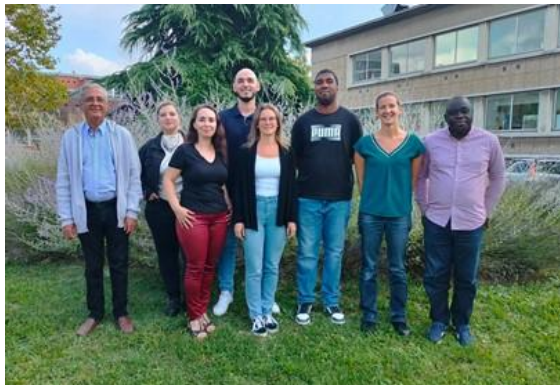




SUPPORT FROM EURL

FMD EU-RL

Eurl-fmd@anses.fr
<http://eurl-fmd.anses.fr>



**Biology of Picornaviruses Team (BioPic)
(Animal Health Laboratory/Virology Unit)**



**Service for Exotic viruses and
vector borne diseases**

O/ME-SA/SA-2018 in Germany

10/01 Outbreak reported by Germany in Brandenburg

11/01 Identification O/ME-SA/SA-2018 by FLI and shared VP1 sequence with EURL

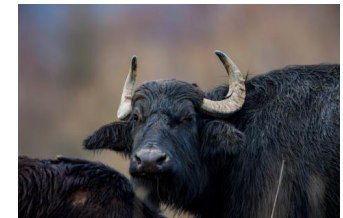
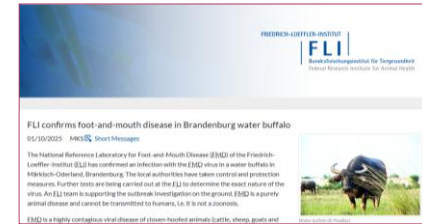
11/01 EURL shared rtRT-PCR protocol specific for SA-2018 previously developed with FLI

14/01 EURL received from FLI 1 isolate and 5 samples from one dead buffalo

14/01 Confirmation FMDV by EURL (All samples pos by rtRT-PCR)

Nature of the sample	Ct value	Result
	3D/IRES	
Lung	22.51/24.12	Pos
Intestine	29.56/30.57	Pos
Spleen	30.85/31.21	Pos
Lymph node	26.16/26.94	Pos
Tonsils	30.19/31.18	Pos

15/01 SA-2018 rtRT-PCR protocol shared with all NRLs and publication on the EURL website



Bubalus bubalis, water buffalo

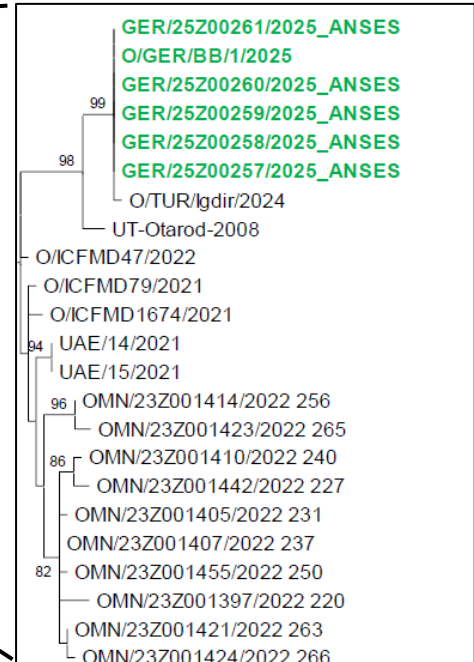
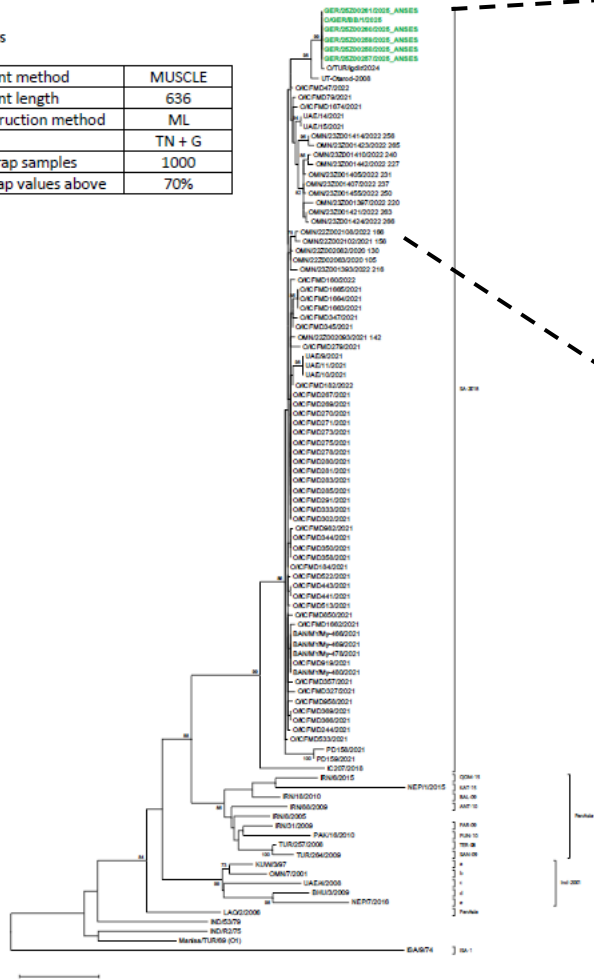


