

**Regional FMD situation,
recent circulating genetic
lineages,
&
Vaccine strains, vaccine
selection for FMD**

WELNET FMD

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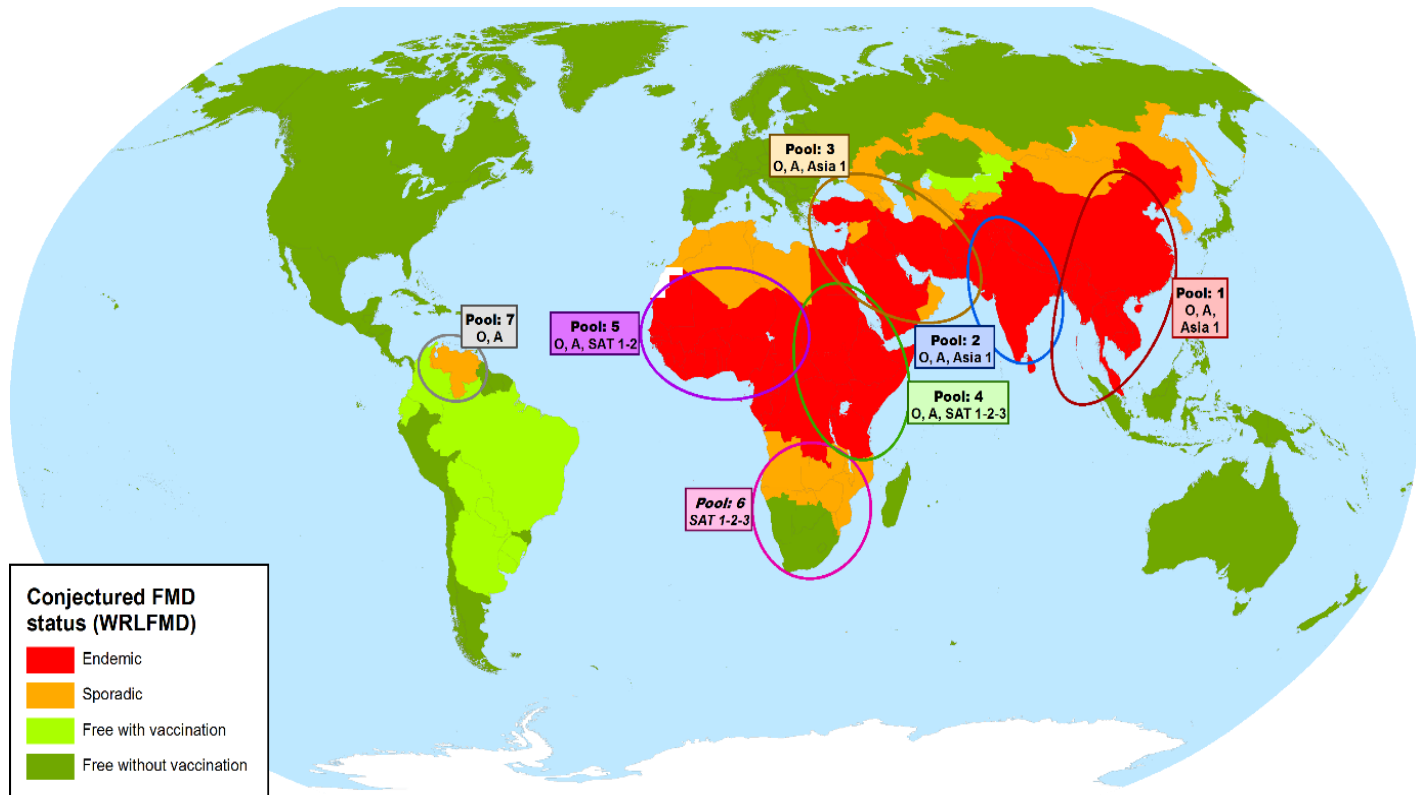
Dr. Don King
Head of the Vesicular Disease Reference Laboratory
Group
The Pirbright Institute

WELNET FMD

Conjectured global status

Endemic pools

- Virus ecosystems that maintain specific FMD virus strains
- Seven FMDV serotypes with an unequal distribution
 - No reported serotype C outbreaks since 2004 (Kenya and Brazil)
- Control via (tailored) vaccination and supporting diagnostics



