



HAL
open science

MOLECULAR EPIDEMIOLOGY OF FOOT-AND-MOUTH DISEASE VIRUS O/EA-3: A RECENT TRANSBOUNDARY EMERGENCE IN NORTH AFRICA (2017-2019)

Souheyla Benfrid, Sandra Blaise-Boisseau, Jemma Wadsworth, Antonello Di Nardo, Andrew Shaw, Aurore Romey, Anthony Relmy, Rémi Faucheux, Valerie Mioulet, Donald P. King, et al.

► **To cite this version:**

Souheyla Benfrid, Sandra Blaise-Boisseau, Jemma Wadsworth, Antonello Di Nardo, Andrew Shaw, et al.. MOLECULAR EPIDEMIOLOGY OF FOOT-AND-MOUTH DISEASE VIRUS O/EA-3: A RECENT TRANSBOUNDARY EMERGENCE IN NORTH AFRICA (2017-2019). GFRA 2019, Oct 2019, Bangkok / Thailand, Thailand. anses-04524330

HAL Id: anses-04524330

<https://anses.hal.science/anses-04524330>

Submitted on 28 Mar 2024

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - NonCommercial - NoDerivatives 4.0 International License

MOLECULAR EPIDEMIOLOGY OF FMDV O/EA-3: A RECENT TRANSBOUNDARY EMERGENCE IN NORTH AFRICA

Benfrid Souheyla¹, Blaise-Boisseau S¹, Wadsworth J², Di Nardo A², Shaw A², Romey A¹, Relmy A¹, Faucheu R¹, Mioulet V¹, King DP², Knowles NJ² & Bakkali Kassimi L¹
¹ Laboratoire de Santé Animale de Maisons-Alfort, UMR 1161 virologie, INRA, Ecole Nationale Vétérinaire d'Alfort, ANSES, Université Paris-Est, 94700 Maisons-Alfort, France
² The Pirbright Institute, Ash Road, Pirbright, Woking, Surrey GU24 0NF, UK

THE Pirbright INSTITUTE

VIR UMR 1161 INRA - ANSES - ENVA

anses
French agency for food, environmental and occupational health & safety
Investigate, evaluate, protect
Souheyla.benfrid@anses.fr



INTRODUCTION

- Foot-and-mouth disease (FMD) remains endemic in Africa, with 5 out of its 7 viral serotypes currently circulating across the continent¹.
- In 2018 and 2019, FMDV outbreaks related to an unprecedented lineage of the serotype O were recorded in West and North Africa, causing numerous outbreaks in more than 17 countries.
- To better control FMD, we need a comprehensive understanding of the virus diffusion in this region of Africa at the local and inter-regional levels.
- In this work, we tried to identify and trace the circulation of this FMDV O new incursion in West and North Africa using phylogenetic analysis.