FMD EURL

16/01 VP1 sequencing

Analysis parameters

Sequence alignment method	MUSCLE
Sequence alignment length	636
Phylogeny reconstruction method	ML
Model used	TN + G
Number of bootstrap samples	1000
Displaying bootstrap values above	70%



100%
homology

Most closely related sequences

Virus name	Serotype	Topotype	Lineage	Length	Identity (best hit)
O/TUR/Igdir/2024	O	ME-SA	SA-2018	633	99.84
UT-Otarod-2008	O	ME-SA	SA-2018	639	98.89
O/ICFMD270/2021	O	ME-SA	SA-2018	639	98.10
O/ICFMD271/2021	O	ME-SA	SA-2018	639	98.10
O/ICFMD291/2021	O	ME-SA	SA-2018	639	98.10
O/ICFMD280/2021	O	ME-SA	SA-2018	639	98.10
O/ICFMD302/2021	O	ME-SA	SA-2018	639	98.10
O/ICFMD267/2021	O	ME-SA	SA-2018	639	98.10
O/ICFMD79/2021	O	ME-SA	SA-2018	639	98.10
O/ICFMD285/2021	O	ME-SA	SA-2018	639	98.10
O/ICFMD275/2021	O	ME-SA	SA-2018	639	98.10

➤ **Most closely related sequence:**
O/TUR/Igdir/2024



24/01 vaccine matching test performed by EURL and result provided to FLI and EC

Vaccine strain	Heterologous Titre	r1
O-3039 BI	2.0	0.28
O-PanAsia2 BI	2.25	0.35
O1 Manisa BI	2.15	0.63

Effective vaccines available



Bubalus bubalis, water buffalo

O/ME-SA/PanAsia-2^{ANT-10} in Hungary

06/03 Outbreak in dairy farm in Győr-Moson-Sopron county, close to the border with Slovakia, reported by Hungary

