Genome Sequences of SAT 2 Foot-and-Mouth Disease Viruses from Egypt and Palestinian Autonomous Territories (Gaza Strip)

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Two foot-and-mouth disease virus (FMDV) genome sequences have been determined for isolates collected from recent field outbreaks in North Africa (Egypt) and the Middle East (Palestinian Autonomous Territories). These data represent the first examples of complete genomic sequences for the FMDV SAT 2 topotype VII, which is thought to be endemic in countries immediately to the south of the Sahara desert. Further studies are now urgently required to provide insights into the epidemiological links between these outbreaks and to define the pathogenicity of this emerging lineage.

Foot-and-mouth disease virus (FMDV; family *Picornaviridae*, genus *Aphthovirus*) causes a highly contagious vesicular disease that affects cloven-hoofed animals (5). FMDV exists as seven antigenically and genetically distinct serotypes (O, A, C, Asia 1, Southern African Territories [SAT] 1, SAT 2, and SAT 3) that can be subdivided into a number of temporally and spatially distributed topotypes (6). FMD is endemic in Africa, Asia, and parts of South America and has the potential to cause sporadic outbreaks in many other parts of the world (7). During 2012, cases of FMD due to SAT 2 have been reported in domesticated livestock outside sub-Saharan Africa, which is the usual geographical range of this serotype (6). This upsurge of outbreaks has affected countries in North Africa (Libya and Egypt) and the Middle East (Palestinian Autonomous Territories [PAT] and Bahrain). Virus diversity is high among SAT serotypes, especially for the SAT 2 serotype, which is composed of at least 14 topotypes (2). Analysis of VP1 (1D) sequences (undertaken in our laboratory) demonstrates that SAT 2 FMDVs from Libya, Egypt, and PAT belong to topotype VII, whereas the FMDVs from Bahrain belong to topotype IV.

Genome sequences of two closely related FMDV isolates from Egypt and PAT (Gaza Strip) that were classified within the SAT2/VII/Ghb-12 lineage have been determined (ABI 3730 DNA analyzer; Applied Biosystems) using an overlapping reverse transcription-PCR (RT-PCR) strategy (primers are available from the authors on request). The assembled genomes (SeqMan Pro v10; DNASTar Inc.) are 8,134 (Egypt) and 8,133 (PAT) nucleotides (nt) in length and share 99.5% nucleotide identity. They differ by 42 nt substitutions distributed throughout the genome as well as by a single insertion located at position 1016 in the 5' untranslated region (UTR) of the Egyptian virus. Within the polyprotein, 9/38 nt substitutions were nonsynonymous, encoding three and six amino acid changes in structural and nonstructural proteins, respectively. Prior to this study, only four other complete SAT 2 FMDV genomes were available in GenBank (3, 8) and none were from topotype VII. In addition, four partial sequences were available for SAT 2 FMDV L fragments (1, 4) (J. W. I. Newman, S. Ortlep, and A. M. Q. King, unpublished data). One of these partial sequences (GenBank accession number [FJ461346](#), collected from buffalo in Murchison Falls National Park in Uganda in 2002 [4]) represented the only SAT 2 virus from topotype VII

and shared the closest nucleotide identity (87.3 to 87.4%) to the new sequences generated in this study.

In Egypt, these recent outbreaks have affected more than 80,000 animals and have been associated with a high mortality rate (particularly in young cattle <2 months of age) in excess of 20% (ProMED-mail, archive number 20120506.1124542). However, comparative analysis has not revealed any obvious genomic changes in these recent sequences that may explain this apparent severity of disease. Further work is now urgently required to define the epidemiology of these recent outbreaks as well as to better understand factors that may have impact on the virulence in infected animals.

Nucleotide sequence accession numbers. The GenBank accession numbers for SAT2/EGY/9/2012 and PAT/1/2012 are [JX014255](#) and [JX014256](#), respectively.

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