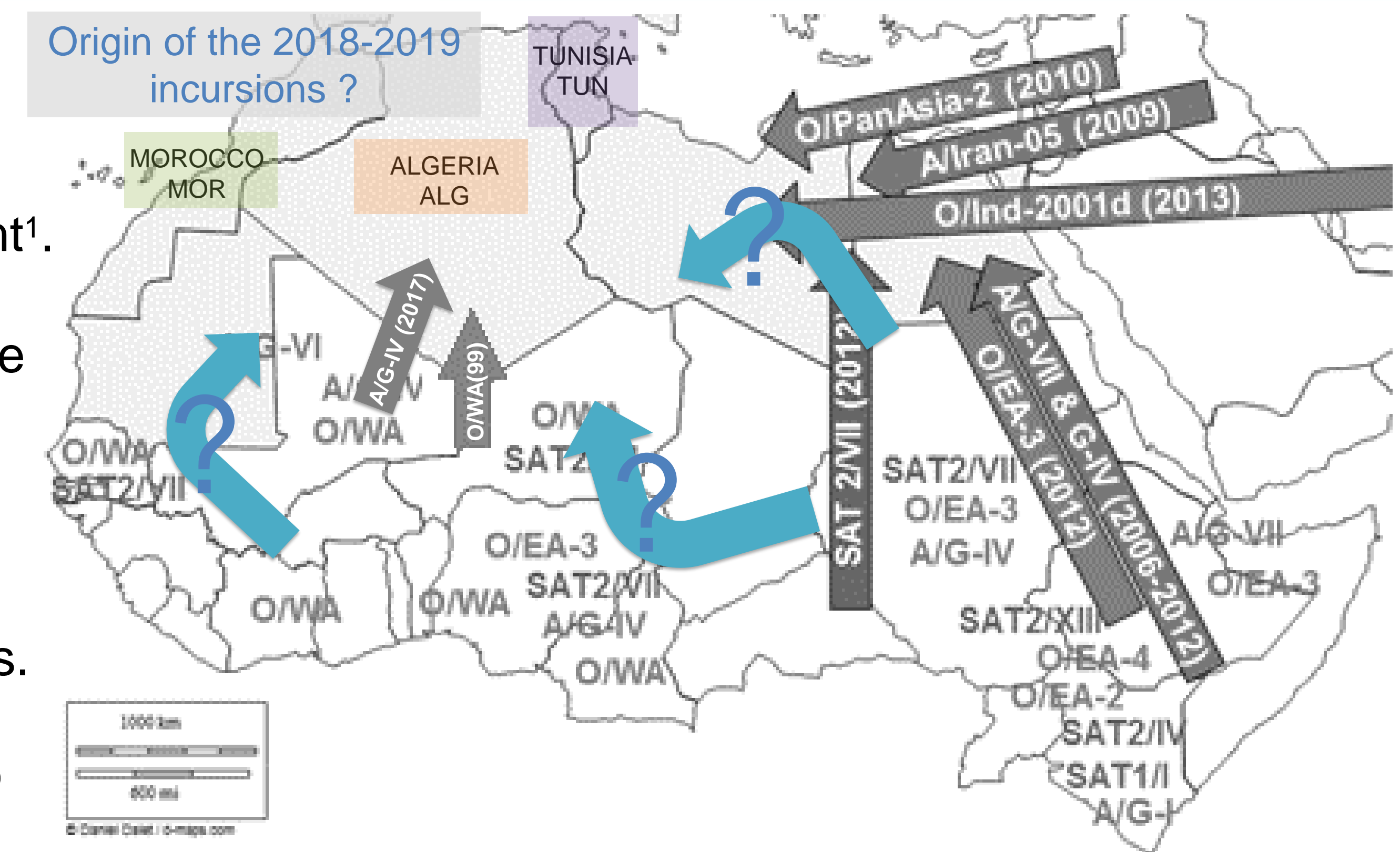


Figure 1: Known circulation of FMDV topotypes in East, West and North Africa (Adapted from Alessandro Ripani, OIE, GF-TAD 2015)

QUICK FACTS

- > 400 FMDV outbreaks reported in Maghreb in 2018-2019
- > O/EA-3 toptype incursions
- > 62 clinical samples from 12 affected countries
- > VP1 phylogenetic analysis

METHODS

- 2018-2019 outbreaks census (EMPRES-FAO/Promed/WAHIS-OIE) 2,3,4
- Sample sequencing at Pirbright or ANSES.
- Phylogenetic analysis (ANSES).

