NIH Public Access
Author Manuscript
Arch Virol. Author manuscript; available in PMC 2012 August 01.

Published in final edited form as:
Arch Virol. 2011 August ; 156(8): 1397–1413. doi:10.1007/s00705-011-1006-z.

Uniformity of Rotavirus Strain Nomenclature Proposed by the Rotavirus Classification Working Group (RCWG)

Jelle Matthijnssens[1], **Max Ciarlet**[2], **Sarah M. McDonald**[3], **Houssam Attoui**[4], **Krisztián Bányai**[5], **J. Rodney Brister**[6], **Javier Buesa**[7], **Mathew D. Esona**[8], **Mary K. Estes**[9], **Jon R. Gentsch**[8], **Miren Iturriza-Gómara**[10], **Reimar Johne**[11], **Carl D. Kirkwood**[12], **Vito Martella**[13], **Peter P.C. Mertens**[4], **Osamu Nakagomi**[14], **Viviana Parreño**[15], **Mustafizur Rahman**[16], **Franco M. Ruggeri**[17], **Linda J. Saif**[18], **Norma Santos**[19], **Andrej Steyer**[20], **Koki Taniguchi**[21], **John T. Patton**[3], **Ulrich Desselberger**[22], and **Marc Van Ranst**[1]

[1]Laboratory of Clinical & Epidemiological Virology, Department of Microbiology & Immunology, Rega Institute for Medical Research, University of Leuven, Belgium

[2]Clinical Research and Development, Novartis Vaccines & Diagnostics, Inc, Cambridge, Massachusetts 02139, USA

[3]Laboratory of Infectious Diseases, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD 20892 USA

[4]Vector-Borne Diseases Program, Institute for Animal Health, Ash Road, Pirbright, Surrey GU24 0NF, UK

[5]Veterinary Medical Research Institute, Hungarian Academy of Sciences, H-1143 Budapest, Hungária krt. 21, Hungary

[6]National Center for Biotechnology Information, National Library of Medicine, National Institutes of Health, Bethesda, MD, USA 20892

[7]Department of Microbiology and Ecology, School of Medicine, University of Valencia, Avda. Blasco Ibáñez, 17, 46010 Valencia, Spain

[8]Centers for Disease Control and Prevention, National Center for Immunization and Respiratory Diseases, Division of Viral Diseases, Atlanta, GA, USA

[9]Departments of Molecular Virology and Microbiology and Medicine –GI, Baylor College of Medicine, Houston, USA

[10]Enteric Virus Unit, Virus Reference Department, Centre for Infection, Health Protection Agency, Colindale, London, United Kingdom

[11]Federal Institute for Risk Assessment, Berlin, Germany

[12]Enteric Virus Research Group, Murdoch Childrens Research Institute, Royal Children's Hospital Parkville, Victoria, Australia

[13]Department of Veterinary Public Health, University of Bari, Italy

[14]Department of Molecular Microbiology and Immunology, Nagasaki University, Nagasaki 852-8523, Japan

[15]Instituto de Virología, CICVyA, INTA Castelar, Buenos Aires, Argentina

Corresponding author: Jelle Matthijnssens, Laboratory of Clinical & Epidemiological Virology, Department of Microbiology & Immunology, Rega Institute for Medical Research, Minderbroedersstraat 10, B-3000 Leuven, Belgium, Tel.: 32-16-332166, Fax: 32-16-332131, jelle.matthijnssens@uz.kuleuven.ac.be.

NIH-PA Author Manuscript
NIH-PA Author Manuscript
NIH-PA Author Manuscript

NIH-PA Author Manuscript

NIH-PA Author Manuscript

NIH-PA Author Manuscript

[16]Laboratory of Virology, ICDDR, B: Mohakhali, Dhaka-1212, Bangladesh

[17]Department of Veterinary Public Health & Food Safety, Istituto Superiore di Sanità, Rome, Italy

[18]Food Animal Health Research Program, Ohio Agricultural Research and Development Center, The Ohio State University, Wooster OH 44691, USA

[19]Departamento de Virologia, Instituto de Microbiologia, Universidade Federal do Rio de Janeiro, Brazil

[20]University of Ljubljana, Faculty of Medicine, Institute of Microbiology and Immunology, Zaloska 4, SI-1104 Ljubljana, Slovenia

[21]Department of Virology and Parasitology, Fujita Health University School of Medicine, Toyoake, Aichi 470-1192, Japan

[22]Department of Medicine, University of Cambridge, Addenbrooke's Hospital, Cambridge, U.K

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 cut-off 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. A 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 50 new genotypes: as of January 2011, new genotypes for VP7 (G20–G26), 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 identified in humans, cows, pigs, horses, mice, South American camelids (guanaco and vicuña), chickens, turkeys, pheasants, and bats. With 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, 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.

Keywords

Rotavirus; Classification; Nomenclature; Strain; Nomenclature guidelines

Introduction

Rotaviruses (RVs) are members of the *Reoviridae* family and cause severe diarrheal illness in the young of various animal species (24). 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 (69). RVs possess a genome consisting of 11 segments of double-stranded (ds) RNA (24). Most segments encode a single polypeptide, allowing the virus to express six structural viral proteins (VPs) and five non-structural proteins (NSPs) (24). However, in some group A RV strains, a second open-reading frame (ORF) is detected in genome

NIH-PA Author Manuscript

NIH-PA Author Manuscript

NIH-PA Author Manuscript

segment 11, leading to the expression of another protein product (NSP6) (33) in addition to NSP5. The viral particle has icosahedral symmetry and is composed of three concentric protein layers (24, 62). VP7 and VP4 are the components of the outermost protein layer (outer capsid), and each carries neutralizing epitopes (24). The middle protein layer (inner capsid) is composed of VP6 and surrounds the inner layer (the core shell) which is composed of VP2 (62). Comprised 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 (24). The RV NSPs have various functions in the replication and morphogenesis of RV progeny and in evasion of the host immune response (24). Based on the antigenic properties of VP6, RVs have been subdivided into 5 serological species (A–E) and two additional tentative species (F and G) according to the International Committee on Taxonomy of Viruses (ICTV) (3, 75). 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 identified in animals, mostly birds (3, 54). Epidemiologically, RVA is the most important for human infection and disease and have been classified further using various approaches. Specifically, RVA have been categorized based on the: (i) antigenic properties of VP6, VP7, and VP4 (subgroups, G-serotypes, and P-serotypes, respectively); (ii) 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 analyses (genotypes) (24, 50). Due to the segmented nature of the RV genome, reassortment events can occur after co-infection between RV strains belonging to the same group/species both *in vitro* and *in vivo* (26, 32, 61). Numerous examples of such gene exchanges are available in literature for RVA strains (46, 54). Recent data also suggests that reassortment involving the NSP1-encoding genome segment may have occurred between ancestral strains of avian RVA and RVD (87). 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 RV groups can be thought of as unique viral species (3).

In April 2008, a nucleotide sequence-based, complete genome classification system was developed for RVA strains (51). This system assigns a specific genotype to each of the 11 RV genome segments according to established nucleotide percent cut-off 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 (51). Full genome analyses have increased our recognition of the relatedness between animal and human RV strains, and highlights the relevance of a common nomenclature for both animal and public health. To maintain, evaluate, and develop this system, a Rotavirus Classification Working Group (RCWG) was formed (52), which includes researchers worldwide.

In this article, we report on the current status of genotype diversity for RVA strain 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) (94), 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 strains (9). 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

NIH-PA Author Manuscript

NIH-PA Author Manuscript

NIH-PA Author Manuscript

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 (45).

