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GENOME ANNOUNCEMENT

Complete Genome Sequence of a Novel Human Enterovirus C (HEV-C117) Identified in a Child with Community-Acquired Pneumonia

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The new enterovirus C-117 strain belongs to the human enterovirus C species in the *Picornaviridae* family. We describe the characterization of the complete genome of this strain identified in a respiratory specimen of a child enrolled in the Community-Acquired Pneumonia Pediatric Research Initiative (CAP-PRI) study evaluating the etiology of community-acquired pneumonia (CAP).

Enteroviruses (EVs) are small, nonenveloped, positive-stranded RNA viruses of between 7,000 and 7,500 nucleotides that include three genomic regions (P1, P2, and P3). The P1 region encodes four structural capsid proteins (VP4, VP2, VP3, and VP1), whereas P2 and P3 encode seven nonstructural proteins (2A, 2B, 2C, 3A, 3B, 3C, and 3D) (6). Divergences within the VP1 region are used to classify EVs, of which there are four known species: human enterovirus A (HEV-A) to HEV-D (1, 5). To date, HEV-C has been shown to consist of 23 types (3) (http://www.picornaviridae.com/enterovirus/hev-c/hev-c.htm), including the new type EV-C117 (GenBank accession number JQ446368).

We here report the characterization of this new HEV type. The EV-C117 strain was found in a 45-month-old female Lithuanian child hospitalized because of community-acquired pneumonia. PCR using primers targeting the VP1 region, as described elsewhere (4), showed that her nasopharyngeal sample was positive for enterovirus. The complete genome sequence was obtained using degenerated primers designed by means of the multiple alignment of the EV-C104 and EV-C109 genomes available in GenBank and additional primers designed on the basis of the results of the first and subsequent rounds of sequencing. These primer sequences are available on request. The terminal sequences were confirmed by means of rapid amplification of the cDNA ends (RACE) using a 5′/3′ RACE kit (Roche, Mannheim, Germany). The sequences were aligned using ClustalX 2.1 (8); the phylogenetic trees were constructed using MEGA 5 (7); and the bootscan and similarity plot analyses were made using SimPlot 3.5.1.

The genome of the EV-C117 strain consists of 7,363 nucleotides, excluding the poly(A) tail tract. The 5′ untranscribed region (UTR) contains 672 nucleotides, and the 3′ UTR consists of 70 nucleotides. Downstream of the 5′ UTR, the genome contains a large open reading frame of 6,621 bases, which encodes a potential polyprotein precursor of 2,206 amino acids. The base composition of the full genome is 27.8% A, 23.6% C, 24.4% G, and 24.2% U.

The VP1 has 297 amino acids, and the results of pairwise similarity analysis show that it shares 78.7% amino acid and 70% nucleotide identity with VP1 of EV104 (2) and 77.4% amino acid and 69.1% nucleotide identity with VP1 of EV109 (9). The P2 and P3 region genome sequences showed greater identity to the corresponding sequences of the EV-C104 AK11 strain isolated in Japan than the P1 region sequences. Analysis of the sequence from the 5′ UTR to the end of the 2C gene showed high bootstrap support for clustering with the EV-C109 virus; the sequence from 2C to the end of the genome supported clustering with EV-C104 strain AK11. In addition, preliminary bootscan analysis showed the presence of one putative recombinant site in the 2C/3A region. Overall, the P3 region showed the greatest identity with that of EV-C104 strain AK11. These findings suggest a recombinant origin of the virus and therefore the independent evolution of the different genome regions. However, further extensive analyses are needed to clarify its origin.

Nucleotide sequence accession number. The EV-C117 genome sequence has been deposited in GenBank under accession number JX262382.

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