



FMD in Libya

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Libya



History of FMD in Libya:

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Source: <http://www.wrlfmd.org/>

<u>Serotype</u>	<u>Years</u>
FMDV-O:	1959, 1962, 1967-1968, 1972, 1981-1983, 1988-1989, 1994, 2010-2013
FMDV-A:	1979, 2009
FMDV-C:	0000
FMDV-Asia 1:	0000
FMDV-SAT 1:	0000
FMDV-SAT 2:	2003, 2012
FMDV-SAT 3:	0000

History of vaccination in Libya

- ❑ Mass vaccination for all animal (small ruminants and cattle)
- ❑ All animals vaccinated during 2013/2014.
- ❑ All animals vaccinated during 2014/2015.
- ❑ A single injection of FMD vaccine.
- ❑ Sheep and Goat once per year, cattle twice per year.
- ❑ Mainly cattle vaccinated during In 2015/2016.
- ❑ Last vaccination was on June 2016.

Sep 2018 in IZSLER – Training

Supported by IZSLER and EuFMD



4 ELISA Kits (2 NSP – 2 SP) provided by IZSLER (Brescia, Italy) by the end of May 2019 during OIE meeting in Paris.



Recent work on FMD

- ▶ Continuous support by EuFMD and IZSLER
- ▶ EuFMD has organized a Technical meeting on 21-22 March 2019 to support FMD risk-based strategy of Libya



FMD Samples

- ▶ Hundreds of sera samples collected
- ▶ Stored in Tripoli lab and ready for shipment
- ▶ All samples will be shipped to IZSLER in Italy for testing and confirmation
- ▶ Facing difficulties regarding samples shipment!

Current FMD outbreak

- ▶ It was not possible to send clinical and serum samples outside Libya
- ▶ NCAH succeeded in sending clinical samples on FTA cards to IZSLER lab in Brescia (end of May 2019)
- ▶ On 4/6/2019 Emiliana sent the results as FMD positive for serotype O (O/EA-3)
- ▶ ON 7/6/2019 Emiliana and her lab team succeeded in sequencing VP1 gene

FMD during April-May 2019



FMDV Genotyping report

Samples sequenced: **O/LIB/Misrata/2019** (IZSLER_19_194010/2)
 Region sequenced: 846 nt including VP1 (VP1 gene length: 636nt)
 RT-PCR primers: O-1C283F/EUR-2B52R (for 1st round RT-PCR)
 O-1C583F/EUR-2B52R (for 2nd round PCR)

