol 9:238
48. Martella V, Ciarlet M, Camarda A, Pratelli A, Tempesta M, Greco G, Cavalli A, Elia G, Decaro N, Terio V, Bozzo G, Camero M, Buonavoglia C (2003) Molecular characterization of the VP4, VP6, VP7, and NSP4 genes of lapine rotaviruses identified in Italy: emergence of a novel VP4 genotype. Virology 314:358–370
49. Martella V, Ciarlet M, Bányai K, Lorusso E, Cavalli A, Corrente M, Elia G, Arista S, Camero M, Desario C, Decaro N, Lavazza A, Buonavoglia C (2006) Identification of a novel VP4 genotype carried by a serotype G5 porcine rotavirus strain. Virology 346:301–311
50. Martella V, Bányai K, Matthijnssens J, Buonavoglia C, Ciarlet M (2009) Zoonotic aspects of rotaviruses. Vet Microbiol 140:246–255
51. Martella V, Potgieter AC, Lorusso E, De Grazia S, Giammanco GM, Matthijnssens J, Bányai K, Ciarlet M, Lavazza A, Decaro N, Buonavoglia C (2011) A feline rotavirus G3P[9] carries traces of multiple reassortment events and resembles rare human G3P[9] rotaviruses. J Gen Virol 92:1214–1221
52. Matthijnssens J, Rahman M, Martella V, Xuelei Y, De Vos S, De Leener K, Ciarlet M, Buonavoglia C, Van Ranst M (2006) Full genomic analysis of human rotavirus strain B4106 and lapine rotavirus strain 30/96 provides evidence for interspecies transmission. J Virol 80:3801–3810
53. Matthijnssens J, Rahman M, Yang X, Delbeke T, Arijs I, Kabue JP, Muyembe JJ, Van Ranst M (2006) G8 rotavirus strains isolated in the Democratic Republic of Congo belong to the DS-1-like genogroup. J Clin Microbiol 44:1801–1809
54. Matthijnssens J, Ciarlet M, Heiman E, Arijs I, Delbeke T, McDonald SM, Palombo EA, Iturriza-Gómara M, Maes P, Patton JT, Rahman M, Van Ranst M (2008) 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 82:3204–3219
55. Matthijnssens J, Ciarlet M, Rahman M, Attoui H, Bányai K, Estes MK, Gentsch JR, Iturriza-Gómara M, Kirkwood CD, Martella V, Mertens PP, Nakagomi O, Patton JT, Ruggeri FM, Saif LJ, Santos N, Steyer A, Taniguchi K, Desselberger U, Van Ranst M (2008) Recommendations for the classification of

group A rotaviruses using all 11 genomic RNA segments. Arch Virol 153:1621–1629
56. Matthijnssens J, Rahman M, Van Ranst M (2008) Two out of the 11 genes of an unusual human G6P[6] rotavirus isolate are of bovine origin. J Gen Virol 89:2630–2635
57. Matthijnssens J, Bilcke J, Ciarlet M, Martella V, Bányai K, Rahman M, Zeller M, Beutels P, Van Damme P, Van Ranst M (2009) Rotavirus disease and vaccination: impact on genotype diversity. Future Microbiol 4:1303–1316
58. Matthijnssens J, Potgieter CA, Ciarlet M, Parreno V, Martella V, Bányai K, Garaicoechea L, Palombo EA, Novo L, Zeller M, Arista S, Gerna G, Rahman M, Van Ranst M (2009) Are human P[14] rotavirus strains the result of interspecies transmissions from sheep or other ungulates belonging to the mammalian order of Artiodactyla? J Virol 83:2917–2929
59. Matthijnssens J, Taraporewala ZF, Yang H, Rao S, Yuan L, Cao D, Hoshino Y, Mertens PP, Carner GR, McNeal M, Sestak K, Van Ranst M, Patton JT (2009) Simian rotaviruses possess divergent gene constellations originating from interspecies transmission and reassortment. J Virol 84:2013–2026
60. Matthijnssens J, Joelsson DB, Warakomski DJ, Zhou T, Mathis PK, van Maanen MH, Ranheim TS, Ciarlet M (2010) Molecular and biological characterization of the 5 human-bovine rotavirus (WC3)-based reassortant strains of the pentavalent rotavirus vaccine, RotaTeq(R). Virology 403:111–127