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 3 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 16 th –20 th, 2011) and the 11th International Symposium on dsRNA Viruses in San Juan, Puerto Rico (November 27 th –December 1 st, 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 in RVs identified in a variety of host species including humans, cows, pigs, horses, mice, chickens, turkeys, pheasants, South American camelids, and bats. Several of these new genotypes have been published (1, 18, 23, 30, 42, 55, 56, 81, 83, 86, 90). For several other strains, such as RVA/Human-tc/ITA/260-97/1997/G3P[3] (HQ661112-HQ661122), RVA/Cow-tc/JPN/Dai-10/2007/G24P[33] (AB513836-AB513837 and AB573070-AB573078), RVA/Mouse-tc/USA/ETD_822/XXXX/G16P[16] (GQ479947-GQ479957), RVA/Pig-wt/JPN/FGP51/2009/G4P[34] (AB571046-AB571047), and RVA/Pig-wt/JPN/TJ4-1/2010/G26P[unknown] (AB605258), at present only the GenBank accession numbers are available. Table 2 shows RV strains of all recognised genotypes that are not represented in Table 1.

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 become available. The complete genomes of 4 human RVB strains were recently sequenced and analyzed by Yamamoto and colleagues, bringing the total number of genomes to 8 (7 human RVB strains and a single murine RVB strain) (67, 98). 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 8 strains: the porcine strain Cowden and 7 human strains detected in the UK, Japan, China, Bangladesh and India (11, 14, 99). The first complete genome sequence of a RVD strain (RVD/chicken-wt/DEU/05V0049/2005/GXP[X]), was published recently (87). Furthermore, the complete genome sequences of two Novel Adult Diarrhea Rotavirus (NADRV) strains (RVX/Human-tc/CHN/NADRV-J19/1997/GXP[X], and RVX/Human-wt/BAN/NADRV-B219/2002/GXP[X]), causing diarrhea in adults, have been determined (37, 67, 100). These NADRV strains have not yet been assigned to a RV group/species by ICTV. Recently, VP6

NIH-PA Author Manuscript

NIH-PA Author Manuscript

NIH-PA Author Manuscript

sequence information was obtained for avian RVF and RVG strains (38). 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 recently published (54).

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, which 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).

- *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, or other as appropriate. In case the sample was obtained from the environment (i.e., sewage, soil, river, lake, ocean or similar), “Env” should be used. In case 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 identified should be used followed by “-wt”.
- *Country of identification*: using a unique 3-letter abbreviation code for each country according to: https://www.cia.gov/library/publications/the-world-factbook/appendix/appendix-d.html. In case 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*: 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 or

NIH-PA Author Manuscript

NIH-PA Author Manuscript

NIH-PA Author Manuscript

clinically important information, as long as the number of characters is less than/equal to 15.

- *Year of identification*: using the "yyyy" format. In case 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 identified should be used.
- *G-type*: 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*: 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.

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 which has been tissue culture adapted, 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 used cell lines or animal 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, or iii) RV strain 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, or other as appropriate. In case the sample was obtained from the environment (i.e., sewage, soil, river, lake, ocean or similar), "Env" should be used. In case 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 wildtype (-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 identified should be used followed by "-wt".
- *Country of identification*: using a unique 3-letter abbreviation code for each country according to: https://www.cia.gov/library/publications/the-world-factbook/appendix/appendix-d.html. In case 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 in the common name or the metadata, see below).
- *Common name*: See section A) above
- *Year of identification*: using the "yyyy" format. In case 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 identified should be used.

NIH-PA Author Manuscript

NIH-PA Author Manuscript

NIH-PA Author Manuscript

- *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 unambigously

These guidelines apply to any RV strain in which small deliberate changes have been introduced (examples: chemically mutagenised RV strain, moderately modified RV strain using reverse genetics techniques, etc.) or RV strains passaged in 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, or other as appropriate. In case the sample was obtained from the environment (i.e., sewage, soil, river, lake, ocean or similar), “Env” should be used. In case the species of origin is unknown, “X” should be used. The second component is “-lab” (lab engineered) to distinguish from wildtype (-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 identified should be used followed by “-wt”.
- *Country of identification*: using a unique 3-letter abbreviation code for each country according to: https://www.cia.gov/library/publications/the-world-factbook/appendix/appendix-d.html. In case 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 in the common name or the metadata, see below).
- *Common name*: See section A) above.
- *Year of identification*: using the “yyyy” format. In case 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 identified 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 2.

NIH-PA Author Manuscript

NIH-PA Author Manuscript

NIH-PA Author Manuscript

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, 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 introduced changes and the used methods 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*: 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 3.

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.

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 was identified (in case of a vaccine containing a tissue culture adapted strain) or developed (in 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*: 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 or equal than 15.

NIH-PA Author Manuscript

NIH-PA Author Manuscript

NIH-PA Author Manuscript

- *Year of identification*: The year in which the RV strain was identified (in case of a vaccine containing a tissue culture adapted strain) or developed (in 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 3.

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, which was identified in nature from any host (e.g., a vaccine strain identified 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", as long as none of the "parents" of the reassorted strains belong to categories b, c, or d
- Genotypes of remaining 9 RNA segments according to RCWG guidelines (52)
- Species/group (RVA, RVB, RVC, RVD, RVE, RV F, 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

NIH-PA Author Manuscript

NIH-PA Author Manuscript

NIH-PA Author Manuscript

- 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” as 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) (16, 27, 79, 80) or World Health Organization (WHO) ref schemes
- Clinical outcome: dehydration (using WHO or Gorelick ref schemes) (34, 96), 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 electrolytes solutions, antibiotic, anti-diarrheic or other unspecific treatment before and/or after sample collection
- Sample derive from a single case of diarrhea or an outbreak. In 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; thorough-bred or standard-bred horses, etc)

Analyses specific information

- Was sequencing performed on stool, rectal swab, intestinal content, other type of sample of the patient, environmental sample or on 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?

NIH-PA Author Manuscript

NIH-PA Author Manuscript

NIH-PA Author Manuscript

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 strain, RV vaccine strains, as well as RV strains that have been generated or engineered in a laboratory using reassortment or reverse genetics procedures. This standardized naming procedure is reminiscent of the nomenclature guidelines for influenza viruses and will be very useful for future analyses. However, this system will only succeed if the entire research community supports and adheres to the proposed guidelines. It should be noted that the terms “RV groups” and “RV species” are used interchangeably.

Towards utilizing the large amount of RV nucleotide sequence data, a 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 (9, 77) and the resources developed at the Los Alamos National Laboratory for hepatitis C virus (HCV) (41) and for human immunodeficiency virus (HIV) (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 3 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.

Acknowledgments

J. Matthijnssens is supported by an FWO (Fonds voor Wetenschappelijk Onderzoek) postdoctoral fellowship. S. McDonald and J. Patton are supported by the Intramural Research Program of the National Institute of Allergy and Infectious Diseases, National Institutes of Health. K. Bányai was supported by the Hungarian Scientific Research Fund (OTKA PD76364). J. Buesa is supported by the Consolider-Ingenio 2010 Program (FUN-C-FOOD CSD2007-063) of the Spanish Ministry of Science. R. Johne is supported by a grant of Deutsche Forschungsgemeinschaft (JO369/4-1). CD Kirkwood is supported by an NHMRC Career Development Award (607347). V. Martella was supported by the Ministry of Health, Ricerca finalizzata 2007 “Zoonosi e infezioni virali esotiche: fronteggiare le emergenze attraverso un approccio integrato fra medicina umana e veterinaria”. F.M. Ruggeri is supported by the Ministry of Health, CCM “Rotanet-Italy” Programme.