Regional FMD Situation

- FMD is endemic in WestEurasia (WE)region
 - Serotype **O**, **A** and **Asia1** is circulated dynamically
 - In Pakistan and Iran
 - increased number of outbreak due to **Asia1** in Pakistan
 - **A** and **O** more in Iran
 - Only serotype **O** causes outbreak in Turkey
 - Sporadically virus circulated in sometime in the remained area in WE
 - Recently O/ME-SA/Ind2001e incursioned to Russia and Kazakhstan as well as North Africa

FMDV Genetic Lineages Circulated in WE

- Currently circulated Genetic lineages for in WestEurasia (WE) region
 - O/ME-SA/PanAsia-2^{QOM-15}
 - O/ME-SA/PanAsia-2^{ANT-10},
 - (recently in Iran, partially in Türkiye and ME)
 - O/ME-SA/Ind2001e
 - A/ASIA/Iran-05 (FAR-11 and SIS-13)
 - A/ASIA/G-VII (?)
 - ASIA1/SINDH08

Headline events 2021/22

Tunisia

Jan 2022

O/EA-3

A (untyped) – Libya

O (untyped) - Libya

Russian Federation

Dec 2021

O/ME-SA/Ind-2001e

Kazakhstan

Jan 2022

O/ME-SA/Ind-2001e

Indonesia

O/ME-SA/Ind-200e

Namibia/Zambia

July 2021

O/EA-2

South Africa

KwaZulu-Natal:

