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VIRUSES

Genome Sequences of Crimean-Congo Hemorrhagic Fever Virus Strains Isolated in South Africa, Namibia, and Turkey

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ABSTRACT We report here the full-length sequences of 16 historical isolates of Crimean-Congo hemorrhagic fever orthonairovirus (CCHFV) obtained in Turkey, Namibia, and South Africa. The strains may be useful for future work to develop molecular diagnostics or viral evolution studies.

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Crimean-Congo hemorrhagic fever orthonairovirus (CCHFV), a member of the family *Nairoviridae*, is the causative agent of a severe hemorrhagic fever disease (Crimean-Congo hemorrhagic fever [CCHF]). CCHFV is endemic to the Middle East, western and central Asia, southeastern Europe, and Africa. The wide geographic distribution of the disease is due to the broad range of CCHFV's primary vectors, which are hard-bodied ticks of the genus *Hyalomma* (1). In nature, CCHFV is capable of infecting a wide range of mammals and birds but is known to cause disease only in humans (2). Human infections are the result of either direct contact with *Hyalomma* ticks or exposure to infected animal or human bodily fluids. Exposure to infectious human bodily fluids has been the main cause of several nosocomial outbreaks (3–6).

Here, we report the complete sequences of 16 CCHFV strains isolated from humans or ticks from South Africa, Namibia, and Turkey. The African CCHFV strains were isolated in South Africa in the 1980s and propagated initially in suckling mouse brains (2 to 5 passages) and once in SW-13 cells. The Turkish strains were isolated in 2004 from anonymized patient samples with confirmed CCHFV infection and propagated once in Vero-E6 and once in SW-13 cells. Strains SPU_94_85_813055, and SPU_134_87_813049 were isolated from fatal CCHF cases from South Africa or Namibia, while SPU_41_84_813060, and SPU_264_84_2_813058 were isolated from surviving patients in South Africa. CCHFV strain SPU_D8_81_7_813051 was isolated from ticks collected in South Africa. The clinical outcomes or history of the Turkish patients is not known.

All virus stocks were clarified by low-speed (1,200 × *g* for 5 min) centrifugation. In order to determine the sequences of the full-length, negative-sense, trisegmented RNA genome of the CCHFV isolates, samples were inactivated and processed using the MagMAX pathogen RNA/DNA kit (Thermo Fisher Scientific), according to the manufacturer's instructions (7). cDNA sequencing libraries were generated from purified RNA using Illumina's TruSeq stranded total RNA library prep kit, without depletions (8). The libraries were sequenced using the Illumina MiniSeq platform with version 3 chemistry and paired-end sequencing (2 × 151 cycles). Sequences were assembled using Geneious version 9.1.4. We obtained full coverage for all segments of all isolates.

The sequence data made available in this report will provide valuable information for the design of novel molecular diagnostic tests and for future evolutionary and epidemiological analyses of CCHFV strains.

Accession number(s). The genome sequences of the CCHFV strains are deposited in GenBank under the accession numbers MF511207, MF511224, and MF511190 (Tur_2004_813048); MF511208, MF511225, and MF511191 (Tur_2004_813135); MF511209, MF511226, and MF511192 (Tur_2004_813137); MF511210, MF511227, and MF511193 (Tur_2004_813139); MF511211, MF511228, and MF511194 (Tur_2004_813141); MF511212, MF511195, and MF511229 (Tur_2004_813143); MF511213, MF511230, and MF511196 (Tur_2004_813145); MF511214, MF511231, and MF511197 (Tur_2004_813147); MF511215, MF511232, and MF511198 (Tur_2004_813149); MF511216, MF511233, and MF511199 (Tur_2004_813151); MF511217, MF511234, and MF511200 (Tur_2004_813153); MF511218, MF511235, and MF511201 (SPU134_87_813049); MF511219, MF511236, and MF511202 (SPUD8_81_7_813051); MF511221, MF511238, and MF511204 (SPU94_85_813055); MF511222, MF511239, and MF511205 (SPU264_84_2_813058); and MF511223, MF511240, and MF511206 (SPU41_84_813060).

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