Number of samples	Country	Location	Species	Date collected
1	Ethiopia	Gaweta, Keffa Zone, SMNPR	cattle	07/01/2018
3	Burkina Faso	Pv Sabou, Sabou, Bouklemde, Centre-Ouest	cattle	07/02/2018
3	Burkina Faso	Bougoumsine, Saaba, Kadogo, Centre	cattle	07/06/2018
3	Guinea-Conakry	x	cattle	07/10/2018
1	Senegal	Bandafassi, Arrondissement of Bandafassi, Kedougou Department, Kedougou Region	cattle	07/11/2018
1	Senegal	Kaolack, Kaolack Region	cattle	07/12/2018
1	Algeria	El Bayadh	sheep	07/17/2018
1	Burkina Faso	Sawadogo, Zinare, Ouhritenga, Plateau-Central	cattle	07/18/2018
1	Algeria	Ghardaia	goat	07/19/2018
1	Algeria	Bouinan, Centre, Blida	cattle	07/20/2018
1	Senegal	Bandia, Sindia, Mbour, Thies Region	cattle	07/20/2018
1	Algeria	Mekla, Centre, Tizi Ouzou	cattle	07/21/2018
2	Gambia	x	cattle	07/23/2018
4	Ethiopia	Kewet, North Shewa Zone, Amhara	cattle	07/24/2018
1	Senegal	Koumpentoum, Tambacounda Region	swine	07/28/2018
1	Sierra Leone	Quidudu, Kono, Eastern, Eastern	cattle	07/29/2018
1	Senegal	Sebkoutane, Rufisque, Rufisque Department, Dakar	cattle	07/29/2018
2	Mauritania	Hodh el Charqui, Tiji	cattle	07/30/2018
1	Ivory Coast	Bingerville	swine	07/30/2018
1	Ivory Coast	Port-Bouet	swine	07/30/2018
1	Ivory Coast	Yopougon-Arto	swine	07/30/2018
1	Algeria	Tizi-Ouzou	cattle	07/30/2018
2	Mauritania	Hodh El Charqui, Tiji	cattle	07/30/2018
2	Ethiopia	Albeko, South Wollo Zone, Amhara	cattle	07/31/2018
2	Ethiopia	Weirababu, South Wollo Zone, Amhara	cattle	07/31/2018
1	Senegal	Tilene, Ziguinchor, Ziguinchor Region	cattle	07/31/2018
1	Mauritania	Hodh El Charqui, Guersavoine	sheep	08/01/2018
1	Mauritania	Brakna, Aleg	cattle	08/01/2018
3	Algeria	Ghardaia	goat	12/19/2018
2	Algeria	El Bayadh	cattle	12/25/2018
1	Algeria	Tizi-Ouzou	cattle	12/30/2018
4	Tunisia	unknown	cattle	01/07/2019
1	Tunisia	Sidi Bouzid	cattle	07/13/2019
3	Morocco	Khouribga	cattle	07/15/2019
1	Morocco	Sidi Bennour	cattle	07/15/2019
1	Tunisia	Jendouba	cattle	07/17/2019
2	Maroc	Oulad sidi Chehman	cattle	01/08/2019