Outbreak confirmed by the NRL → **rtRT-PCR positive**



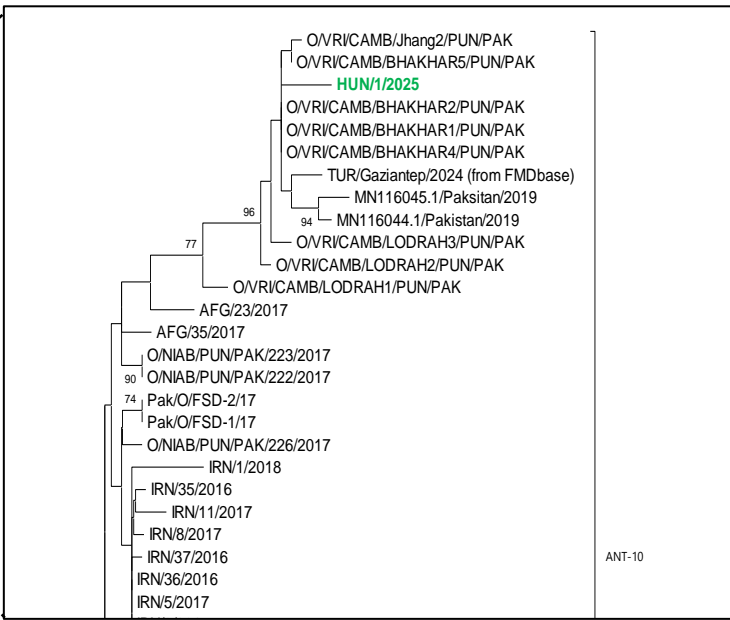
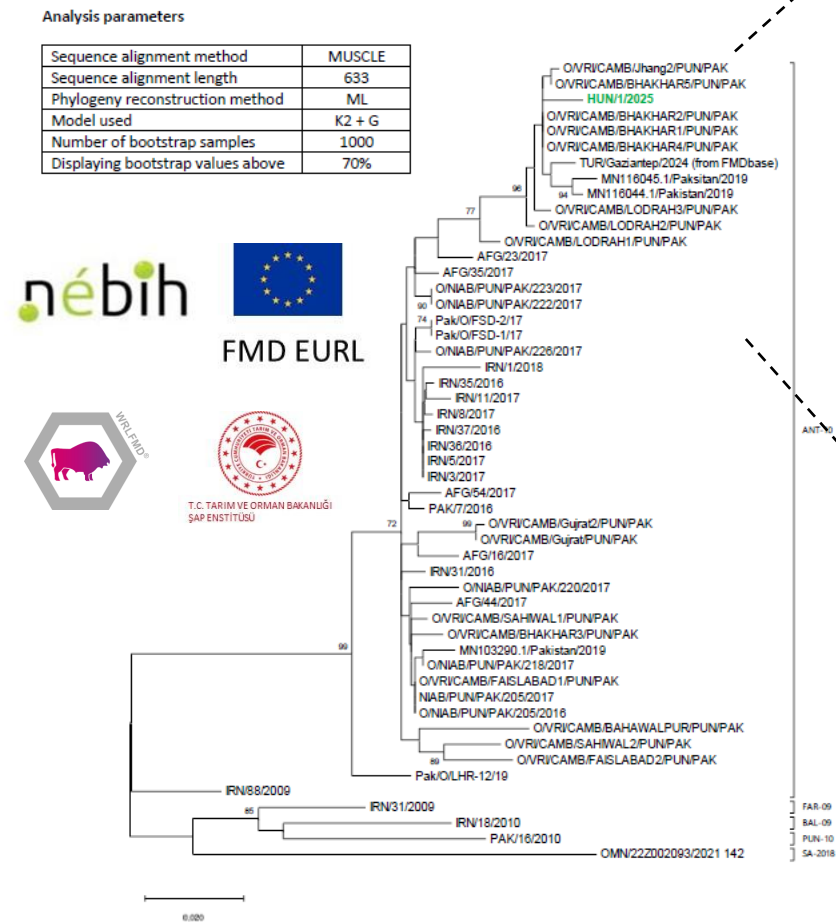
08/03 Hungarian NRL identified O/ME-SA/PanAsia-2^{ANT-10} after VP1 sequencing and shared sequence with EURL