SAT 2 – 2021

2022: New SAT 2 outbreaks in Gauteng and North-West Provinces

Eastern Mediterranean

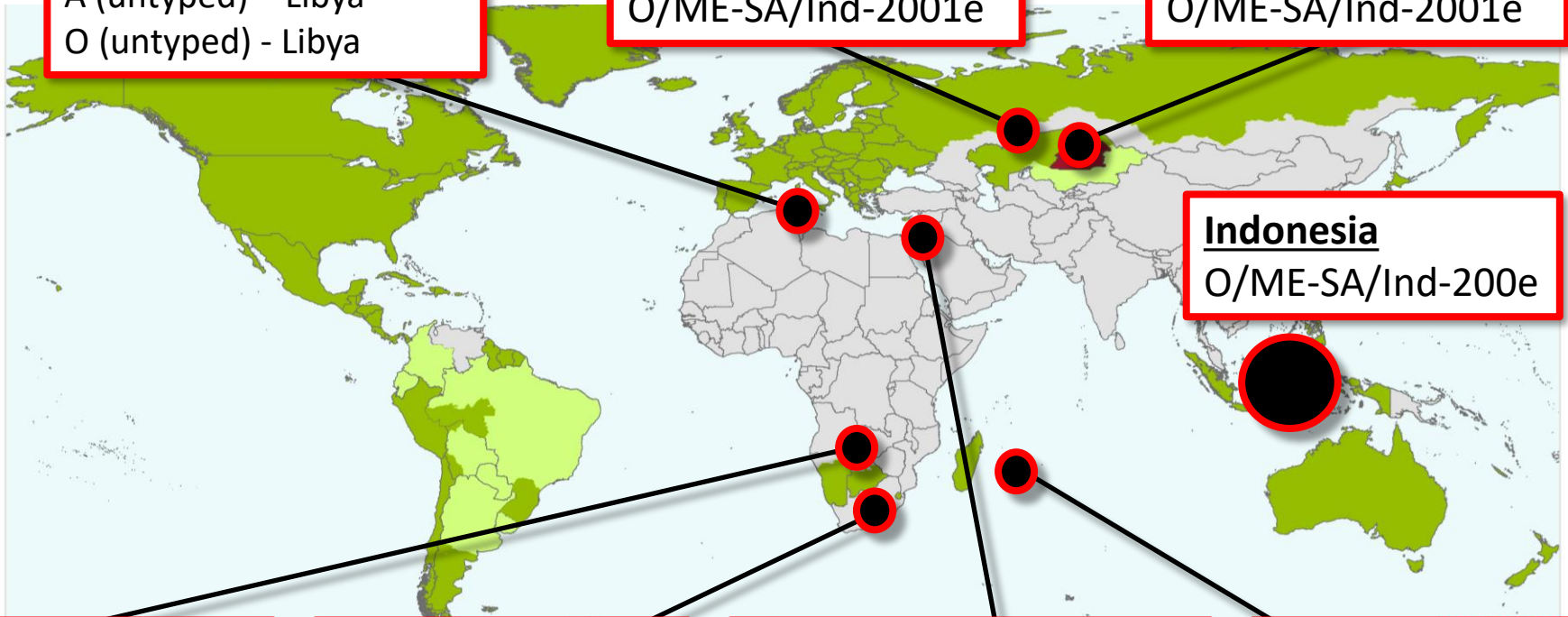
Dec 2021-on-going

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

Mauritius

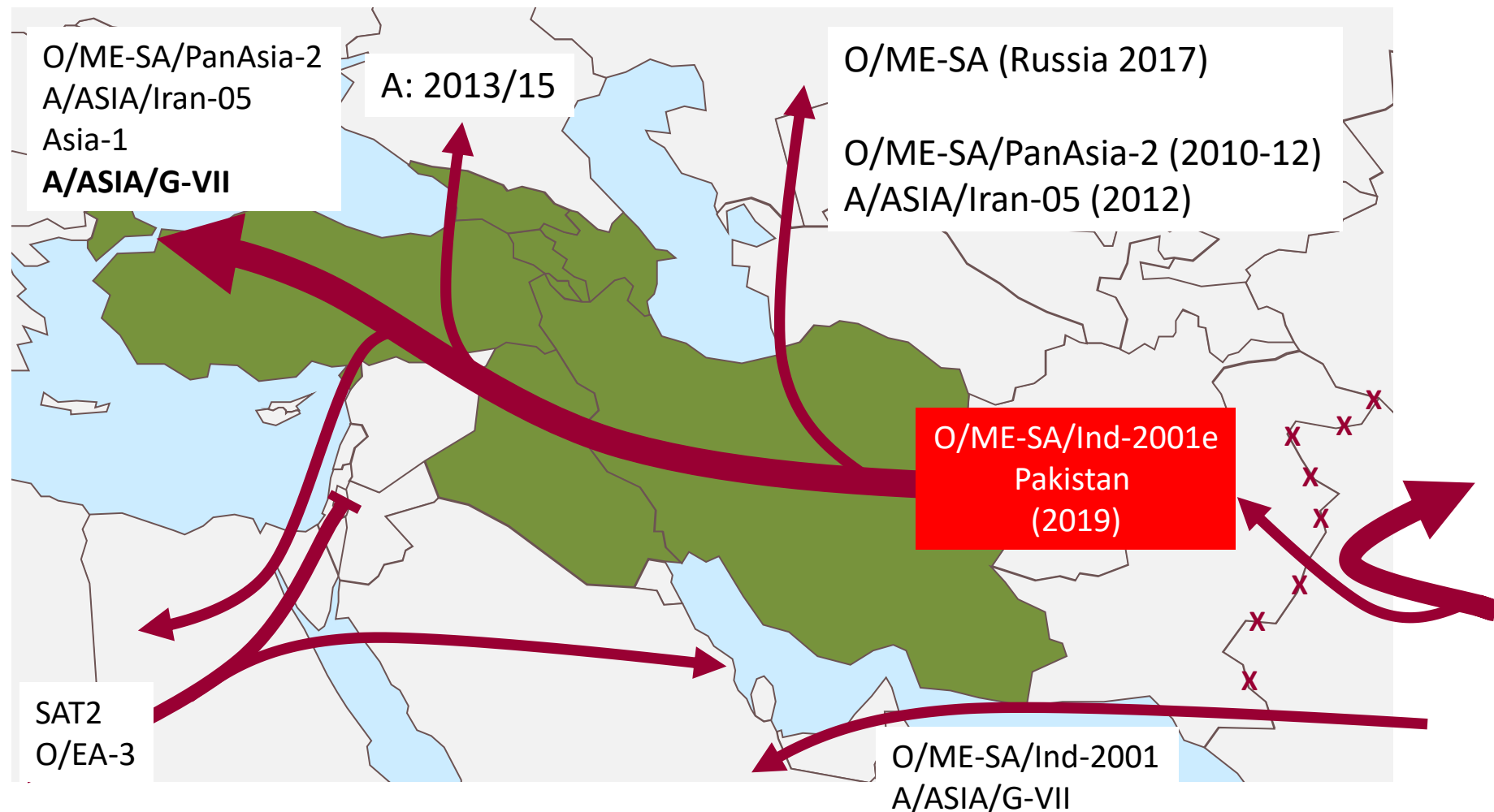
March 2021

O/ME-SA/Ind-200e



Risk pathways


Simplified summary and conjectured routes by which FMDV spreads
- to understand transmission pathways and help identify future FMDV lineages that threaten the region



FMDV transmission pathways: West EurAsia

Evolutionary and Ecological Drivers Shape the Emergence and Extinction of Foot-and-Mouth Disease Virus Lineages

MBE
Open Access

Antonello Di Nardo ^{*,1} Luca Ferretti,² Jemma Wadsworth,¹ Valerie Mioulet,¹ Boris Gelman,³ Sharon Karniely,³ Alexey Scherbakov,⁴ Ghulam Ziay,⁵ Fuat Özyörük,⁶ Ünal Parlak,⁷ Pelin Tuncer-Göktuna,⁷ Reza Hassanzadeh,⁸ Mehdi Khalaj,⁸ Seyed Mohsen Dastoor,⁸ Darab Abdollahi,⁸ Ehtisham-ul-Haq Khan,⁹ Muhammad Afzal,¹⁰ Manzoor Hussain,¹⁰ Nick J. Knowles,¹ and Donald P. King¹

