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Isolation and molecular characterization of foot-and-mouth disease virus strains circulating in the Sultanate of Oman between 2018 and 2023

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Introduction: Foot-and-mouth disease is a highly contagious and infectious transboundary viral disease of cloven-hoofed animal species. The disease causes massive economic impacts due to production losses and restrictions on movement and trade of livestock and their products. In the Sultanate of Oman, FMD is endemic and the circulating foot-and-mouth disease virus (FMDV) strains have not been well-investigated. The current study aimed at characterizing FMDV from samples collected from clinically infected livestock between 2018 and 2023.

Methods: A total of 199 oral epithelial tissue samples were collected from suspected FMD cases from cattle, sheep and goats in ten governorates between 2018 and 2023. Based on the results of rtRT-PCR, viruses were isolated using the porcine Instituto Biologico-Rim Suino-2 cell lines. Isolated viruses were sequenced and genetically characterized to demonstrate the relatedness of Oman isolates with other isolated viruses circulating in the region.

Results: One-hundred sixty-five (82.91%) samples showed a positive result for FMDV genome. Out of 131 samples cultured on IBRS-2 cell line, 92 (70.23%) samples (from 2018 to January 2022) were successfully isolated and characterized. The remaining 39 samples from FMD outbreaks between 2022 and January 2023 are being analyzed and will be included in the final analysis. The phylogenetic analysis revealed that FMDV of serotype O belonged to two topotypes East Africa (EA) and Middle-East South-Asian (ME-SA) and to the following lineages: EA-3, ME-SA /PANASIA-2ANT-10, ME-SA/SA-2018, and ME-SA/IND/2001e. The O/EA-3 strains from Oman were most closely related to viruses from Ethiopia (2020 and 2021) (99.1-99.8%). There was a close connection between ME-SA/IND/2001e viral lineage from Oman to those from Bhutan and India in 2018 (98.7-99.7%). Whereas, the ME-SA/PanAsia-2ANT-10 viruses from FMD outbreak in 2020 and 2021 showed close similarities to the viruses from Iran in 2020 (99.4-99.5%) and Pakistan and UAE (in 2021) (98.3%) respectively. Finally, the ME-SA/SA-2018 viral lineage was related to viruses from India (in 2018) and the UAE (in 2021). Interestingly, FMDV serotype A/AFRICA/G-I was reported for the first time and was clustered with viruses from Bahrain in 2021 (93.5% to 99.5%) and Kenya in 2017 (93.4% to 99.1%).

Conclusion: This study revealed that the FMDV of serotype O was the dominant strain circulating in most of the study area, followed by serotype A. These findings support the need to establish a national control strategy based on risk analysis as well as the vaccination-based control measures. Vaccine matching study is recommended to be employed to find out the cross-protection provided by the vaccine against the field strains.