nébih

08/03 Phylogenetic analysis

EURL genotyping report confirmed O/ME-SA/PanAsia-2^{ANT-10}

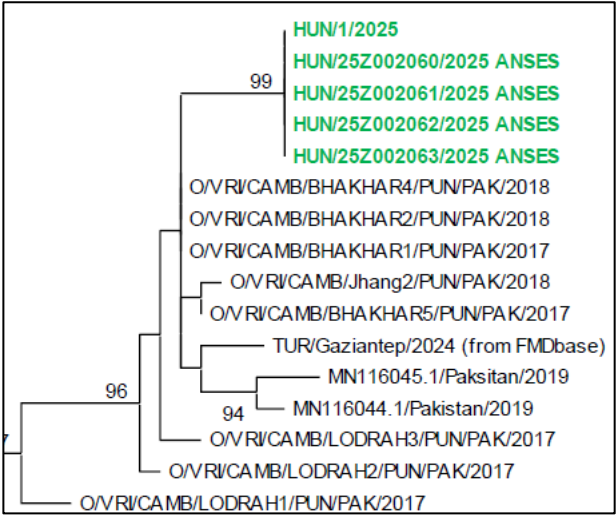
Most closely related to isolates from Pakistan (2017, 2018) 99.22% and Türkiye (2024) 98.58%



Most closely related sequences

Virus Name	Serotype	Topotype	Lineage	Sublineage	Length	Identity (best hit)
O/VR/CAMB/BHAKHAR2/PUN/PAK	O	ME-SA	PanAsia-2	ANT-10	639	99.22
O/VR/CAMB/BHAKHAR1/PUN/PAK	O	ME-SA	PanAsia-2	ANT-10	639	99.22
O/VR/CAMB/BHAKHAR4/PUN/PAK	O	ME-SA	PanAsia-2	ANT-10	639	99.22
O/VR/CAMB/BHAKHAR5/PUN/PAK	O	ME-SA	PanAsia-2	ANT-10	639	99.06
O/VR/CAMB/Jhang2/PUN/PAK	O	ME-SA	PanAsia-2	ANT-10	639	98.90
O/VR/CAMB/LODRAH3/PUN/PAK	O	ME-SA	PanAsia-2	ANT-10	639	98.75
O/VR/CAMB/LODRAH2/PUN/PAK	O	ME-SA	PanAsia-2	ANT-10	639	98.75
TUR/Gaziantep/2024 (from FMDbase)	O	ME-SA	PanAsia-2	ANT-10	633	98.58
MN116044.1/Pakistan/2019	O	ME-SA	PanAsia-2	ANT-10	634	98.11
O/VR/CAMB/LODRAH1/PUN/PAK	O	ME-SA	PanAsia-2	ANT-10	639	97.65

- 10/03** Samples arrived at EURL (4 Epithelium; 4 blood; 1 serum)
- 10/03** Confirmation FMDV by EURL (7/8 samples positive in rtRT-PCR)
- 11/03** FMDV isolated from the 4 epithelium samples
- 11/03** VP1 sequencing from isolates: 100% homology
- 02/04** VP1 sequence from second outbreak (Level received from NRL. 100% homology



Vaccine matching

O/ME-SA/PanAsia-2^{ANT-10} Hungary

24/01 vaccine matching test performed by EURL and result provided to NRL and EC

Vaccine strain	Heterologous Titre	r1
O-3039 BI	1.70	0.18
O-PanAsia2 BI	2.30	0.28
O1 Manisa BI	2.00	0.56

Effective vaccine available



Data to be updated

O/ME-SA/PanAsia-2^{ANT-10} in Slovakia

- 21/03: FMD outbreak confirmed by NRL in 3 dairy farms by rtRT-PCR
- 26/03: NRL sequenced VP1 and identified O/ME-SA/PanAsia-2^{ANT-10}
- Sequence shared with EURL. 100% homology with Hungarian strain