NIH-PA Author Manuscript

NIH-PA Author Manuscript

NIH-PA Author Manuscript

References

1. Abe M, Ito N, Masatani T, Nakagawa K, Yamaoka S, Kanamaru Y, Suzuki H, Shibano K, Arashi Y, Sugiyama M. Whole genome characterization of new bovine rotavirus G21P[29] and G24P[33] strains provides evidence for interspecies transmission. J Gen Virol. 2011
2. Baggi F, Peduzzi R. 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. 2000; 38:3681–5. [PubMed: 11015383]
3. Ball, LA. The universal taxonomy of viruses in theory and practice. In: Fauquet, CM.; Mayo, MA.; Maniloff, J.; Desselberger, U.; Ball, LA., editors. Virus Taxonomy: Eight Report of the International Committee on taxonomy of Viruses. Elsevier, Academic Press; Amsterdam, Holland: 2005. p. 3-8.
4. Bányai K, Esona MD, Kerin TK, Hull JJ, Mijatovic S, Vasconez N, Torres C, de Filippis AM, Gentsch JR. Molecular characterization of a rare, human-porcine reassortant rotavirus strain, G11P[6], from Ecuador. Arch Virol. 2009 Sep 18. [Epub ahead of print].
5. Banyai K, Esona MD, Mijatovic S, Kerin TK, Pedreira C, Mercado J, Balmaseda A, Perez MC, Patel MM, Gentsch JR. Zoonotic bovine rotavirus strain in a diarrheic child, Nicaragua. J Clin Virol. 2009; 46:391–3. [PubMed: 19775934]
6. Banyai K, Martella V, Molnar P, Mihaly I, Van Ranst M, Matthijnssens J. Genetic heterogeneity in human G6P[14] rotavirus strains detected in Hungary suggests independent zoonotic origin. J Infect. 2009
7. Banyai K, Mijatovic-Rustempasic S, Hull JJ, Esona MD, Freeman MM, Frace AM, Bowen MD, Gentsch JR. 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. 2011; 83:532–9. [PubMed: 21264876]
8. Bányai K, Papp H, Dandar E, Molnar P, Mihaly I, Van Ranst M, Martella V, Matthijnssens J. Whole genome sequencing and phylogenetic analysis of a zoonotic human G8P[14] rotavirus strain. Infect Genet Evol. 2010; 10:1140–1144. [PubMed: 20471499]
9. Bao Y, Bolotov P, Dernovoy D, Kiryutin B, Zaslavsky L, Tatusova T, Ostell J, Lipman D. The influenza virus resource at the National Center for Biotechnology Information. J Virol. 2008; 82:596–601. [PubMed: 17942553]
10. Barman P, Ghosh S, Das S, Varghese V, Chaudhuri S, Sarkar S, Krishnan T, Bhattacharya SK, Chakrabarti A, Kobayashi N, Naik TN. 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. 2004; 42:2816–8. [PubMed: 15184480]
11. Bremont M, Juste-Lesage P, Chabanne-Vautherot D, Charpilienne A, Cohen J. Sequences of the four larger proteins of a porcine group C rotavirus and comparison with the equivalent group A rotavirus proteins. Virology. 1992; 186:684–92. [PubMed: 1310192]
12. Chen Y, Wen Y, Liu X, Xiong X, Cao Z, Zhao Q, Yu Y, Yin X, Li C, Fan Y. Full genomic analysis of human rotavirus strain TB-Chen isolated in China. Virology. 2008; 375:361–73. [PubMed: 18329063]
13. Chen Y, Zhu W, Sui S, Yin Y, Hu S, Zhang X. Whole genome sequencing of lamb rotavirus and comparative analysis with other mammalian rotaviruses. Virus Genes. 2009; 38:302–10. [PubMed: 19214729]
14. Chen Z, Lambden PR, Lau J, Caul EO, Clarke IN. Human group C rotavirus: completion of the genome sequence and gene coding assignments of a non-cultivatable rotavirus. Virus Res. 2002; 83:179–87. [PubMed: 11864750]
15. Chitambar SD, Arora R, Chhabra P. Molecular characterization of a rare G1P[19] rotavirus strain from India: evidence of reassortment between human and porcine rotavirus strains. J Med Microbiol. 2009; 58:1611–5. [PubMed: 19679684]
16. Clark HF, Borian FE, Bell LM, Modesto K, Gouvea V, Plotkin SA. Protective effect of WC3 vaccine against rotavirus diarrhea in infants during a predominantly serotype 1 rotavirus season. J Infect Dis. 1988; 158:570–87. [PubMed: 2842405]

NIH-PA Author Manuscript

NIH-PA Author Manuscript

NIH-PA Author Manuscript

17. Cohen J, Lefevre F, Estes MK, Bremont M. Cloning of bovine rotavirus (RF strain): nucleotide sequence of the gene coding for the major capsid protein. Virology. 1984; 138:178–82. [PubMed: 6093360]

18. Collins PJ, Martella V, Buonavoglia C, O'Shea H. Identification of a G2-like porcine rotavirus bearing a novel VP4 type, P[32]. Vet Res. 2010; 41:73. [PubMed: 20663474]

19. De Grazia S, Giammanco GM, Potgieter CA, Matthijnssens J, Bányai K, Platia MA, Colomba C, Martella V. Unusual assortment of segments in 2 rare human rotavirus genomes. Emerg Infect Dis. 2010; 16:859–62. [PubMed: 20409385]

20. Dyall-Smith ML, Elleman TC, Hoyne PA, Holmes IH, Azad AA. Cloning and sequence of UK bovine rotavirus gene segment 7: marked sequence homology with simian rotavirus gene segment 8. Nucleic Acids Res. 1983; 11:3351–62. [PubMed: 6304629]

21. El-Attar L, Dhaliwal W, Howard CR, Bridger JC. Rotavirus cross-species pathogenicity: molecular characterization of a bovine rotavirus pathogenic for pigs. Virology. 2001; 291:172–82. [PubMed: 11878886]

22. 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. Genomic characterization of human rotavirus G10 strains from the African Rotavirus Network: relationship to animal rotaviruses. Infect Genet Evol. 2011; 11:237–41. [PubMed: 20934537]

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. Reassortant Group A Rotavirus from Straw-colored Fruit Bat (Eidolon helvum). Emerg Infect Dis. 2010; 16:1844–1852. [PubMed: 21122212]

24. Estes, M.; Kapikian, A. Rotaviruses. In: Knipe, DM.; Howley, PM.; Griffin, DE.; Lamb, RA.; Martin, MA.; Roizman, B.; Straus, SE., editors. Fields Virology. 5. Kluwer Health/Lippincott, Williams and Wilkins; Philadelphia: 2007. p. 1917-1974.