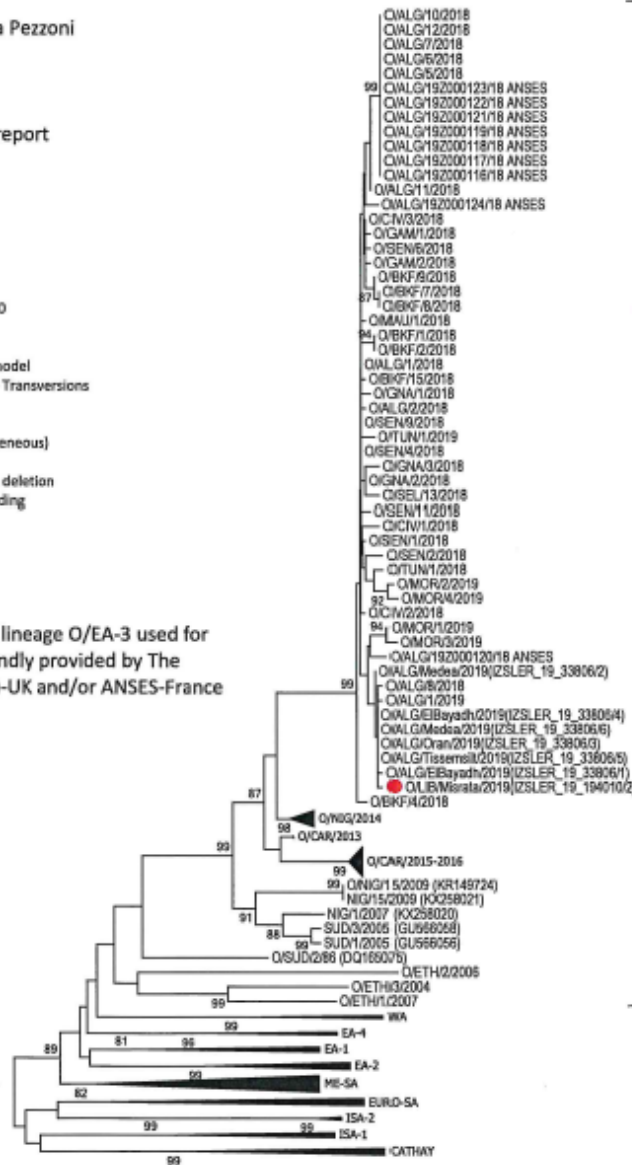
Reported by: Giulia Pezzoni

● virus sequenced in this report

Analysis

Analysis: Phylogeny Reconstruction
 Scope: All Selected Taxa
 Statistical Method: Neighbor-joining
Phylogeny Test
 Test of Phylogeny: Bootstrap method
 No. of Bootstrap Replications ——— 1000
Substitution Model
 Substitutions Type : Nucleotide
 Model/Method: Kimura 2-parameter model
 Substitutions to Include d: Transitions + Transversions
Rates and Patterns
 Rates among Sites: Uniform rates
 Pattern among Lineages: Same (Homogeneous)
Data Subset to Use
 Gaps/Missing Data Treatment: Pairwise deletion
 Codons Included: 1st+2nd+3rd+Non-Coding
 No. of Sites : 636nt (VP1 gene)
 No of Bootstrap Reps = 1000

Most of the sequences of the lineage O/EA-3 used for the phylogenetic tree were kindly provided by The Pirbright Institute (FMD-WRL)-UK and/or ANSES-France



O/EA-3

Serotype O
 Topotype EA-3

99.7-99.8% with Algerian viruses

- ▶ Don King the head Pirbright lab kindly provided us with all vaccine matching results for this serotype

Sample Ref. #	Topotype	O 3039	O ₁ Manisa	O/TUR/5/2009	Country
ETH/13/2018	EA-3	0.34	0.21	0.38	ETHIOPIA
ETH/16/2018	EA-3	0.21	0.15	0.31	ETHIOPIA
ALG/01/2018	EA-3	0.51	0.37	0.46	ALGERIA
ALG/02/2018	EA-3	0.45	0.34	0.59	ALGERIA
GAM/01/2018	EA-3	0.45	0.3	0.52	GAMBIA
SEN/02/2018	EA-3	0.38	0.3	0.49	SENEGAL
SEN/11/2018	EA-3	0.63	0.39	0.54	SENEGAL
SEL/13/2018	EA-3	0.79	0.58	0.28	SIERRA LEONE
BKF/04/2018	EA-3	1	0.87	0.93	BURKINA FASO
BKF/09/2018	EA-3	0.74	0.66	0.68	BURKINA FASO
PAT/01/2018	EA-3	0.65	0.46	0.56	PALESTINIAN AUTONOMOUS TERRITORIES
ALG/01/2019	EA-3	0.5	0.33	0.52	ALGERIA
ALG/05/2018	EA-3	0.85	0.51	0.62	ALGERIA
ETH/20/2018	EA-3	0.41	0.46	0.36	ETHIOPIA
ETH/23/2018	EA-3	0.47	0.56	0.56	ETHIOPIA
ALG/11/2018	EA-3	0.81	0.58	0.81	ALGERIA
CIV/03/2018	EA-3	0.59	0.46	0.76	COTE DIVOIRE
GNA/03/2018	EA-3	0.55	0.4	0.5	GUINEA
TUN/01/2019	EA-3	0.51	0.46	0.47	TUNISIA

- ▶ NCAH is trying to provide bivalent vaccine (O-Manisa + O3039 and A): **REMESA support in this regard would be appreciated**

Special thanks to:

- ▶ IZSLER (Brescia - Italy)
- ▶ EuFMD
- ▶ FAO
- ▶ OIE
- ▶ REMESA