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First Full Genome Sequence of a Human Enterovirus A120, Isolated in Madagascar

Richter Razafindratsimandresy,a Marie-Line Joffret,b,c Francis Delpeyroux,b,c Jean-Michel Heraud,a and R.R. and M.-L.J. contributed equally to this work.

We report the first complete genome sequence of an enterovirus isolate belonging to the human enterovirus A species of the Picornaviridae family and to type A120 (EV-A120). The EV-A120 isolate MAD-2741-11 was obtained from the stool of a healthy child living on Madagascar Island. The isolate genome was amplified by a reverse transcription-PCR method, and the consensus sequence was determined.

The genus Enterovirus in the family Picornaviridae comprises related viruses associated with either asymptomatic infection or various clinical syndromes, including respiratory illness, gastroenteritis, meningitis, encephalitis, and paralytic syndromes (1). Seven enterovirus (EV) species are known to infect humans: human enteroviruses (HEV) A, B, C, and D and human rhinoviruses A, B, and C (see http://www.picornaviridae.com/enterovirus/enterovirus.htm). They are classified according to their nucleotidic identity and peptidic similarity rates within the VP1 region (2, 3). Enteroviruses are small, nonenveloped viruses. The RNA genome is an ~7.5-kb single-stranded, positive-sense, polyadenylated molecule, with a single long open reading frame (ORF) flanked by 5′ and 3′ untranslated regions (UTRs) (4). This report describes the sequence of an EV-A120 isolate belonging to a new enterovirus type characterized from a partial genome sequence and recently reported (GenBank accession no. KF700245). The two VP1 sequences shared 81.0% nt and 94.6% amino acid identities, in agreement with values for isolates belonging to the same enterovirus type (8). The P2 and P3 genomic sequences of isolate MAD-2741-11 shared, respectively, 82% and 88% nt identities with those of one of the closest enteroviruses of species A, the coxsackievirus A10 isolate CVA10/SD/CHN/09 (GenBank accession no. HQ728262). The whole polypeptides of the two isolates shared 86% amino acid identity, in agreement with values for isolates belonging to identical enterovirus species (3). These data indicated that isolate MAD-2741-11 can be unambiguously characterized as an EV-A120 isolate. To our knowledge, this work describes the first full genome sequence of this type of human enterovirus.

Nucleotide sequence accession number. The genome sequence of the isolate MAD-2741-11 has been deposited in the ENA database as that of an EV-A120 isolate under the accession no. LK021688.

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