25. Feng N, Sen A, Nguyen H, Vo P, Hoshino Y, Deal EM, Greenberg HB. Variation in antagonism of the interferon response to rotavirus NSP1 results in differential infectivity in mouse embryonic fibroblasts. J Virol. 2009; 83:6987–94. [PubMed: 19420080]

26. Garbarg-Chenon A, Bricout F, Nicolas JC. Serological characterization of human reassortant rotaviruses. J Virol. 1986; 59:510–3. [PubMed: 3016313]

27. Georges-Courbot MC, Monges J, Siopathis MR, Roungou JB, Gresenguet G, Bellec L, Bouquety JC, Lanckriet C, Cadoz M, Hessel L, et al. Evaluation of the efficacy of a low-passage bovine rotavirus (strain WC3) vaccine in children in Central Africa. Res Virol. 1991; 142:405–11. [PubMed: 1663261]

28. Ghosh S, Alam MM, Ahmed MU, Talukdar RI, Paul SK, Kobayashi N. Complete genome constellation of a caprine group A rotavirus strain reveals common evolution with ruminant and human rotavirus strains. J Gen Virol. 2010; 91:2367–73. [PubMed: 20505013]

29. Ghosh S, Gatheru Z, Nyangao J, Adachi N, Urushibara N, Kobayashi N. 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. 2011; 83:367–76. [PubMed: 21181935]

30. Ghosh S, Gatheru Z, Nyangao J, Adachi N, Urushibara N, Kobayashi N. 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. 2010; 11:57–63. [PubMed: 21035567]

31. Ghosh S, Kobayashi N, Nagashima S, Chawla-Sarkar M, Krishnan T, Ganesh B, Naik TN. Full genomic analysis and possible origin of a porcine G12 rotavirus strain RU172. Virus Genes. 2010; 40:382–388. [PubMed: 20157771]

32. Gombold JL, Ramig RF. Analysis of reassortment of genome segments in mice mixedly infected with rotaviruses SA11 and RRV. J Virol. 1986; 57:110–6. [PubMed: 3001336]

33. Gonzalez RA, Torres-Vega MA, Lopez S, Arias CF. In vivo interactions among rotavirus nonstructural proteins. Arch Virol. 1998; 143:981–96. [PubMed: 9645203]

34. Gorelick MH, Shaw KN, Murphy KO. Validity and Reliability of Clinical Signs in the Diagnosis of Dehydration in Children. pediatrics. 1997; 99:E6. [PubMed: 9113963]

NIH-PA Author Manuscript

NIH-PA Author Manuscript

NIH-PA Author Manuscript

35. Grice AS, Lambden PR, Caul EO, Clarke IN. Sequence conservation of the major outer capsid glycoprotein of human group C rotaviruses. J Med Virol. 1994; 44:166–71. [PubMed: 7852957]
36. Ito H, Sugiyama M, Masubuchi K, Mori Y, Minamoto N. Complete nucleotide sequence of a group A avian rotavirus genome and a comparison with its counterparts of mammalian rotaviruses. Virus Res. 2001; 75:123–38. [PubMed: 11325467]
37. Jiang S, Ji S, Tang Q, Cui X, Yang H, Kan B, Gao S. 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. 2008; 89:2622–9. [PubMed: 18796732]
38. Johne R, Otto P, Roth B, Lörhen U, Belnap D, Reetz J, Trojnar E. Sequence analysis of the VP6-encoding genome segment of avian group F and G rotaviruses. Virology. 2011 Accepted for publication.
39. Khamrin P, Maneekarn N, Peerakome S, Chan-it W, Yagyu F, Okitsu S, Ushijima H. Novel porcine rotavirus of genotype P[27] shares new phylogenetic lineage with G2 porcine rotavirus strain. Virology. 2007; 361:243–52. [PubMed: 17215015]
40. Khamrin P, Maneekarn N, Peerakome S, Yagyu F, Okitsu S, Ushijima H. Molecular characterization of a rare G3P[3] human rotavirus reassortant strain reveals evidence for multiple human-animal interspecies transmissions. J Med Virol. 2006; 78:986–94. [PubMed: 16721863]
41. Kuiken C, Hraber P, Thurmond J, Yusim K. The hepatitis C sequence database in Los Alamos. Nucleic Acids Res. 2008; 36:D512–6. [PubMed: 18025038]
42. Lamhoujeb S, Cook A, Pollari F, Bidawid S, Farber J, Mattison K. Rotaviruses from Canadian farm samples. Arch Virol. 2010; 155:1127–37. [PubMed: 20517624]
43. Liprandi F, Gerder M, Bastidas Z, Lopez JA, Pujol FH, Ludert JE, Joelsson DB, Ciarlet M. A novel type of VP4 carried by a porcine rotavirus strain. Virology. 2003; 315:373–80. [PubMed: 14585340]
44. Ludert JE, Feng N, Yu JH, Broome RL, Hoshino Y, Greenberg HB. Genetic mapping indicates that VP4 is the rotavirus cell attachment protein in vitro and in vivo. J Virol. 1996; 70:487–93. [PubMed: 8523562]
45. Maes P, Matthijnssens J, Rahman M, Van Ranst M. RotaC: a web-based tool for the complete genome classification of group A rotaviruses. BMC Microbiol. 2009; 9:238. [PubMed: 19930627]
46. Martella V, Bányai K, Matthijnssens J, Buonavoglia C, Ciarlet M. Zoonotic aspects of rotaviruses. Vet Microbiol. 2009; 140:246–255. [PubMed: 19781872]
47. 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. Identification of a novel VP4 genotype carried by a serotype G5 porcine rotavirus strain. Virology. 2006; 346:301–11. [PubMed: 16364388]
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. Molecular characterization of the VP4, VP6, VP7, and NSP4 genes of lapine rotaviruses identified in italy: emergence of a novel VP4 genotype. Virology. 2003; 314:358–70. [PubMed: 14517088]
49. Martella V, Potgieter C, Lorusso E, De Grazia S, Giammanco G, Matthijnssens J, Banyai K, Ciarlet M, Lavazza A, Decaro N, Buonavoglia C. A feline rotavirus G3P[9] carries traces of multiple reassortment events and resembles rare human G3P[9] rotaviruses. J Gen Virol. 2011
50. Matthijnssens J, Bilcke J, Ciarlet M, Martella V, Bányai K, Rahman M, Zeller M, Beutels P, Van Damme P, Van Ranst M. Rotavirus disease and vaccination: impact on genotype diversity. Future Microbiol. 2009; 4:1303–16. [PubMed: 19995190]
51. 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. 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; 82:3204–3219. [PubMed: 18216098]
52. 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. Recommendations for the classification of group A rotaviruses using all 11 genomic RNA segments. Arch Virol. 2008; 153:1621–9. [PubMed: 18604469]