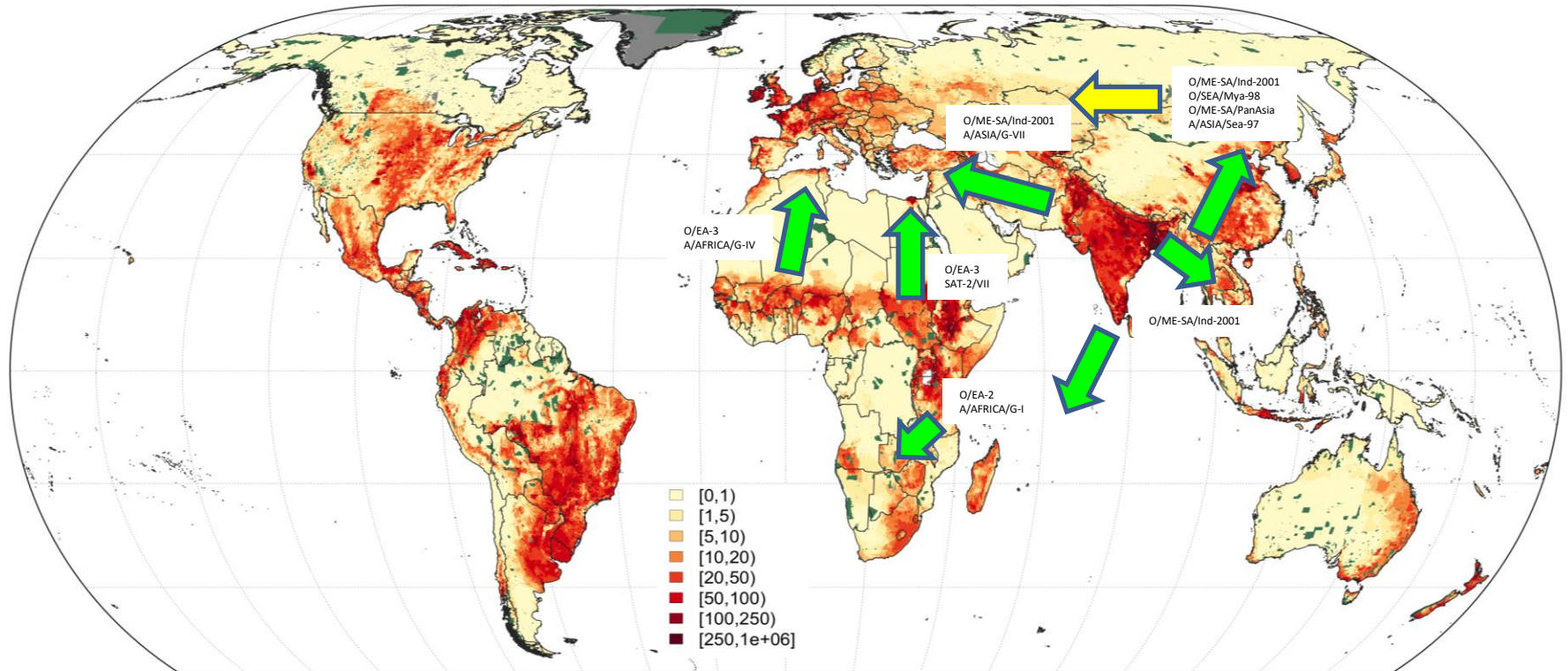
Mol. Biol. Evol. 38(10):4346–4361

- New paper reviews ~2500 VP1 sequences collected in West EurAsia countries since 2000 for three endemic lineages:
 - O/ME-SA/PanAsia-2, A/ASIA/Iran-05 and serotype Asia 1
- Endemic infection is characterised by alternating “waves” of the three FMDV serotypes with a periodicity of ~ 3 years
- Highlights the importance of Pakistan, Afghanistan and Iran as countries that generate new FMDV genetic diversity/variants
- Describes an east-to-west viral conveyer in the region that distribute new viruses across the region where viruses move at ~730 km/year (ave)

Trans-pool movements of FMDV since 2015

Some of the underlying causes:

- Movement of animals (increased demand for animal protein)
- Migration of people with animal products
- New opportunities (road building)

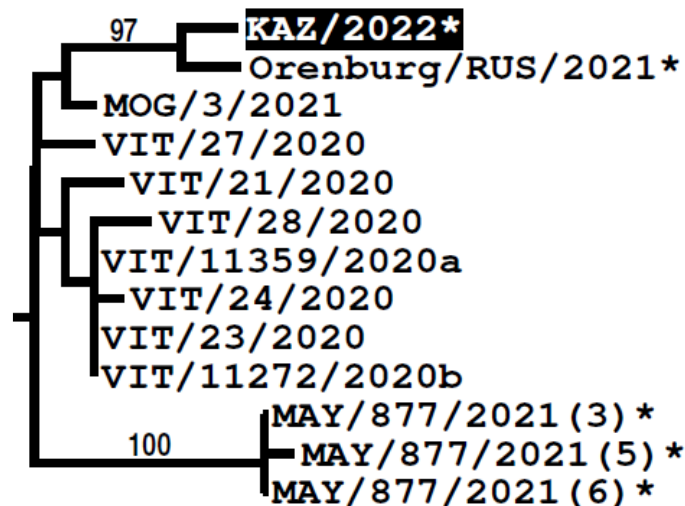


Cattle density map

Robinson et al., 2007

O/ME-SA/Ind-2001e in the Russian Federation

- December 2021
- New FMD outbreaks in cattle, Orenburg, Russia
- Located in southern FMD vaccination buffer zone close to the border with Kazakhstan
- Caused by O/ME-SA/Ind-2001e lineage
- FMD outbreaks due to O/ME-SA/Ind-2001e also reported in an FMD-free (without vaccination) zone in Kazakhstan
- Sequences* demonstrate 98.9% nt identity to virus from Mongolia (2021