Table 1: Characteristics of the samples collected from West and North Africa

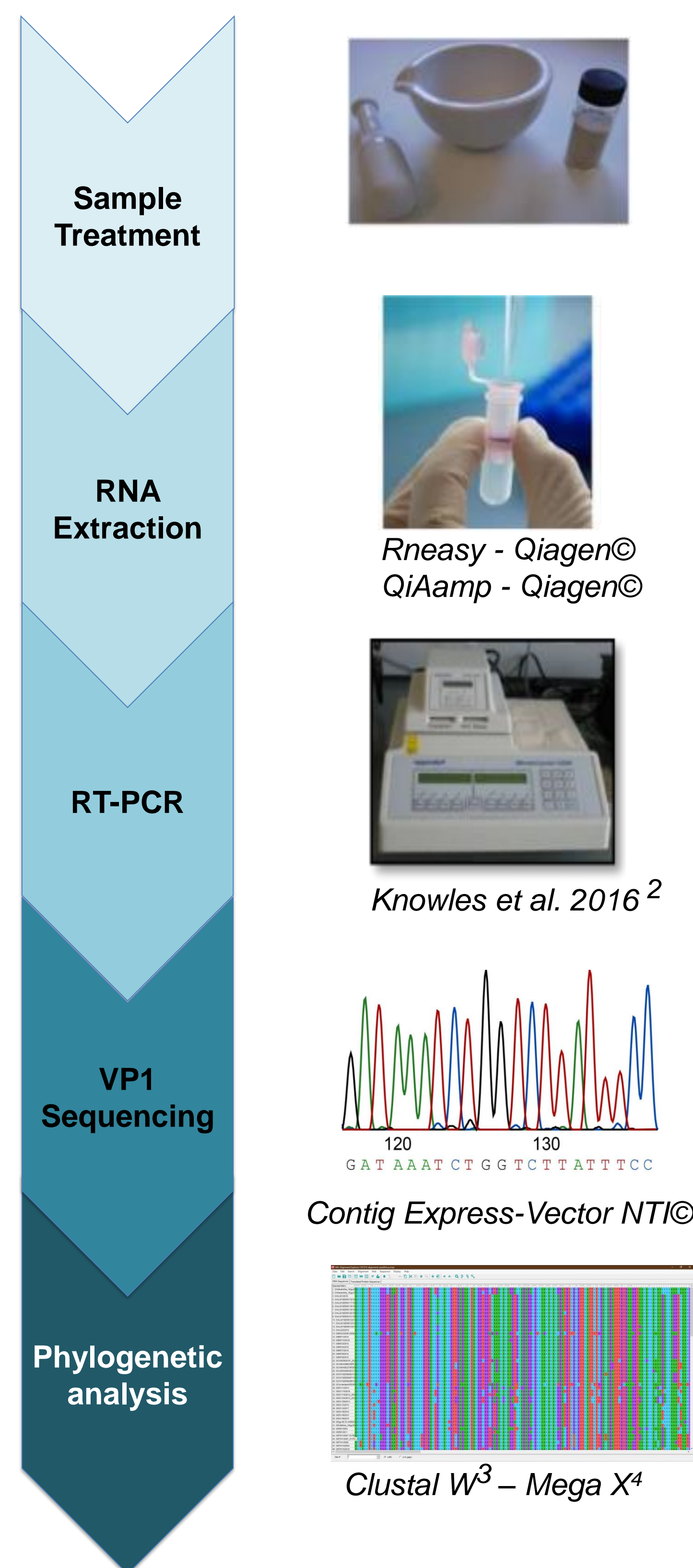


Figure 2: Workflow used for the analysis of FMDV-infected sampled

RESULTS

- The FMDV viruses circulating in 2018-2019 in the Maghreb region clustered with the O/EA-3 toptype.
- The Maghreb FMDV viruses did not cluster with the strains responsible for the 2017 outbreaks in Egypt.
- The O/EA-3 viruses showed a 99% identity with strains circulating in Nigeria in 2016.
- The O/EA-3 strain from North Africa shares a strong similarity with viruses circulating in West Africa: Nigeria, Central African Republic (C.A.R.), Senegal, Burkina Faso, Ivory Coast, Gambia, Guinea and Sierra Leone.
- Algeria probably suffered from multiple incursions as viruses circulating in this country cluster in different branches on the phylogenetic tree.
- Tunisia probably suffered from at least two incursions as presented in the phylogenetic tree.
- Morocco suffered from two incursions, probably originating from the same path.