NIH-PA Author Manuscript

NIH-PA Author Manuscript

NIH-PA Author Manuscript

53. Matthijnssens J, Joelsson DB, Warakomski DJ, Zhou T, Mathis PK, van Maanen MH, Ranheim TS, Ciarlet M. Molecular and biological characterization of the 5 human-bovine rotavirus (WC3)-based reassortant strains of the pentavalent rotavirus vaccine, RotaTeq(R). Virology. 2010; 403:111–127. [PubMed: 20451234]
54. Matthijnssens J, Martella V, Van Ranst M. Priority Paper Evaluation: Genomic evolution, host-species barrier, reassortment and classification of rotaviruses. Future Virology. 2010; 5:385–390.
55. 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. 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. 2009; 83:2917–29. [PubMed: 19153225]
56. Matthijnssens J, Rahman M, Ciarlet M, Zeller M, Heylen E, Nakagomi T, Uchida R, Hassan Z, Azim T, Nakagomi O, Van Ranst M. Reassortment of human rotavirus gene segments into G11 rotavirus strains. Emerg Infect Dis. 2010; 16:625–30. [PubMed: 20350376]
57. Matthijnssens J, Rahman M, Martella V, Xuelei Y, De Vos S, De Leener K, Ciarlet M, Buonavoglia C, Van Ranst M. Full genomic analysis of human rotavirus strain B4106 and lapine rotavirus strain 30/96 provides evidence for interspecies transmission. J Virol. 2006; 80:3801–10. [PubMed: 16571797]
58. Matthijnssens J, Rahman M, Van Ranst M. Two out of the 11 genes of an unusual human G6P[6] rotavirus isolate are of bovine origin. J Gen Virol. 2008; 89:2630–5. [PubMed: 18796733]
59. Matthijnssens J, Rahman M, Yang X, Delbeke T, Arijs I, Kabue JP, Muyembe JJ, Van Ranst M. G8 rotavirus strains isolated in the Democratic Republic of Congo belong to the DS-1-like genogroup. J Clin Microbiol. 2006; 44:1801–9. [PubMed: 16672410]
60. 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. Simian rotaviruses possess divergent gene constellations originating from interspecies transmission and reassortment. J Virol. 2009; 84:2013–2026. [PubMed: 19939934]
61. Maunula L, Von Bonsdorff CH. Frequent reassortments may explain the genetic heterogeneity of rotaviruses: analysis of Finnish rotavirus strains. J Virol. 2002; 76:11793–800. [PubMed: 12414921]
62. McClain B, Settembre E, Temple BR, Bellamy AR, Harrison SC. X-ray crystal structure of the rotavirus inner capsid particle at 3.8 A resolution. J Mol Biol. 2010; 397:587–99. [PubMed: 20122940]
63. McDonald SM, Matthijnssens J, McAllen JK, Hine E, Overton L, Wang S, Lemey P, Zeller M, Van Ranst M, Spiro DJ, Patton JT. Evolutionary dynamics of human rotaviruses: balancing reassortment with preferred genome constellations. PLoS Pathog. 2009; 5 Epub 2009 Oct 23.
64. Mijatovic-Rustempasic S, Banyai K, Esona M, Foytich K, Bowen MD, Gentsch JR. Genome sequence based molecular epidemiology of unusual US Rotavirus A G9 strains isolated from Omaha, USA between 1997 and 2000. Infect Genet Evol. 2011
65. Mori Y, Borgan MA, Ito N, Sugiyama M, Minamoto N. Sequential analysis of nonstructural protein NSP4s derived from Group A avian rotaviruses. Virus Res. 2002; 89:145–51. [PubMed: 12367757]
66. Mukherjee B, Ghosh S, Bagchi P, Dutta D, Chattopadhyay N, Kobayashi N, Chawla-Sarkar M. 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. Clinical Microbiology and Infection. 2011 In press.
67. Nagashima S, Kobayashi N, Ishino M, Alam MM, Ahmed MU, Paul SK, Ganesh B, Chawla-Sarkar M, Krishnan T, Naik TN, Wang YH. Whole genomic characterization of a human rotavirus strain B219 belonging to a novel group of the genus Rotavirus. J Med Virol. 2008; 80:2023–33. [PubMed: 18814255]
68. Okada J, Kobayashi N, Taniguchi K, Urasawa S. Analysis on reassortment of rotavirus NSP1 genes lacking coding region for cysteine-rich zinc finger motif. Arch Virol. 1999; 144:345– 53. [PubMed: 10470258]

NIH-PA Author Manuscript

NIH-PA Author Manuscript

NIH-PA Author Manuscript

69. Parashar UD, Burton A, Lanata C, Boschi-Pinto C, Shibuya K, Steele D, Birmingham M, Glass RI. Global mortality associated with rotavirus disease among children in 2004. J Infect Dis. 2009; 200(Suppl 1):S9–S15. [PubMed: 19817620]
70. Pietsch C, Petersen L, Patzer L, Liebert UG. Molecular characteristics of German G8P[4] rotavirus strain GER1H-09 suggest that an update of G8 genotyping and subclassification are required. J Clin Microbiol. 2009; 47:3569–3576. [PubMed: 19741083]
71. Qian YA, Jiang BM, Saif LJ, Kang SY, Ishimaru Y, Yamashita Y, Oseto M, Green KY. Sequence conservation of gene 8 between human and porcine group C rotaviruses and its relationship to the VP7 gene of group A rotaviruses. Virology. 1991; 182:562–9. [PubMed: 1850919]
72. Rahman M, Matthijnssens J, Saiada F, Hassan Z, Heylen E, Azim T, Van Ranst M. 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. 2010; 10:746–754. [PubMed: 20441801]
73. Rahman M, Matthijnssens J, Yang X, Delbeke T, Arijs I, Taniguchi K, Iturriza-Gomara M, Iftekharuddin N, Azim T, Van Ranst M. Evolutionary history and global spread of the emerging G12 human rotaviruses. J Virol. 2007; 81:2382–90. [PubMed: 17166908]
74. Ramani S, Iturriza-Gómara M, Jana AK, Kuruvilla KA, Gray JJ, Brown DW, Kang G. 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. 2009; 45:237–44. [PubMed: 19505846]
75. Ramig, RF.; Ciarlet, M.; Mertens, PPC.; Dermody, TS. Rotavirus. In: Fauquet, CM.; Mayo, MA.; Maniloff, J.; Desselberger, U.; Ball, LA., editors. Virus Taxonomy: Eight Report of the International Committee on Taxonomy of Viruses. Elsevier, Academic Press; Amsterdam, Holland: 2005. p. 484-496.
76. Rao CD, Gowda K, Reddy BS. 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. 2000; 276:104–13. [PubMed: 11021999]
77. Resch W, Zaslavsky L, Kiryutin B, Rozanov M, Bao Y, Tatusova TA. Virus variation resources at the National Center for Biotechnology Information: dengue virus. BMC Microbiol. 2009; 9:65. [PubMed: 19341451]
78. Rippinger CM, Patton JT, McDonald SM. Complete genome sequence analysis of candidate human rotavirus vaccine strains RV3 and 116E. Virology. 2010; 405:201–13. [PubMed: 20580391]
79. Ruuska T, Vesikari T. A prospective study of acute diarrhoea in Finnish children from birth to 2 1/2 years of age. Acta Paediatr Scand. 1991; 80:500–7. [PubMed: 1872172]
80. Ruuska T, Vesikari T. Rotavirus disease in Finnish children: use of numerical scores for clinical severity of diarrhoeal episodes. Scand J Infect Dis. 1990; 22:259–67. [PubMed: 2371542]
81. Schumann T, Hotzel H, Otto P, Johne R. Evidence of interspecies transmission and reassortment among avian group A rotaviruses. Virology. 2009; 386:334–343. [PubMed: 19249805]
82. Small C, Barro M, Brown TL, Patton JT. Genome heterogeneity of SA11 rotavirus due to reassortment with “O” agent. Virology. 2007; 359:415–24. [PubMed: 17059839]
83. Solberg OD, Hasing ME, Trueba G, Eisenberg JN. Characterization of novel VP7, VP4, and VP6 genotypes of a previously untypeable group A rotavirus. Virology. 2009; 385:58–67. [PubMed: 19131083]
84. Steyer A, Poljsak-Prijatelj M, Barlic-Maganja D, Jamnikar U, Mijovski JZ, Marin J. Molecular characterization of a new porcine rotavirus P genotype found in an asymptomatic pig in Slovenia. Virology. 2007; 359:275–82. [PubMed: 17078990]
85. Trask SD, Taraporewala ZF, Boehme KW, Dermody TS, Patton JT. Dual selection mechanisms drive efficient single-gene reverse genetics for rotavirus. Proc Natl Acad Sci U S A. 2010; 107:18652–7. [PubMed: 20937889]
86. Trojnar E, Otto P, Johne R. The first complete genome sequence of a chicken group A rotavirus indicates independent evolution of mammalian and avian strains. Virology. 2009; 386:325–33. [PubMed: 19246068]

NIH-PA Author Manuscript

NIH-PA Author Manuscript

NIH-PA Author Manuscript

87. Trojnar E, Otto P, Roth B, Reetz J, Johne R. The genome segments of a group D rotavirus possess group A-like conserved termini but encode group-specific proteins. J Virol. 2010; 84:10254–65. [PubMed: 20631147]

88. Tsugawa T, Hoshino Y. 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. 2008; 230:344–353. [PubMed: 18789808]

89. Tsunemitsu H, Saif LJ, Jiang BM, Shimizu M, Hiro M, Yamaguchi H, Ishiyama T, Hirai T. Isolation, characterization, and serial propagation of a bovine group C rotavirus in a monkey kidney cell line (MA104). J Clin Microbiol. 1991; 29:2609–13. [PubMed: 1663512]

