

Full-Genome Sequence of a Rare Human G3P[9] Rotavirus Strain

Slavica Mijatovic-Rustempasic,^a Sunando Roy,^a Michele Sturgeon,^a Kunchala Rungsririyachai,^a Mathew D. Esona,^a Dona DeGroat,^b Xuan Qin,^b Margaret M. Cortese,^a Michael D. Bowen^a

Division of Viral Diseases, National Center for Immunization and Respiratory Diseases, Centers for Disease Control and Prevention, Atlanta, Georgia, USA^a; Department of Laboratories & Pathology, Seattle Children's Hospital, Seattle, Washington, USA^b

This is a report of the complete genomic sequence of a rare rotavirus group A G3-P[9]-I2-R2-C2-M2-A3-N2-T1-E2-H3 strain designated RVA/Human-wt/USA/12US1134/2012/G3P[9].

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Address correspondence to Michael D. Bowen, mkb6@cdc.gov.

Group A rotaviruses (RVAs) possess a segmented double-stranded RNA (dsRNA) genome composed of 11 segments encoding six structural proteins (VPs) and five or six nonstructural proteins (NSPs) (1). The classification nomenclature for the VP7, VP4, VP6, VP1-3, and NSP1-5/6 genes uses the notation Gx-P[x]-Ix-Rx-Cx-Mx-Ax-Nx-Tx-Ex-Hx, with x indicating the numbers of the corresponding genotypes (2). The majority of human RVA strains possess either the Wa-like genogroup 1 constellation (I1-R1-C1-M1-A1-N1-T1-E1-H1) or the DS-1-like genogroup 2 constellation (I2-R2-C2-M2-A2-N2-T2-E2-H2), which is believed to have origins with the porcine or the bovine RVAs, respectively (3). A smaller group of RVA strains have the AU-1-like genogroup 3 constellation (I3-R3-C3-M3-A3-N3-T3-E3-H3), which originated from feline RVAs (3, 4). Genogroup 3 RVAs cause rare human disease with limited transmission (5).

Here, we report the full-genome sequence of rotavirus strain RVA/Human-wt/USA/12US1134/2012/G3P[9] (12US1134), detected in a stool sample collected through the National Rotavirus Strain Surveillance System (7) from a 6-year-old who was treated at the Seattle's Children Hospital, Seattle, WA, in 2012. Rotavirus dsRNA was extracted from the sample using TRIzol (Invitrogen), followed by DNase I treatment, and then was separated from single-stranded RNA by LiCl precipitation. The sequencing templates were prepared by using sequence-independent whole-genome reverse transcription-PCR (RT-PCR) amplification (8), with slight modifications. PCR amplicons were sequenced by the Illumina MiSeq 150 paired-end method by the Genomics Lab, HudsonAlpha Institute for Biotechnology, AL. Illumina sequence reads were analyzed using CLC Genomics Workbench 6.0. A combination of *de novo* assembly and subsequent mapping to a G3P[9] reference strain was used to obtain the full-length genome of strain 12US1134. The sizes of full-length segments 1 to 11 were 3,302, 2,687, 2,591, 2,359, 1,578, 1,356, 1,075, 1,059, 1,062, 751, and 667 bp, and the open reading frames (ORFs) for these segments were 3,267, 2,643, 2,508, 2,328, 1,476, 1,194, 942, 954, 981, 528, and 597 bp, respectively. The genotype assignment for each gene was accomplished using the RotaC online classification tool (<http://rotac.regatools.be/>) and BLAST (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>).

The full-genotype constellation for strain 12US1134 is G3-P[9]-I2-R2-C2-M2-A3-N2-T1-E2-H3. This strain is nearly identical (98.9 to 99.8% nucleotide identity) to G3P[9] strain 0537, described previously (9), but only a partial sequence for strain 0537 was reported. This is the first complete RVA sequence with the genotype G3-P[9]-I2-R2-C2-M2-A3-N2-T1-E2-H3.

Several full-genome sequences of G3P[9] RVA strains of feline or human origin have been reported (6, 10). G3P[9] strains of human origin (PAI58/96, PAH136/96, and 0537) have a relatively stable genetic constellation, G3-P[9]-I2-R2-C2-M2-A3-(N1/N2)-(T1/T6)-E2-H3, and carry a DS-1 backbone, which differentiates them from most G3P[9] strains of feline origin.

Full-genome studies help expand our knowledge of the genetic diversity and origin of uncommon rotavirus genotypes and highlight the need for continuous monitoring of RVA strains for timely recognition of novel or rare genotypes, including in post-vaccine introduction settings.

Nucleotide sequence accession numbers. The full-genomic sequence of the G3P[9] rotavirus strain 12US1134 has been deposited in GenBank under accession no. [KF500514](https://www.ncbi.nlm.nih.gov/nuccore/KF500514) to [KF500524](https://www.ncbi.nlm.nih.gov/nuccore/KF500524).

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