

**Abstract:**

Viral hemorrhagic fever has re-emerged in the United Arab Emirates (UAE) since November 1993. Genomic RNA of Crimean-Congo hemorrhagic virus (C-CHFV) was detected by a newly developed, nested reverse transcriptase polymerase chain reaction (RT-PCR) in the sera of four (25.0%) of 16 suspected cases of viral hemorrhagic fever. The RT-PCR was based on oligonucleotide primers deduced from the small RNA segment encoding the nucleoprotein of the virus. By comparison with a nucleotide sequence of a C-CHFV isolate from a Chinese sheep, a divergence of 10.0-11.8% was detected in the C-CHFV variants causing the UAE outbreak. In the four positive sera, three phylogenetically distinct C-CHFV variants were amplified and confirmed by direct sequencing of the PCR fragments. These C-CHFV sequences were obtained directly from sera of infected humans without prior propagation in cell culture. The RT-PCR allows rapid detection of genomic C-CHFV RNA in clinical specimens and study of the molecular epidemiology of this infection.