90. Ursu K, Kisfali P, Rigo D, Ivanics E, Erdelyi K, Dan A, Melegh B, Martella V, Bányai K. Molecular analysis of the VP7 gene of pheasant rotaviruses identifies a new genotype, designated G23. Arch Virol. 2009; 154:1365–9. [PubMed: 19593592]

91. Varghese V, Das S, Singh NB, Kojima K, Bhattacharya SK, Krishnan T, Kobayashi N, Naik TN. Molecular characterization of a human rotavirus reveals porcine characteristics in most of the genes including VP6 and NSP4. Arch Virol. 2004; 149:155–72. [PubMed: 14689281]

92. Varghese V, Ghosh S, Das S, Bhattacharya SK, Krishnan T, Karmakar P, Kobayashi N, Naik TN. Characterization of VP1, VP2 and VP3 gene segments of a human rotavirus closely related to porcine strains. Virus Genes. 2006; 32:241–7. [PubMed: 16732476]

93. Vonderfecht SL, Huber AC, Eiden J, Mader LC, Yolken RH. Infectious diarrhea of infant rats produced by a rotavirus-like agent. J Virol. 1984; 52:94–8. [PubMed: 6090714]

94. Wang S, Sundaram JP, Spiro D. VIGOR, an annotation program for small viral genomes. BMC Bioinformatics. 2010; 11:451. [PubMed: 20822531]

95. Wang YH, Kobayashi N, Nagashima S, Zhou X, Ghosh S, Peng JS, Hu Q, Zhou DJ, Yang ZQ. Full genomic analysis of a porcine-bovine reassortant G4P[6] rotavirus strain R479 isolated from an infant in China. J Med Virol. 2010; 82:1094–102. [PubMed: 20419827]

96. WHO. THE TREATMENT OF DIARRHOEA - A manual for physicians and other senior health workers. 2005

97. Xie JX, Duan ZJ, Li DD, Li BW, Lan B, Li YQ, Kong XY, Zhang Q, Li J. Detection of bovine rotavirus G10P[11] in a diary farm in Daqing, China. Bing Du Xue Bao. 2010; 26:407–9. [PubMed: 21043143]

98. Yamamoto D, Ghosh S, Ganesh B, Krishnan T, Chawla-Sarkar M, Alam MM, Aung TS, Kobayashi N. Analysis of genetic diversity and molecular evolution of human group B rotaviruses based on whole genome segments. J Gen Virol. 2010; 91:1772–1781. [PubMed: 20200192]

99. Yamamoto D, Ghosh S, Kuzuya M, Wang Y, Zhou X, Chawla-Sarkar M, Paul SK, Ishino M, Kobayashi N. Whole genomic characterization of human group C rotaviruses: identification of two lineages in VP3 gene. J Gen Virol. 2010; 92:361–369. [PubMed: 21048036]

100. Yang H, Makeyev EV, Kang Z, Ji S, Bamford DH, van Dijk AA. 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. 2004; 106:15–26. [PubMed: 15522443]

101. Yang JH, Kobayashi N, Wang YH, Zhou X, Li Y, Zhou DJ, Hu ZH, Ishino M, Alam MM, Naik TN, Ahmed MU. Phylogenetic analysis of a human group B rotavirus WH-1 detected in China in 2002. J Med Virol. 2004; 74:662–7. [PubMed: 15484272]

NIH-PA Author Manuscript NIH-PA Author Manuscript NIH-PA Author Manuscript

Table 1

RV strains possessing novel genotypes assigned by the RCWG since its formation in April 2008 (51, 52). Strain name, available genotype constellation and publication are shown. Novel assigned genotypes are in bold.

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**									(83)
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	(55)
RVA/Chicken-tc/DEU/02V0002G3/2002/G19P[30]	G19	**P[30]**	I11	**R6**	**C6**	**M7**	**A16**	**N6**	**T8**	E10	**H8**	(86)
RVA/Turkey-tc/DEU/03V0002E10/2003/G22P[35]	**G22**	**P[35]**	I4								H4	(81), N.P.
RVA/Chicken-tc/DEU/06V0661/2006/G19P[31]	G19	**P[31]**	I11								H8	(81)
RVA/Human-wt/NPL/KTM368/2004/G11P[25]	G11	P[25]	**I12**	R1	C1	M1	A1	N1	T1	E1	H1	(56)
RVA/Human-tc/ITA/260-97/1997/G3P[3]	G3	P[3]	I3	R3	C3	M3	**A15**	N2	T3	E3	H6	N.P.
RVA/Horse-wt/ARG/E30/1993/G3P[12]	G3	P[12]	I6	R2	C2	M3	A10	N2	T3	E2	**H7**	N.P.
RVA/Pig-wt/IRL/61/07-ire/2007/G2P[32]	G2	**P[32]**	I5							E9		(18)
RVA/Pheasant-wt/HUN/Phea14246/2008/G23P[?]	**G23**											(90)
RVA/Pig-wt/CAN/CE-M-06-0003/2005/G2P[27]	G2	P[27]	**I14**									(42)
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**	N.P.
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]**										N.P.
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**											N.P.
RVA/Horse-tc/GBR/L338/1991/G13P[18]	G13	P[18]	I6	**R9**	**C9**	M6	A6	**N9**	**T12**	**E14**	**H11**	N.P.

[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 (52), before this can be confirmed.

An open space refers to: genotype not known, as sequencing has not been performed.

Abbreviation: N.P., not published.

NIH-PA Author Manuscript NIH-PA Author Manuscript NIH-PA Author Manuscript

Table 2

List of RV strains representing all 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	(51)
RVA/Human-wt/BGD/Dhaka16-03/2003/G1P[8]	G1	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	(72)
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/NIV929893/1992/G1P[19]	G1	P[19]	I1							E1		(15)
RVA/Pig-wt/SVN/P21-5/2004/G1P[27]	G1	P[27]								E9		(84)
RVA/Human-tc/USA/DS-1/1976/G2P1B[4]	G2	P[4]	I2	R2	C2	M2	A2	N2	T2	E2	H2	(51)
RVA/Human-wt/CHN/TB-Chen/1996/G2P[4]	G2	P[4]	I2	R2	C2	M2	A2	N2	T2	E2	H2	(12)
RVA/Human-wt/USA/LB2744/2006/G2P[4]	G2	P[4]	I2	R2	C2	M2	A2	N2	T2	E2	H2	(7)
RVA/Pig-wt/ESP/34461-4/2003/G2P[23]	G2	P[23]	I5							E1	H1	(39)
RVA/Pig-wt/THA/CMP034/2000/G2P[27]	G2	P[27]	I5							E9	H1	(39)
RVA/Simian-tc/ZAF/SA11-H96/1958/G3P5B[2]	G3	P[2]	I2	R2	C5	M5	A5	N5	T5	E2	H5	(82)
RVA/Simian-tc/USA/RRV/1975/G3P[3]	G3	P[3]	I2	R2	C3	M3	A9	N2	T3	E3	H6	(60)
RVA/Human/USA/HCR3A/1984/G3P[3]	G3	P[3]	I3	R3	C2	M3	A9	N2	T3	E3	H6	(88)
RVA/Cat-tc/AUS/Cat97/1984/G3P[3]	G3	P[3]	I3	R3	C2	M3	A9	N2	T3	E3	H6	(88)
RVA/Dog-tc/USA/CU-1/1982/G3P[3]	G3	P[3]	I3	R3	C2	M3	A9	N2	T3	E3	H6	(88)
RVA/Human-wt/THA/CMH222/2001/G3P[3]	G3	P[3]	I8							E3		(40)
RVA/Human-tc/AUS/RV3/1977/G3P2A[6]	G3	P[6]	I1	R1	C1	M1	A1	N1	T1	E1	H1	(78)
RVA/Cow-lab/GBR/PP-1/1976/G3P[7]	G3	P[7]					A3			E8		(21)
RVA/Pig-tc/VEN/A131/1988/G3P9[7]	G3	P[7]	I5	R1	C2	M1	A1	N1	T1	E1	H1	(51)
RVA/Human-tc/USA/P/1974/G3P1A[8]	G3	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	(51)
RVA/Human-wt/USA/DC5544-Bethesda/1991/G3P[8]	G3	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	(63)
RVA/Cat-wt/ITA/BA222/2005/G3P[9]	G3	P[9]	I2	R2	C2	M2	A3	N1	T3	E2	H3	(49)
RVA/Human-tc/ITA/PAH136/1996/G3P[9]	G3	P[9]	I2	R2	C2	M2	A3	N1	T6	E2	H3	(19)
RVA/Human-tc?/ITA/PAI58/1996/G3P[9]	G3	P[9]	I2	R2	C2	M2	A3	N2	T6	E2	H3	(19)
RVA/Cat-tc/AUS/Cat2/1984/G3P[9]	G3	P[9]	I3	R3	C2	M3	A3	N1	T6	E3	H3	(88)
RVA/Human-tc/JPN/AU-1/1982/G3P3[9]	G3	P[9]	I3	R3	C3	M3	A3	N3	T3	E3	H3	(51)

