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THE FIRST ISOLATION, MOLECULAR DETECTION AND PHYLOGENETIC ANALYSIS OF FOOT-AND-MOUTH DISEASE A/AFRICA/G-I IN THE SULTANATE OF OMAN

Wafa Ahmed Al-Rawahi^{3,4}, Jemma Wadsworth¹, Hayley M. Hicks¹, Nick J. Knowles¹, Antonello Di Nardo¹, Donald P. King¹, Souheila Benfrid², Sandra Blaise-Boisseau², Mathilde Gondard², Caroline Michaud², Anthony Relmy², Aurore Romey², Anne-Laure Salomez², Morgan Sarry², Stephan Zientara², Senan Baqir⁴, Elshafie Ibrahim Elshafie⁵, Aliya Al-Ansari⁴, Cindy Bernlein-Cottet² and Labib Bakkali –Kassimi²

¹The Pirbright Institute, Ash Road, Pirbright, Woking, Surrey, GU24 0NF, United Kingdom

²ANSES, Laboratory for Animal Health, UMR1161 (ANSES, INRAE, EnvA), 14 Rue Pierre et Marie Curie, 94706 Maisons-Alfort, France.

³Central Laboratory of Animal Health, Ministry of Agriculture, Fisheries Wealth and Water Resources, Muscat PC. 100, Sultanate of Oman

⁴Department of Biology, College of Sciences, Sultan Qaboos University, Muscat PC. 123, Sultanate of Oman

⁵Department of Animal and Veterinary Sciences, College of Agricultural and Marine Sciences, Sultan Qaboos University, Muscat PC. 123, Sultanate of Oman

Introduction

Foot and mouth disease (FMD) is a highly infectious, contagious and economically devastating vesicular viral disease of cloven-hoofed animal species (Alexandersen and Mowat, 2005). FMD causes enormous economic losses to the animal production sector in endemic countries resulting from the restriction on the international trade of animals and animal products, reduced animal productivity, the high mortality rate of young animals and the control and surveillance costs (Knight-Jones and Rushton, 2013).

The Middle East region is mainly endemic of O, A and Asia1 serotypes and is at high risk through the trade of live animals from Asia and Africa. The exchange of livestock with Africa through Egypt or the sea from Eritria, Djibouti, Sudan and Somalia contributed to the prevalence of the disease in the area (Rweyemamu, et al., 2008).

The Sultanate of Oman is considered an FMD endemic country.

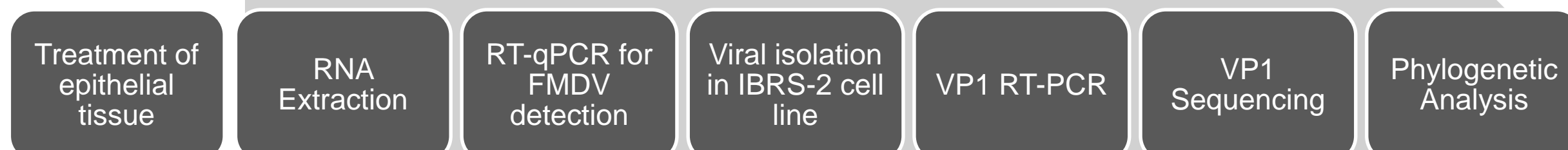
This study was aimed at isolating and characterizing the FMDV responsible of outbreaks occurred in the Sultanate of Oman between 2018 and 2021.

Methodology

A total of 13 oral epithelial tissue samples were collected from suspected FMD outbreaks from farms in four governorates Ash Sharqiyah North, Al Batinah North, Dhofar and Ad Dakhiliyah. Samples were analysed using RT-qPCR targeting the conserved region of the 3D and IRES of the virus. For phylogenetic analysis a conventional PCR assay of the virus isolates was used targeting FMDV VP1 protein-coding sequence. Phylogenetic analysis was conducted using the Maximum Likelihood method based on the Tamura 3-parameter model with other sequence data of selected isolates available in GenBank and WRLFMD.