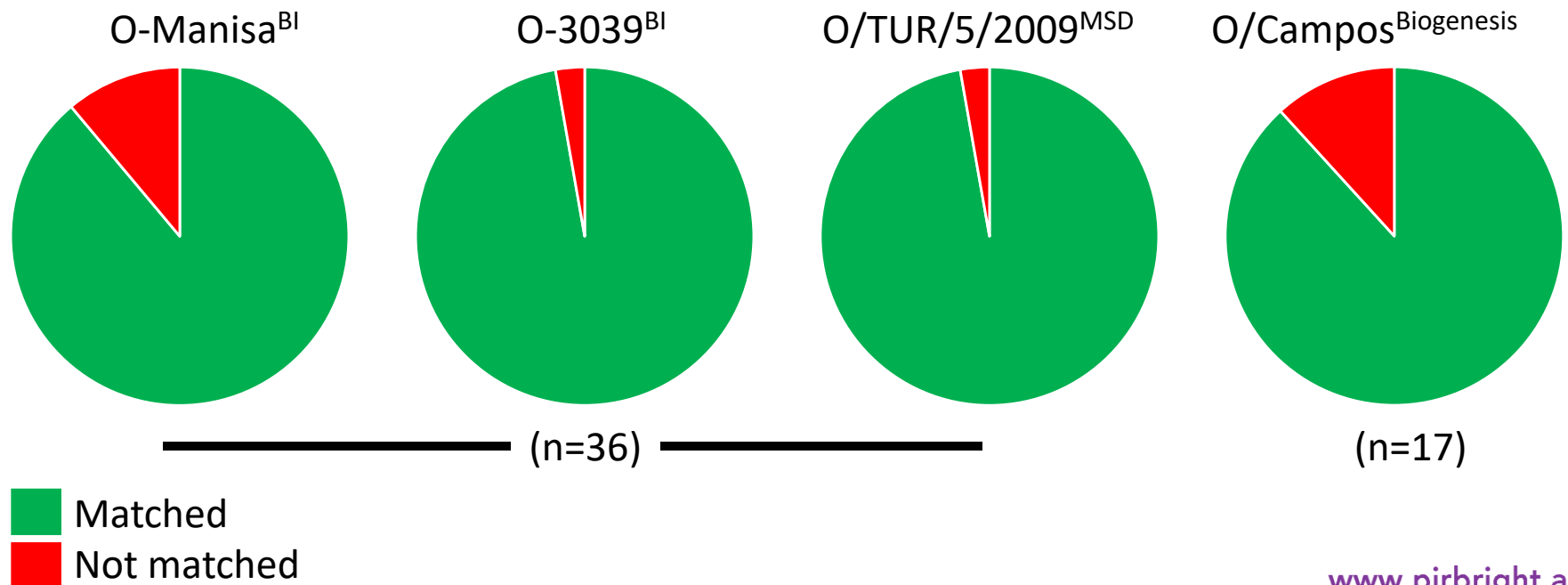


* Thanks to Dr Alexei Scherbakov, ARRIAH, Russia



O/ME-SA/Ind-2001e: vaccine matching (2017-2022)

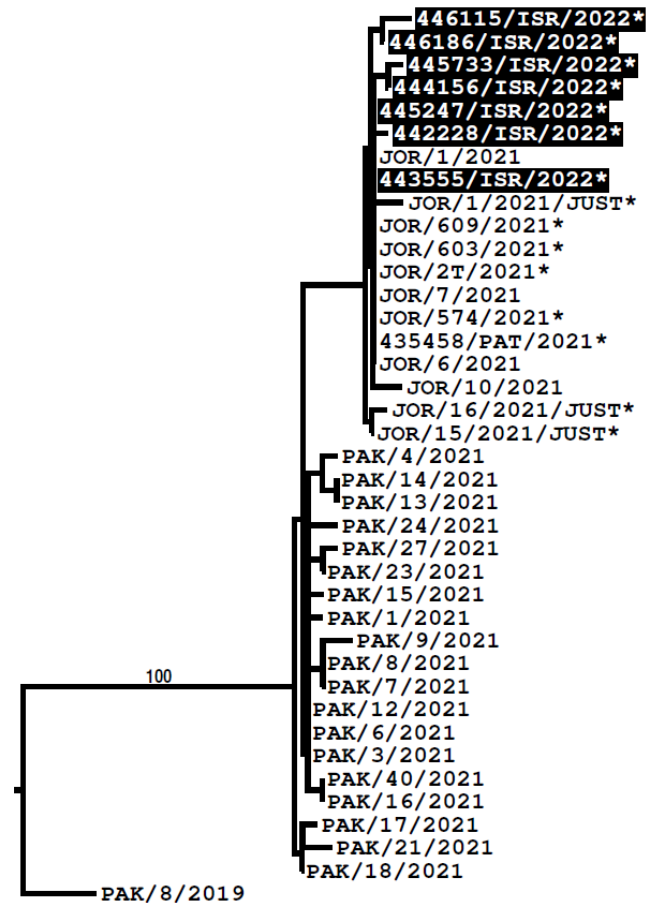
- