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VIRUSES

Near-Complete Genome Sequences of Several New Norovirus Genogroup II Genotypes

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ABSTRACT We report here the near-complete genome sequences of 13 norovirus strains detected in stool samples from patients with acute gastroenteritis from Bangladesh, Ecuador, Guatemala, Peru, Nicaragua, and the United States that are classified into one existing (genotype II.22 [GII.22]), 3 novel (GII.23, GII.24 and GII.25), and 3 tentative novel (GII.NA1, GII.NA2, and GII.NA3) genotypes.

Norovirus is a leading cause of epidemic acute gastroenteritis (AGE) and an important cause of childhood diarrhea worldwide. The WHO estimates that noroviruses annually cause 685 million cases of diarrhea and approximately 200,000 deaths globally (1, 2). Norovirus infection and disease occur throughout life and are associated with an estimated 18% of AGE cases in all age groups (3). Noroviruses are positive-sense single-stranded nonenveloped RNA viruses which belong to the family *Caliciviridae*. These viruses are genetically diverse and can be divided into at least seven genogroups (G), of which viruses from GI, GII, and GIV infect humans (4). GI and GII noroviruses are further divided into 9 and 22 different genotypes, respectively, based on the phylogenetic clustering of the complete capsid protein VP1 (5). Over the past decade, the majority of norovirus infections have been caused by GII.4, but multiple genotypes are cocirculating at any given time.

We detected several tentative new norovirus GII genotypes in fecal specimens from patients with acute gastroenteritis in Bangladesh, Ecuador, Guatemala, Nicaragua, Peru, and the United States using routine dual typing of partial regions of the 3′ open reading frame 1 (ORF1) and 5′ ORF2 (6). Using shotgun metagenomics sequencing, near-complete genomes were assembled using 34,983 reads generated by Illumina MiSeq next-generation sequencing (7). The lengths of the near-complete genomes of 13 strains ranged from 7,204 to 7,395 nucleotides, with short regions missing at the 5′ ends. The designation of new norovirus genotypes is dictated by the internationally accepted 2×SD criterion of VP1 amino acid divergence, as well as agreement among the Norovirus Working Group (5) that new genotypes need to be supported by VP1 sequences from at least two different countries. Single complete VP1 sequences or those from strains from a single

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country that form distinct branches will be preliminarily labeled NA (not assigned). Based on these criteria, we identified a GII.22 strain, strains from three new genotypes (GII.23, GII.24, and GII.25), and strains from three tentative new GII genotypes (GII.NA1 from Peru, GII.NA2 from Peru, and GII.NA3 from Nicaragua). Compared to the VP1 of the phylogenetically closest genotype GII.22 (YURI, GenBank accession number AB083780), pairwise amino acid identities were 78.9 to 79.1% for the GII.23 strains, 79.8 to 80.0% for GII.24 strains, 86.3% for the GII.25 strain, 79.7% for the GII.NA1 strain, 80.1 to 80.2% for the GII.NA.2 strains, and 80.2% for the GII.NA3 strain. The VP1 sequence of strain Hu/BD/2012/GII.P22-GII.22/Dhaka190 clustered closely with the GII.22 prototype strain YURI, and that of strain Hu/BD/2012/GII.P22-GII.25/Dhaka1928 clustered closely with the newly assigned GII.25 strain Beijing53931 (GenBank accession number GQ856469).

Globally, GII.4 viruses have been the predominant genotype for more than a decade, but recently, previously rare genotypes, including GII.17 and GII.2 viruses, have emerged in certain regions of the world (8, 9). In addition, frequent changes in the cocirculating non-GII.4 norovirus genotypes have been reported (6, 10). The identification of three new and three tentative new norovirus genotypes in stool collections from sporadic cases of norovirus gastroenteritis highlights the importance of global norovirus surveillance to monitor changing genotype distributions and identify the emergence of novel genotypes.

Accession number(s). The near-complete genome sequences have been deposited in GenBank with the following accession numbers: MG495082 (Hu/BD/2012/GII.P22-GII.22/Dhaka1940), KR232647 (Hu/EC/2011/GII.P23-GII.23/Quininde1906), MG495080 (Hu/PE/2011/GII.P23-GII.23/Loreto6422), MG551869 (Hu/GT/2012/GII.P23-GII.23/Guatemala City3872), KY225989 (Hu/PE/2013/GII.P24-GII.24/Loreto1972), MG495081 (Hu/PE/2014/GII.P24-GII.24/Loreto6424), MG495084 (Hu/US/2013/GII.P24-GII.24/EdenPrairie5457), MG495085 (Hu/US/2013/GII.P24-GII.24/EdenPrairie5458), MG495083 (Hu/BD/2012/GII.P22-GII.25/Dhaka1928), MG495077 (Hu/PE/2012/GII.PNA1-GII.NA1/Loreto0959), MG495078 (Hu/PE/2012/GII.PNA1-GII.NA1/Loreto1041), MG495079 (Hu/PE/2013/GII.PNA2-GII.NA2/Loreto1257), and KU306738 (Hu/NI/2005/GII.PNA3-GII.NA3/Leon4509).

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We declare no conflicts of interest relevant to this study.

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