Figure 1 & 2: Samples collated from FMD outbreaks in the Sultanate of Oman



Results

Table 1: Representative data for the samples collected from all FMDV serotype A

Sample Number	Governorate	Wilayat	Date of Collection	3D CT value	IRES CT value
OMN 22	Ash Sharqiyah North	Bidiya	21/3/2018	24.55	24.83
OMN 25	Dhofar	Salalah	10/04/2018	21.43	22.39
OMN 26	Al Batinah North	Shinas	20/03/2018	21.74	21.25
OMN 63	Ad Dakhiliyah	Nizwa	17/03/2020	32.77	25.86
OMN 65	Ad Dakhiliyah	Nizwa	17/03/2020	17.30	23.44
OMN 66	Ad Dakhiliyah	Nizwa	17/03/2020	21.38	27.33
OMN 67	Ad Dakhiliyah	Nizwa	17/03/2020	21.81	25.41
OMN 69	Ad Dakhiliyah	Nizwa	17/03/2020	19.13	21.77
OMN 74	Ad Dakhiliyah	Nizwa	17/03/2020	20.25	25.04
OMN 85	Al Batinah North	Sohar	29/01/2020	14.17	16.28
OMN 86	Al Batinah North	Sohar	29/01/2020	16.94	17.09
OMN 87	Al Batinah North	Sohar	29/01/2020	19.71	21.32
OMN 106	Ad Dakhiliyah	Samail	22/12/2020	15.90	27.43
OMN 113	Dhofar	Salalah	15/03/2021	21.89	18.88
OMN 114	Dhofar	Salalah	15/03/2021	18.62	23.59
OMN 115	Dhofar	Salalah	30/03/2021	26.57	32.25

FMDV RNA was detected by the duplex real-time RT-PCR (qRT-PCR) in the thirteen samples collected (Table 2). Both 3D and IRES FMDV genome targets were detected in all samples. The CT values ranged between 15.90 and 32.77 for the 3D target and between 18.88 and 32.25 for the IRES target.

All samples were tested for virus isolation in the IBRS-2 cell line. Cytopathic effects were observed in the form of cell rounding and detachment from the cell monolayer at the first passage for 4 samples and at the second passage for the remaining 9 samples.



Figure 3: Sample OMN115 showed cytopathic effect on IBRS-2 cell line

Results

Phylogenetic analysis of VP1 sequence revealed one group of A isolates of Africa topotype and G-I genotype. The isolates were genetically related to viruses circulating in Kenya in 2017 by 93.4% to 99.1% and in Bahrain in 2021 by 93.5% to 99.5%.