Analysis parameters

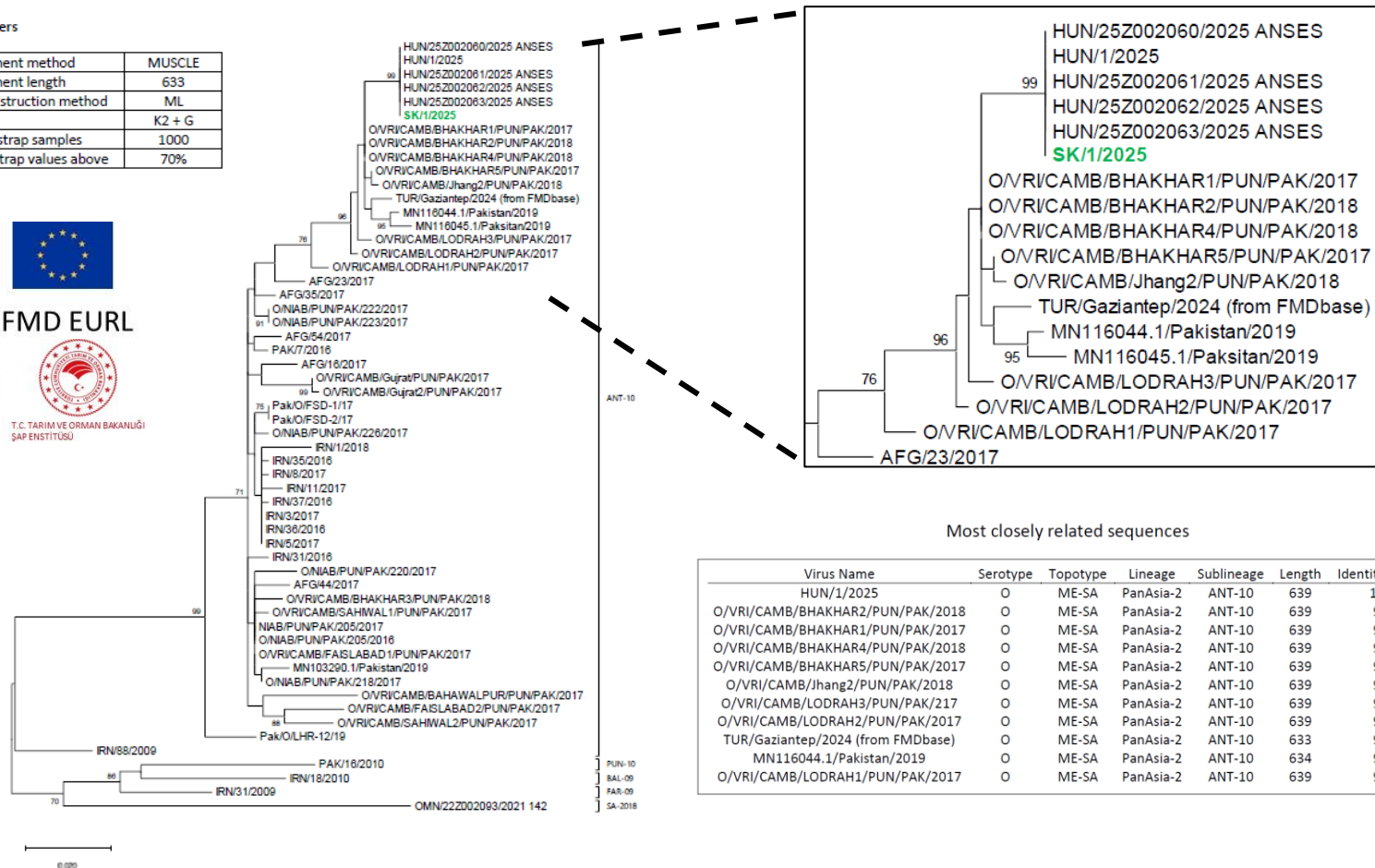
Sequence alignment method	MUSCLE
Sequence alignment length	633
Phylogeny reconstruction method	ML
Model used	K2 + G
Number of bootstrap samples	1000
Displaying bootstrap values above	70%



FMD EURL



T.C. TARIM VE ORMAN BAKANLIĞI
ŞAP ENSTİTÜSÜ



Full Genome Sequencing

04/04 17 Samples from 5 Slovakian outbreaks were received by the EURL
(Medvedov, Narad, Baka, Mala Luc, Plavecky Stvrtok)

07/04 6 Epithelium samples from the other 3 Hungarian outbreaks will be shipped today. (Levél, Darnózseli, Dunakiliti)



Full genome sequencing will be performed on all samples by EURL.



Acknowledgments



EURL Network members



T.C. TARIM VE ORMAN BAKANLIĞI
ŞAP ENSTİTÜSÜ



Thank you for your attention