NIH-PA Author Manuscript
NIH-PA Author Manuscript
NIH-PA Author Manuscript

STRAIN NAME	GENOTYPES											REF.
	VP7	VP4	VP6	VP1	VP2	VP3	NSP1	NSP2	NSP3	NSP4	NSP5	
RVA/Human-wt/BEL/B4106/2000/G3P[14]	G3	P[14]	I2	R2	C2	M3	A9	N2	T6	E5	H3	(57)
RVA/Rabbit-tc/ITA/30/96/1996/G3P[14]	G3	P[14]	I2	R2	C2	M3	A9	N2	T6	E5	H3	(57)
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	(60)
RVA/Human-wt/IND/mani-253/2007/G4P[4]	G4	P[4]	I1	R1	C1	M2	A8	N1	T1	E1	H1	(66)
RVA/Human-wt/IND/mani-362/2007/G4P[6]	G4	P[6]	I1	R1	C1	M1	A8	N1	T1	E1	H1	(66)
RVA/Human-tc/GBR/ST3/1975/G4P2A[6]	G4	P[6]	I1	R1	C1	M1	A1	N1	T1	E1	H1	(51)
RVA/Pig-tc/USA/Gottfried/1983/G4P[6]	G4	P[6]	I1	R1	C1	M1	A8	N1	T1	E1	H1	(56)
RVA/Human-tc/CHN/R479/2004/G4P[6]	G4	P[6]	I5	R1	C1	M1	A1	N1	T7	E1	H1	(95)
RVA/Pig-tc/USA/OSU/1977/G5P9[7]	G5	P[7]	I5	R1	C1	M1	A1	N1	T1	E1	H1	(56)
RVA/Human-tc/BRA/IAL28/1992/G5P[8]	G5	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	(51)
RVA/Pig-tc/VEN/A34/1985/G5P[23]	G5	P[23]								E1		(43)
RVA/Pig-wt/ITA/134/04-15/2003/G5P[26]	G5	P[26]	I5							E1		(47)
RVA/Cow-tc/VEN/BRV033/1990/G6P6[1]	G6	P[1]	I2	R2	C2	M2	A3	N2	T6	E2	H3	(51)
RVA/Cow-tc/FRA/RF/1982/G6P[1]	G6	P[1]	I2	R2	C2	M2	A3	N2	T6	E2	H3	(17)
RVA/Goat-tc/BGD/GO34/1999/G6P[1]	G6	P[1]	I2	R2	C2	M2	A11	N2	T6	E2	H3	(28)
RVA/Cow-tc/USA/WC3/1981/G6P[5]	G6	P[5]	I2	R2	C2	M2	A3	N2	T6	E2	H3	(51)
RVA/Cow-tc/GBR/UK/1973/G6P7[5]	G6	P[5]	I2	R2	C2	M2	A3	N2	T7	E2	H3	(20)
RVA/Human-wt/BEL/B1711/2002/G6P[6]	G6	P[6]	I2	R2	C2	M2	A2	N2	T2	E2	H2	(58)
RVA/Human-wt/IND/HP140/1987/G6P[13]	G6	P[13]	I2	R1	C1	M1				E1	H1	(92)
RVA/Human-wt/BEL/B10925-97/1997/G6P[14]	G6	P[14]	I2	R2	C2	M2	A3	N2	T6	E2	H3	(55)
RVA/Human-wt/HUN/Hun5/1997/G6P[14]	G6	P[14]	I2	R2	C2	M2	A11	N2	T6	E2	H3	(55)
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		(65)
RVA/Guanaco-wt/ARG/Rio_Negro/1998/G8P[1]	G8	P[1]	I2	R5	C2	M2	A13	N2	T6	E12	H3	(55)
RVA/Rhesus-tc/USA/PTRV/1990/G8P[1]	G8	P[1]	I2	R2	C2	M2	A3	N2	T6	E2	H3	(60)
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	(29)

Arch Virol. Author manuscript; available in PMC 2012 August 01.