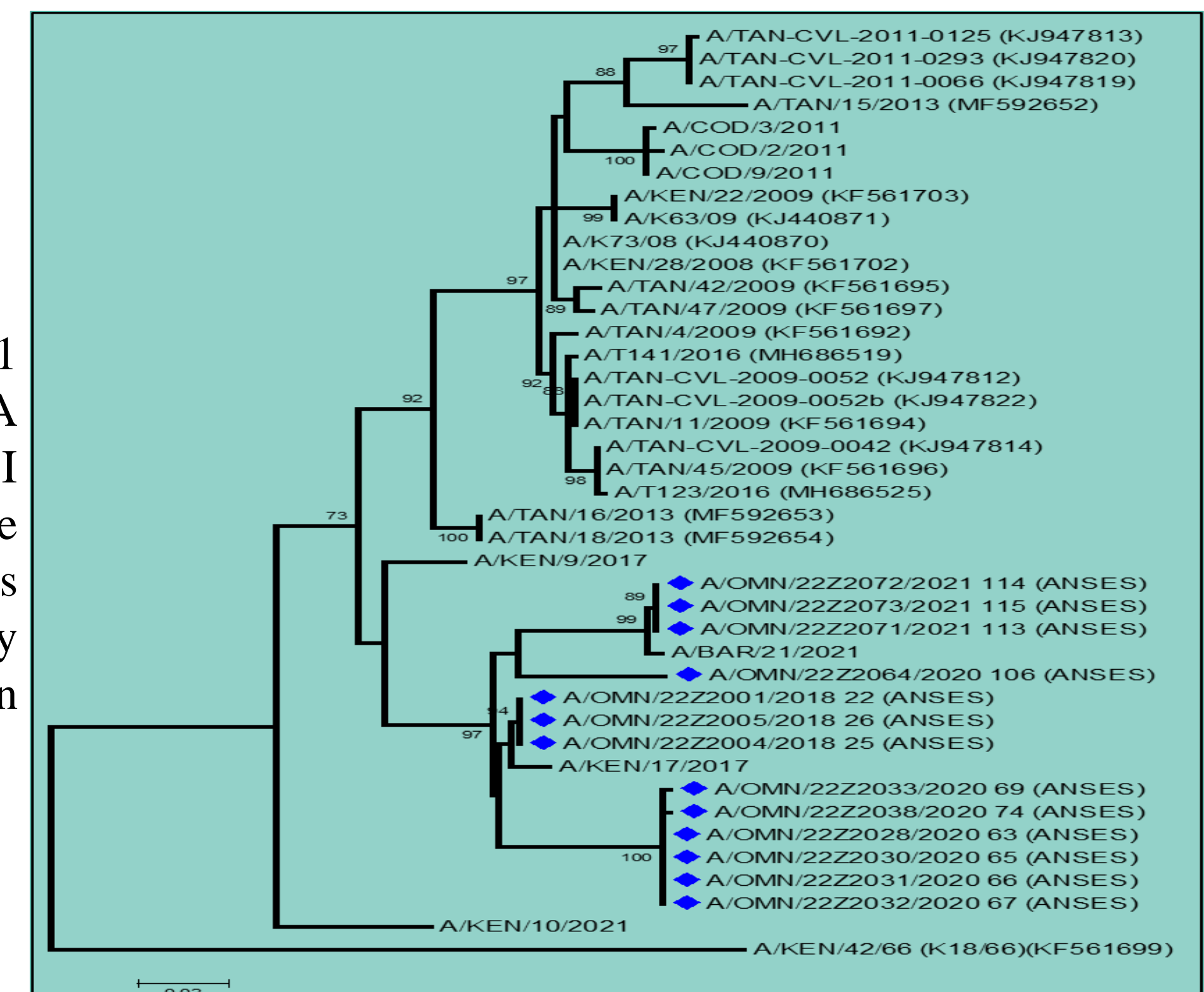
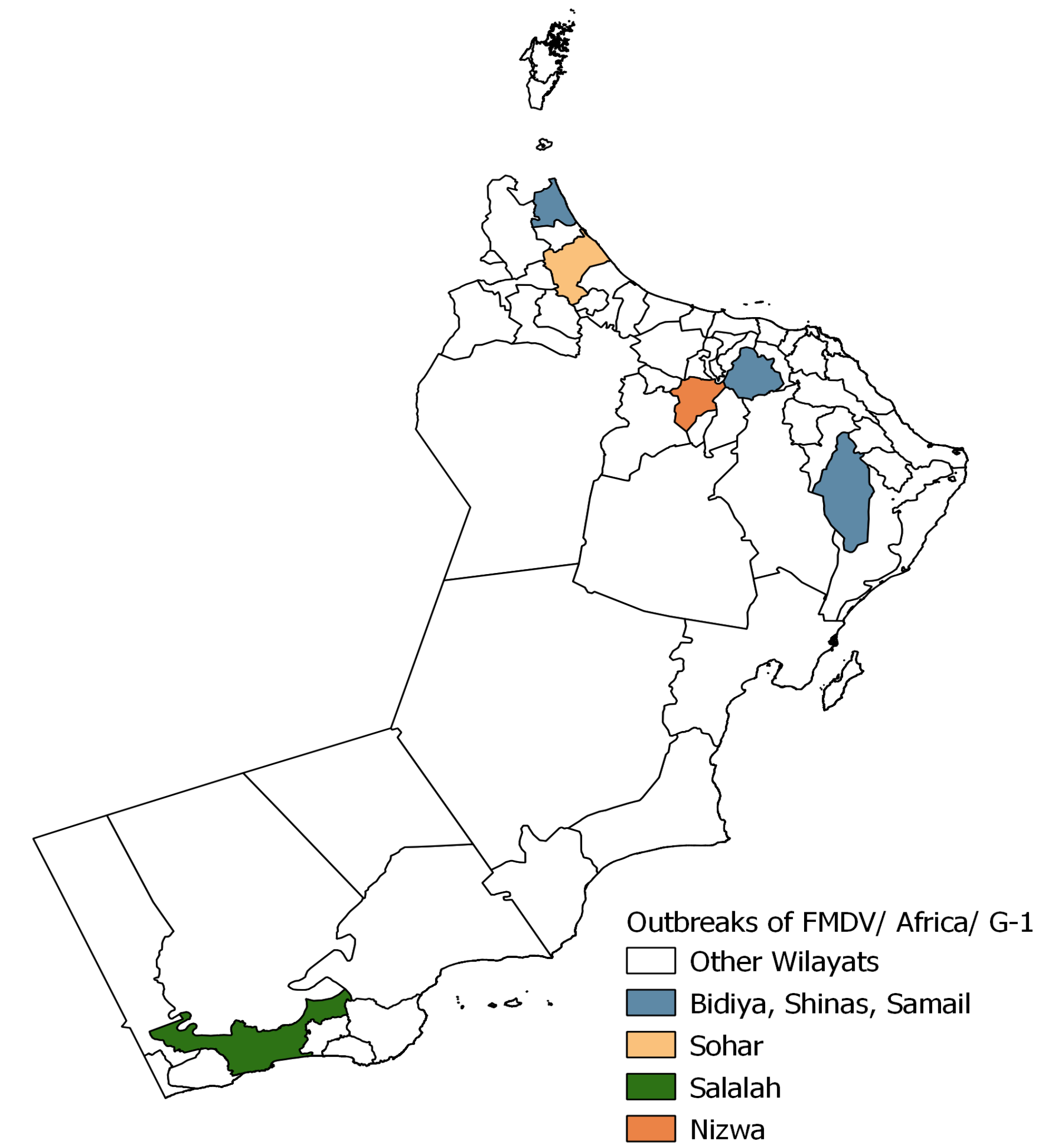


Figure 4: Phylogenetic tree constructed by Maximum Likelihood method based on the Tamura 3-parameter model, showing the relationship between the serotype A viruses isolates from Oman with other contemporary and reference viruses from Genbank and WRLFMD. The percentage of trees in which the associated taxa clustered together is shown next to the branches

FMD serotype A/Africa/G1 in OMAN

The geographical distribution of A/Africa/ G-I lineage in the Sultanate of Oman was found to extend from the northern governorates, Al Batinah North and Ash Sharqiyah North to the Southern governorate, Dhofar in 2018. The outbreaks were still recorded in 2020 in Al Batinah North, Sohar and new reports in two Ad Dhakhilia region Wilayats, Nizwa and Samail. Recently, in 2021, the virus was reemerging again in Dhofar.



Map1: Geographical distribution of FMDV/Africa/G-I in the Sultanate of Oman

Conclusion

This study reported genetic evidence of FMDV circulation from 2018 to 2021 in the Sultanate of Oman with closer links to isolates from the 2017 and 2021 FMD outbreaks in Kenya and Bahrain. This relationship of the Oman isolates to the isolates from East Africa might imply introduction of the virus into Oman from those countries where viruses within Lineage G-I are established.

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