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**Phylogenetic Analysis of Foot-and-Mouth Disease Viruses in the Emirate of Abu Dhabi, United Arab Emirates**

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**Abstract:**

**Background/Objective:** Foot-and-mouth disease (FMD), a highly contagious transboundary viral disease which considered as a major constraint to animal production and international trade. Although FMD is endemic in the United Arab Emirates (UAE) in both wild and domestic animals, the evolution of FMD virus (FMDV) strains circulating in UAE is poorly explored. Understanding the epidemiology and risk factors responsible for FMDV occurrence within the UAE is crucial factor for the effective control of FMD.

**Methods:** Suspected FMD outbreaks in animals farms and market in the Emirate of Abu Dhabi were investigated and clinical samples were collected & tested for FMD-virus(FMDV) using RT-qPCR. The VP1 nucleotide sequences of four samples (*Arabian oryx* n = 1, goat n = 2, and sheep n = 1) were characterized and subjected to phylogenetic analysis.

**Results:** All sequences characterized were classified within the serotype O, Middle East–South Asia topotype (O/ME-SA). The *Arabian oryx* FMD isolate belonged to the PanAsia-2 lineage, the ANT-10 sublineage, and was closely related to the FMDVs recently detected in neighbouring countries. Isolates from and from sheep clustered with the SA-2018 lineage that contained viruses from Bangladesh, India, and Sri Lanka. FMD Outbreaks in Abu Dhabi Emirate were attributed to the lower vaccination coverage and animal movement.

**Conclusion** Epidemiological connections between FMDV sequences collected in the UAE, the Middle East, and neighbouring countries was observed. Increasing of vaccination coverage with strict animal movement controls and implementing other zoo sanitary biosecurity measures are vital to reduce opportunities for the virus to circulate within UAE.

**Keywords:** Phylogenetic Analysis; Foot-and-Mouth Disease; epidemiology