



Genomic Characterization of the First Equine-Like G3P[8] Rotavirus Strain Detected in the United States

Charity Perkins, Slavica Mijatovic-Rustempasic, M. Leanne Ward, Margaret M. Cortese, Michael D. Bowen

Viral Gastroenteritis Branch, Division of Viral Diseases (DVD), National Center for Immunization and Respiratory Diseases (NCIRD), Centers for Disease Control and Prevention, Atlanta, Georgia, USA

ABSTRACT We report here the full coding region sequences for all 11 segments of the first equine-like G3P[8] rotavirus strain detected in the United States, strain RVA/Human-wt/USA/3000390639/2015/G3P[8]. The full genotype constellation of this strain is G3-P[8]-I2-R2-C2-M2-A2-N2-T2-E2-H2.

The genomes of group A rotaviruses (RVAs) are composed of 11 segments of double-stranded RNA (dsRNA) encoding 6 viral structural proteins (VP1 to VP4, VP6, and VP7) and 5 or 6 nonstructural proteins (NSP1 to NSP5 or NSP6) (1). Historically, RVA genotypes were named using a binary system based on the glycosylated G genotype, VP7, and the protease-sensitive P genotype, VP4 (2). Currently, the classification nomenclature for all 11 genes uses the convention Gx-P[x]-Ix-Rx-Cx-Mx-Ax-Nx-Tx-Ex-Hx, with x indicating the number of corresponding genotypes (3). Most human RVA strains possess either the Wa-like constellation of porcine origin (Gx-P[x]-I1-R1-C1-M1-A1-N1-T1-E1-H1) or the DS-1-like constellation of bovine origin (Gx-P[x]-I2-R2-C2-M2-A2-N2-T2-E2-H2) (4). Genotype G3P[8] is commonly detected worldwide in humans (5). The majority of globally circulating G3P[8] strains possess a Wa-like backbone, I1-R1-C1-M1-A1-N1-T1-E1-H1, but reassortant equine-like G3P[8] strains with a DS-1-like backbone were detected recently in Australia, Thailand, Spain, Hungary, and Brazil (5–10). These strains have the consensus genetic constellation G3-P[8]-I2-R2-C2-M2-A2-N1/N2-T2-E2-H2.

Here, we report the complete coding region sequences of all 11 gene segments for strain RVA/Human-wt/USA/3000390639/2015/G3P[8] detected in a stool sample collected in March 2015 through the National Rotavirus Strain Surveillance System from a 2-year-old child in North Carolina, USA. RVA dsRNA was extracted using Trizol reagent (Life Technologies, Inc., Grand Island, NY, USA). Full-genome next-generation sequencing was performed using the Illumina MiSeq platform, following a previously published protocol, and the reads were analyzed using CLC Genomics Workbench version 10 software (11). A combination of *de novo* assembly followed by mapping to reference strains was used to obtain open reading frames (ORFs) for all 11 genes. The ORF lengths are 3,267 (VP1), 2,640 (VP2), 2,508 (VP3), 2,328 (VP4), 1,194 (VP6), 981 (VP7), 1,482 (NSP1), 954 (NSP2), 942 (NSP3), 528 (NSP4), 603 (NSP5), and 276 (NSP6) bp. The NSP6 ORF is nested within the larger NSP5 ORF, as described previously for other rotavirus strains (12). The genotype assignment for each gene was determined using BLAST (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>) searches.

The full genotype constellation of RVA/Human-wt/USA/3000390639/2015/G3P[8] is G3-P[8]-I2-R2-C2-M2-A2-N2-T2-E2-H2. This strain is highly similar to all equine-like G3P[8] strains emerging worldwide, with highest nucleotide (nt) and amino acid (aa) similarities (98.9 to 100%, nt and aa) to European strains (5–8, 10). The nucleotide sequence of the I2 VP6 gene of this strain is identical to that of Spanish and Hungarian

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equine-like G3P[8] strains, and the E2 NSP4 gene is identical to that of a strain detected in Spain (6, 8). Among the described equine-like G3P[8] rotavirus strains, RVA/Human-wt/USA/3000390639/2015/G3P[8] exhibits the lowest degree of genetic identity with strains from Brazil and Thailand (5, 10). Newly emerging equine-like G3P[8] strains are believed to have derived from multiple reassortment events between rotavirus strains of human and animal origin (7, 8). Sequencing of all RVA G3 strains may be necessary to identify the prevalence of equine-like G3P[8] strains globally. This is the first report of an equine-like G3P[8] rotavirus strain detected in the United States.

Accession number(s). The strain RVA/Human-wt/USA/3000390639/2015/G3P[8] coding region sequences have been deposited in GenBank under the accession numbers [MF997035](#) to [MF997045](#).

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