NIH-PA Author Manuscript
NIH-PA Author Manuscript
NIH-PA Author Manuscript

STRAIN NAME	GENOTYPES											REF.
	VP7	VP4	VP6	VP1	VP2	VP3	NSP1	NSP2	NSP3	NSP4	NSP5	
RVA/Cow-tc/THA/A5-13/XXXX/G8P[1]	G8	P[1]					A14					(68)
RVA/Human-wt/DEU/GER1H-09/2009/G8P[4]	G8	P[4]	I2	R2	C2	M2	A2	N2	T2	E2	H2	(70)
RVA/Human-wt/COD/DRC86/2003/G8P[6]	G8	P[6]	I2	R2	C2	M2	A2	N2	T2	E2	H2	(59)
RVA/Human-wt/COD/DRC88/2003/G8P[8]	G8	P[8]	I2	R2	C2	M2	A2	N2	T2	E2	H2	(59)
RVA/Human-tc/IND/69M/1980/G8P4[10]	G8	P[10]	I2	R2	C2	M2	A2	N2	T2	E2	H2	(51)
RVA/Human-wt/HUN/BP1062/2004/G8P[14]	G8	P[14]	I2	R2	C2	M2	A11	N2	T6	E2	H3	(8)
RVA/Sheep-tc/ESP/OVR762/2002/G8P[14]	G8	P[14]	I2	R2	C2	M2	A11	N2	T6	E2	H3	(55)
RVA/Human-wt/BEL/B3458/2003/G9P[8]	G9	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	(51)
RVA/Human-tc/USA/WI61/1983/G9P1A[8]	G9	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	(51)
RVA/Human-wt/USA/OM46/1998/G9P[8]	G9	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	(64)
RVA/Human-wt/USA/OM473/2000/G9P[8]	G9	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	(64)
RVA/Human-tc/IND/116E/1985/G9P[11]	G9	P[11]	I1	R1	C1	M1	A1	N1	T1	E1	H1	(78)
RVA/Human-wt/IND/RMC321/1990/G9P[19]	G9	P[19]	I5	R1	C1	M1	A1	N1	T1	E1	H1	(91)
RVA/Human-wt/IND/mani-97/2006/G9P[19]	G9	P[19]	I5	R1	C1	M1	A8	N1	T1	E1	H1	(66)
RVA/Human-wt/IND/mani-265/2007/G10P[6]	G10	P[6]	I2	R2	C2	M2	A3	N2	T2	E2	H2	(66)
RVA/Human-wt/NGA/6717ARN/2002/G10P[8]	G10	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	(22)
RVA/Human-wt/CIV/6755ARN/2002/G10P[8]	G10	P[8]	I2	R1	C1	M1	A1	N1	T1	E1	H1	(22)
RVA/Human-wt/IND/N155/XXXX/G10P[11]	G10	P[11]	I2	R2	C2	M2	A1	N1	T1	E2	H3	(74)
RVA/Cow-xx/CHN/DQ-75/2008/G10P[11]	G10	P[11]	I2	R2	C2	M2	A3	N2	T6	E2	H3	(97)
RVA/Sheep-tc/CHN/Lamb-NT/XXXX/G10P[15]	G10	P[15]	I10	R2	C2	M2	A11	N2	T6	E2	H3	(13)
RVA/Human-wt/ECU/EC2184/2005/G11P[6]	G11	P[6]	I1	R1	C1	M1	A1	N1	T1	E1	H1	(4)
RVA/Pig-tc/MEX/YM/1983/G11P9[7]	G11	P[7]	I5	R1	C1	M1	A8	N1	T1	E1	H1	(56)
RVA/Pig-tc/VEN/A253/1988/G11P9[7]	G11	P[7]	I5	R1	C2	M1	A1	N1	T1	E1	H1	(51)
RVA/Human-wt/BGD/Dhaka6/2001/G11P[25]	G11	P[25]	I1	R1	C1	M1	A1	N1	T1	E1	H1	(56)
RVA/Human-wt/NPL/KTM368/2004/G11P[25]	G11	P[25]	I12	R1	C1	M1	A1	N1	T1	E1	H1	(56)
RVA/Human-tc/PHL/L26/1987/G12P[4]	G12	P[4]	I2	R2	C2	M1	A2	N1	T2	E2	H1	(73)
RVA/Human-wt/BGD/Dhaka12-03/2003/G12P[6]	G12	P[6]	I1	R1	C1	M1	A1	N1	T1	E1	H1	(73)
RVA/Human-wt/BGD/Matlab13/2003/G12P[6]	G12	P[6]	I1	R1	C1	M1	A1	N1	T2	E1	H1	(73)

NIH-PA Author Manuscript
NIH-PA Author Manuscript
NIH-PA Author Manuscript

STRAIN NAME	GENOTYPES											REF.
	VP7	VP4	VP6	VP1	VP2	VP3	NSP1	NSP2	NSP3	NSP4	NSP5	
RVA/Human-wt/BGD/RV161/2000/G12P[6]	G12	P[6]	I2	R2	C2	M2	A2	N2	T2	E1	H2	(73)
RVA/Human-wt/BGD/RV176-00/2000/G12P[6]	G12	P[6]	I2	R2	C2	M2	A2	N2	T2	E6	H2	(73)
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	(73)
RVA/Human-wt/BGD/Dhaka25-02/2002/G12P[8]	G12	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	(73)
RVA/Human-tc/THA/T152/1998/G12P[9]	G12	P[9]	I3	R3	C3	M3	A12	N3	T3	E3	H6	(73)
RVA/Horse-wt/ARG/E403/2006/G14P[12]	G14	P[12]	I2	R2	C2	M3	A10	N2	T3	E2	H7	N.P.
RVA/Cow-xx/ARG/B383/1998/G15P[11]	G15	P[11]	I2	R5	C2	M2	A13	N2	T6	E12	H3	(55)
RVA/Cow-tc/IND/Hg18/XXXX/G15P[21]	G15	P[21]								E2		(76)
RVA/Mouse-tc/XXX/EHP/1981/G16P[20]	G16	P[20]					A7			E7		(25)
RVA/Turkey-tc/IRL/Ty-1/1979/G17P[17]	G17	P[17]	I4					N4		E4		(65)
RVA/Pigeon-tc/JPN/PO-13/1983/G18P[17]	G18	P[17]	I4	R4	C4	M4	A4	N4	T4	E4	H4	(36)
RVB/Rat-tc/USA/IDIR/1984/G1P[X][b]	G1[b]											(93)
RVB/Human-wt/CHN/WH-1/2002/G2P[X][b]	G2[b]											(101)
RVB/Human-wt/BGD/Bang117/2003/G2P[X][b]	G2[b]											(98)
RVB/Cow-wt/IND/DB176/2001/G3P[X][b]	G3[b]											(10)
RVC/Pig-tc/GBR/Cowden/1982/G1P[1][b]	G1[b]	P[1][b]										(71)
RVC/Cow-tc/JPN/Shintoku/1991/G2P[3][b]	G2[b]	P[3][b]										(89)
RVC/Human-tc/GBR/Bristol/1998/G4P[2][b]	G4[b]	P[2][b]										(35)
RVC/Human-wt/BGD/BS347/2005/G4P[2][b]	G4[b]	P[2][b]										(99)
RVD/chicken-wt/DEU/05V0049/2005/GXP[X]												(87)

[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 strain 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).

An open space refers to: i) genotype not known, as sequencing has not been performed, or ii) genotypes have not yet been established for non-group A RVs.

Abbreviation: N.P., not published.

Arch Virol. Author manuscript; available in PMC 2012 August 01.

NIH-PA Author Manuscript NIH-PA Author Manuscript NIH-PA Author Manuscript

Table 3

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											(2)
RVA/Simian-lab/USA/SA11-tsE/XXXX/G3P[2][b]	G3	P[2]	I2	R2	C5	M5	A5	N2	T5	E2	H5	XX
RVA/Cow-lab/GBR/PP-1/1976/G3P[7][c]	G3	P[7]					A3			E8		(21)
RVA/Labstr/USA/RRV-E4/1996/G3P[20][d]	G3	P[20]	I2	R2	C3	M3	A9	N2	T3	E3	H6	(44)
RVA/Labstr/USA/SA11-huN2/2010/G3P[2][e]	G3	P[2]	I2	R2	C5	M5	A5	N2	T5	E2	H5	(85)
RVA/Vaccine/USA/RotaTeq-WI79-9/1992/G1P7[5][f]	G1	P7[5]	I2	R2	C2	M1	A3	N2	T6	E2	H3	(53)
RVA/Vaccine/USA/RotaTeq-SC2-9/1992/G2P7[5][f]	G2	P7[5]	I2	R2	C2	M1	A3	N2	T6	E2	H3	(53)
RVA/Vaccine/USA/RotaTeq-WI78-8/1992/G3P7[5][f]	G3	P7[5]	I2	R2	C2	M2	A3	N2	T6	E2	H3	(53)
RVA/Vaccine/USA/RotaTeq-BrB-9/1996/G4P7[5][f]	G4	P7[5]	I2	R2	C2	M2	A3	N2	T6	E2	H3	(53)
RVA/Vaccine/USA/RotaTeq-WI79-4/1992/G6P1A[8][f]	G6	P1A[8]	I2	R2	C2	M2	A3	N2	T6	E2	H3	(53)
RVA/Vaccine/USA/Rotarix- RIX4414/1988/G1P1A[8][g]	G1	P1A[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	N.P.

[a] Hypothetical name of a RV strain identified in a river in Switzerland (2).

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

[c] Strain PP-1 is a bovine RV strain wish has been passages several times in the heterologous pig model (21)

[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 (44).

[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 (85).

[f] Hypothetical names of the 5 reassortant RV strain present in the RotaTeq vaccine (53).

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

An open space refers to the genotype not being established/determined.