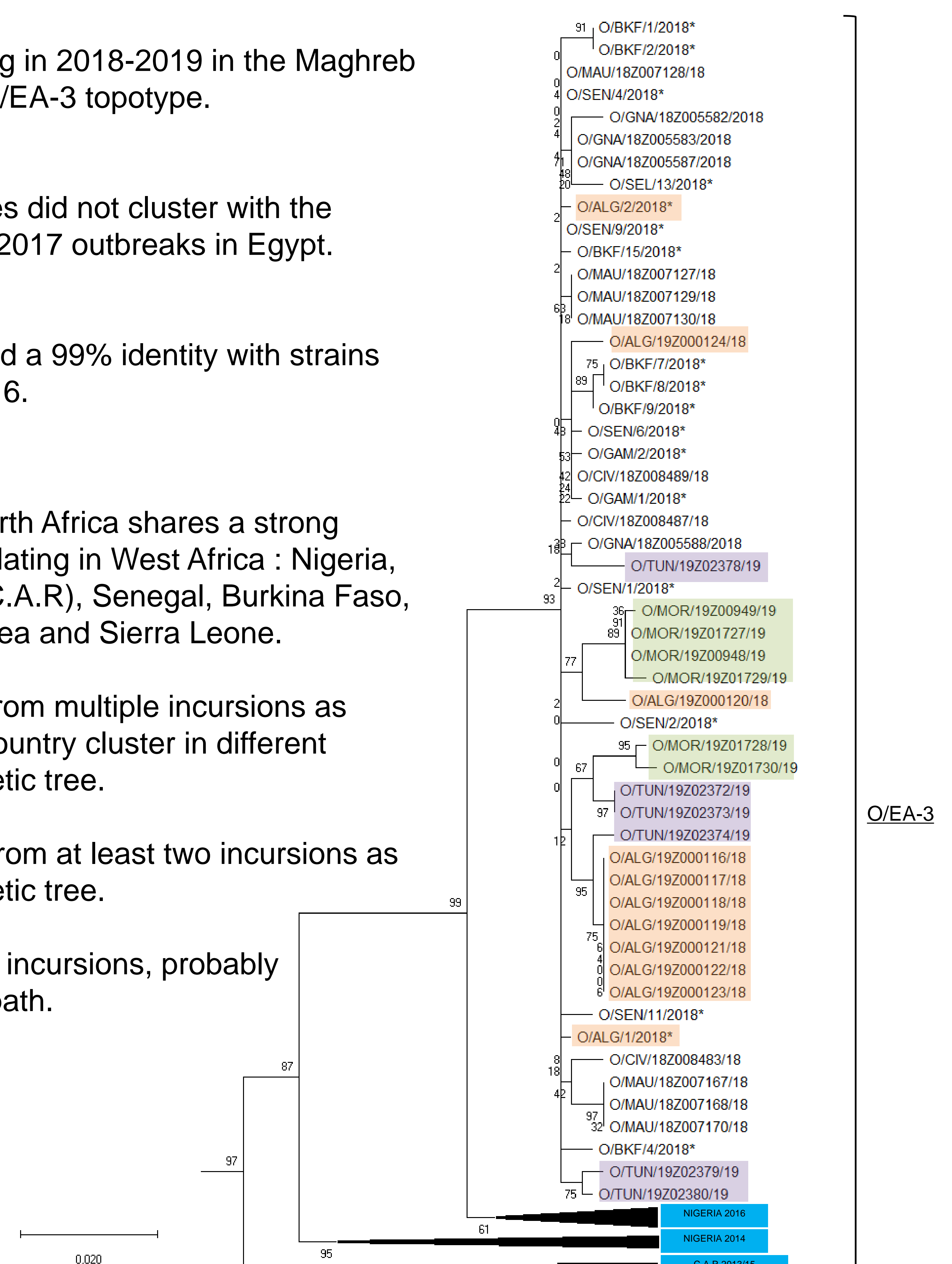


Figure 3: Evolutionary analysis of the O/EA-3 lineage sequences by Maximum Likelihood Method. Sequences from the study were compared to other contemporary and reference sequences available in the NCBI database or in the Pirbright database. The 2018 and 2019 Maghreb viruses were from the O/East-Africa 3 (O/EA-3) toptype as evidenced by the clustering with known O/EA-3 toptype sequences. The O/EA-3 subtree with the highest log likelihood (-12968,78) is shown. Number of bootstrap sample was set to 500. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. This analysis involved 162 nucleotide sequences. There were a total of 639 positions in the final dataset. Evolutionary analyses were conducted in MEGA X⁴.

CONCLUSION AND DISCUSSION

From the phylogenetic analysis, we can infer that the FMDV O/EA-3 lineage disseminated from East Africa to Nigeria, following the Djibouti-Ndjamena highway (Fig 4, pink line). The spread followed further the Ndjamena-Dakar highway (Fig 4, orange line), reaching Burkina Faso and the Ivory Coast. From there, the O/EA-3 lineage spread further to Mauritania, Algeria, Tunisia, and Morocco, probably following the transhumance of cattle through nomadic circulation from Mauritania, Mali and Niger to the Maghreb (Fig 4, dark blue arrows). Full genome sequence data could further help understand if multiple “escapes” of the O/EA-3 virus from East Africa to the West and from the West to Maghreb occurred. Moreover, field data from Mali, Niger, Chad and Libya could help gain knowledge on the temporality of diffusion for this toptype.

Promoting effective control and preventive strategies against invasive FMDV topotypes in the future implies a close monitoring of the main trans-African highways as well as at the nomadic and pastoral circulation areas.

This study helps to develop a comprehensive view of the evolutionary history and dynamics of the O/EA-3 FMD viruses. These findings also provide insights into the complex transboundary nature of the disease and help to understand the risks of future disease incursions into this European neighboring region.

References

- World Reference Laboratory - <http://www.wrlfmd.org/foot-and-mouth-disease/occurrence> (consulted 17/10/2019)
- Knowles et al., VP1 sequencing protocol for foot and mouth disease virus molecular epidemiology, Rev Sci Tech 2016
- Clustal W - improving the sensibility of progressive multiple sequence alignment through sequence weighting
- Kumar S. et al. MEGA-X: molecular evolutionary genetics analysis across computing platforms, 2018.
- Robinson et al. for the Food and Agricultural Organisation (FAO) - cattle density map (2014)
- OECD, An Atlas of the Sahara-Sahel: Geography, Economics and Security, OECD Publishing, Paris 2014 – Hinges of the Saharan Region.