61. Matthijnssens J, Martella V, Van Ranst M (2010) Priority paper evaluation: genomic evolution, host-species barrier, reassortment and classification of rotaviruses. Future Virol 5:385–390
62. Matthijnssens J, Rahman M, Ciarlet M, Zeller M, Heylen E, Nakagomi T, Uchida R, Hassan Z, Azim T, Nakagomi O, Van Ranst M (2010) Reassortment of human rotavirus gene segments into G11 rotavirus strains. Emerg Infect Dis 16:625–630
63. Matthijnssens J, De Grazia S, Piessens J, Heylen E, Zeller M, Giammanco GM, Bányai K, Buonavoglia C, Ciarlet M, Martella V, Van Ranst M (2011) Multiple reassortment and interspecies transmission events contribute to the diversity of feline, canine and feline/canine-like human group A rotavirus strains. Infect Genet Evol (in press)
64. Maunula L, Von Bonsdorff CH (2002) Frequent reassortments may explain the genetic heterogeneity of rotaviruses: analysis of Finnish rotavirus strains. J Virol 76:11793–11800
65. McClain B, Settembre E, Temple BR, Bellamy AR, Harrison SC (2010) X-ray crystal structure of the rotavirus inner capsid particle at 3.8 A resolution. J Mol Biol 397:587–599
66. McDonald SM, Matthijnssens J, McAllen JK, Hine E, Overton L, Wang S, Lemey P, Zeller M, Van Ranst M, Spiro DJ, Patton JT (2009) Evolutionary dynamics of human rotaviruses: balancing reassortment with preferred genome constellations. PLoS Pathog 5(10):e1000634
67. Mijatovic-Rustempasic S, Bányai K, Esona MD, Foytich K, Bowen MD, Gentsch JR (2011) Genome sequence based molecular epidemiology of unusual US Rotavirus A G9 strains isolated from Omaha, USA between 1997 and 2000. Infect Genet Evol 11(2):522–527
68. Mori Y, Borgan MA, Ito N, Sugiyama M, Minamoto N (2002) Sequential analysis of nonstructural protein NSP4s derived from Group A avian rotaviruses. Virus Res 89:145–151
69. Mukherjee B, Ghosh S, Bagchi P, Dutta D, Chattopadhyay N, Kobayashi N, Chawla-Sarkar M (2011) Full genomic analyses of human G4P[4], G4P[6], G9P[19] and G10P[6] strains from north-eastern India evidence for interspecies transmission and complex reassortment events. Clin Microbiol Infect (in press)
70. Nagashima S, Kobayashi N, Ishino M, Alam MM, Ahmed MU, Paul SK, Ganesh B, Chawla-Sarkar M, Krishnan T, Naik TN, Wang YH (2008) Whole genomic characterization of a human rotavirus strain B219 belonging to a novel group of the genus Rotavirus. J Med Virol 80:2023–2033
71. Okada J, Kobayashi N, Taniguchi K, Urasawa S (1999) Analysis on reassortment of rotavirus NSP1 genes lacking coding region for cysteine-rich zinc finger motif. Arch Virol 144:345–353
72. Parashar UD, Burton A, Lanata C, Boschi-Pinto C, Shibuya K, Steele D, Birmingham M, Glass RI (2009) Global mortality associated with rotavirus disease among children in 2004. J Infect Dis 200(Suppl 1):S9–S15
73. Pietsch C, Petersen L, Patzer L, Liebert UG (2009) Molecular characteristics of German G8P[4] rotavirus strain GER1H-09 suggest that an update of G8 genotyping and subclassification are required. J Clin Microbiol 47:3569–3576
74. Qian YA, Jiang BM, Saif LJ, Kang SY, Ishimaru Y, Yamashita Y, Oseto M, Green KY (1991) Sequence conservation of gene 8 between human and porcine group C rotaviruses and its relationship to the VP7 gene of group A rotaviruses. Virology 182:562–569
75. Rahman M, Matthijnssens J, Yang X, Delbeke T, Arijs I, Taniguchi K, Iturriza-Gomara M, Iftekharuddin N, Azim T, Van Ranst M (2007) Evolutionary history and global spread of the emerging G12 human rotaviruses. J Virol 81:2382–2390
76. Rahman M, Matthijnssens J, Saiada F, Hassan Z, Heylen E, Azim T, Van Ranst M (2010) Complete genomic analysis of a Bangladeshi G1P[8] rotavirus strain detected in 2003 reveals a close evolutionary relationship with contemporary human Wa-like strains. Infect Genet Evol 10:746–754
77. Ramani S, Iturriza-Gómara M, Jana AK, Kuruvilla KA, Gray JJ, Brown DW, Kang G (2009) Whole genome characterization of reassortant G10P[11] strain (N155) from a neonate with symptomatic rotavirus infection: identification of genes of human and animal rotavirus origin. J Clin Virol 45:237–244
78. Ramig RF (1983) Isolation and genetic characterization of temperature-sensitive mutants that define five additional recombination groups in simian rotavirus SA11. Virology 130:464–473
79. Ramig RF, Ciarlet M, Mertens PPC, Dermody TS (2005) Rotavirus. In: Fauquet CM, Mayo MA, Maniloff J, Desselberger U, Ball LA (eds) Virus taxonomy: eight report of the international committee on taxonomy of viruses. Elsevier/Academic Press, Amsterdam/Holland, pp 484–496
80. Rao CD, Gowda K, Reddy BS (2000) Sequence analysis of VP4 and VP7 genes of nontypeable strains identifies a new pair of outer capsid proteins representing novel P and G genotypes in bovine rotaviruses. Virology 276:104–113
81. Resch W, Zaslavsky L, Kiryutin B, Rozanov M, Bao Y, Tatusova TA (2009) Virus variation resources at the National Center for Biotechnology Information: dengue virus. BMC Microbiol 9:65
82. Rippinger CM, Patton JT, McDonald SM (2010) Complete genome sequence analysis of candidate human rotavirus vaccine strains RV3 and 116E. Virology 405:201–213
83. Ruuska T, Vesikari T (1990) Rotavirus disease in Finnish children: use of numerical scores for clinical severity of diarrhoeal episodes. Scand J Infect Dis 22:259–267
84. Ruuska T, Vesikari T (1991) A prospective study of acute diarrhoea in Finnish children from birth to 2 1/2 years of age. Acta Paediatr Scand 80:500–507
85. Schumann T, Hotzel H, Otto P, Johne R (2009) Evidence of interspecies transmission and reassortment among avian group A rotaviruses. Virology 386:334–343
86. Small C, Barro M, Brown TL, Patton JT (2007) Genome heterogeneity of SA11 rotavirus due to reassortment with "O" agent. Virology 359:415–424

87. Solberg OD, Hasing ME, Trueba G, Eisenberg JN (2009) Characterization of novel VP7, VP4, and VP6 genotypes of a previously untypeable group A rotavirus. Virology 385:58–67
88. Steyer A, Poljsak-Prijatelj M, Barlic-Maganja D, Jamnikar U, Mijovski JZ, Marin J (2007) Molecular characterization of a new porcine rotavirus P genotype found in an asymptomatic pig in Slovenia. Virology 359:275–282
89. Than VT, Le VP, Lim I, Kim W (2011) Complete genomic characterization of cell culture adapted human G12P[6] rotaviruses isolated from South Korea. Virus Genes [Epub ahead of print]
90. Trask SD, Taraporewala ZF, Boehme KW, Dermody TS, Patton JT (2010) Dual selection mechanisms drive efficient single-gene reverse genetics for rotavirus. Proc Natl Acad Sci USA 107:18652–18657