Acknowledgments



European Reference Laboratory For Foot-and-Mouth Disease

Many thanks to both teams from the FMD WRL and from the FMD EURL. Many thanks to the laboratories of Algeria, Burkina Faso, Central African Republic Côte d'Ivoire, Guinea, Mauritania, Morocco, Nigeria, Senegal, Sierra Leone and Tunisia.

anses.fr

anses

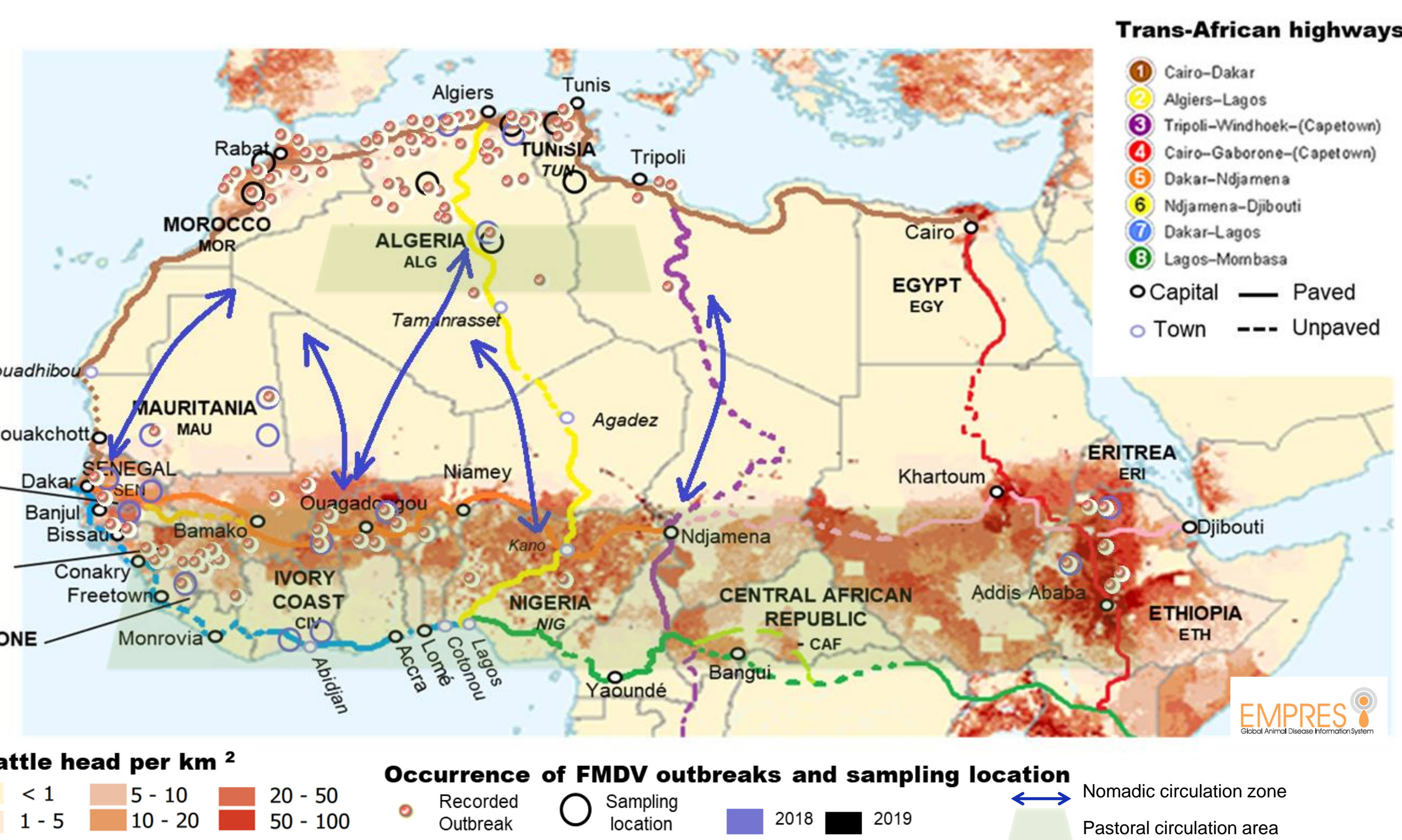


Figure 4: O/EA-3 2018 and 2019 FMDV outbreaks are located alongside the main trans-african highways and pastoral circulation areas. Cattle density map adapted from the Food and Agricultural Organisation (FAO)². Trans-African highways from the African Development Bank Trans-Sahara highway (TSH) project. Outbreak location from EMPRES (FAO): 01/01/18-10/16/19. Sampling location data provided from the respective endemic countries, shared from the Pirbright Institute. Nomadic circulation zones and pastoral circulation areas from OECD (2014)⁶.