91. Trojnar E, Otto P, Johne R (2009) The first complete genome sequence of a chicken group A rotavirus indicates independent evolution of mammalian and avian strains. Virology 386:325–333
92. Trojnar E, Otto P, Roth B, Reetz J, Johne R (2010) The genome segments of a group D rotavirus possess group A-like conserved termini but encode group-specific proteins. J Virol 84:10254–10265
93. Tsugawa T, Hoshino Y (2008) Whole genome sequence and phylogenetic analyses reveal human rotavirus G3P[3] strains Ro1845 and HCR3A are examples of direct virion transmission of canine/feline rotaviruses to humans. Virology 230:344–353
94. Tsunemitsu H, Saif LJ, Jiang BM, Shimizu M, Hiro M, Yamaguchi H, Ishiyama T, Hirai T (1991) Isolation, characterization, and serial propagation of a bovine group C rotavirus in a monkey kidney cell line (MA104). J Clin Microbiol 29:2609–2613
95. Ursu K, Kisfali P, Rigo D, Ivanics E, Erdelyi K, Dan A, Melegh B, Martella V, Bányai K (2009) Molecular analysis of the VP7 gene of pheasant rotaviruses identifies a new genotype, designated G23. Arch Virol 154:1365–1369
96. Varghese V, Das S, Singh NB, Kojima K, Bhattacharya SK, Krishnan T, Kobayashi N, Naik TN (2004) Molecular characterization of a human rotavirus reveals porcine characteristics in most of the genes including VP6 and NSP4. Arch Virol 149:155–172
97. Varghese V, Ghosh S, Das S, Bhattacharya SK, Krishnan T, Karmakar P, Kobayashi N, Naik TN (2006) Characterization of VP1, VP2 and VP3 gene segments of a human rotavirus closely related to porcine strains. Virus Genes 32:241–247
98. Vonderfecht SL, Huber AC, Eiden J, Mader LC, Yolken RH (1984) Infectious diarrhea of infant rats produced by a rotavirus-like agent. J Virol 52:94–98
99. Wang S, Sundaram JP, Spiro D (2010) VIGOR, an annotation program for small viral genomes. BMC Bioinform 11:451
100. Wang YH, Kobayashi N, Nagashima S, Zhou X, Ghosh S, Peng JS, Hu Q, Zhou DJ, Yang ZQ (2010) Full genomic analysis of a porcine-bovine reassortant G4P[6] rotavirus strain R479 isolated from an infant in China. J Med Virol 82:1094–1102
101. WHO (2005) The treatment of diarrhoea—a manual for physicians and other senior health workers. Geneva
102. Xie JX, Duan ZJ, Li DD, Li BW, Lan B, Li YQ, Kong XY, Zhang Q, Li J (2010) Detection of bovine rotavirus G10P[11] in a diary farm in Daqing, China. Bing Du Xue Bao 26:407–409
103. Yamamoto D, Ghosh S, Ganesh B, Krishnan T, Chawla-Sarkar M, Alam MM, Aung TS, Kobayashi N (2010) Analysis of genetic diversity and molecular evolution of human group B rotaviruses based on whole genome segments. J Gen Virol 91:1772–1781
104. Yamamoto D, Ghosh S, Kuzuya M, Wang Y, Zhou X, Chawla-Sarkar M, Paul SK, Ishino M, Kobayashi N (2011) Whole genomic characterization of human group C rotaviruses: identification of two lineages in VP3 gene. J Gen Virol 92:361–369
105. Yang H, Makeyev EV, Kang Z, Ji S, Bamford DH, van Dijk AA (2004) Cloning and sequence analysis of dsRNA segments 5, 6 and 7 of a novel non-group A, B, C adult rotavirus that caused an outbreak of gastroenteritis in China. Virus Res 106:15–26
106. Yang JH, Kobayashi N, Wang YH, Zhou X, Li Y, Zhou DJ, Hu ZH, Ishino M, Alam MM, Naik TN, Ahmed MU (2004) Phylogenetic analysis of a human group B rotavirus WH-1 detected in China in 2002. J Med Virol 74:662–667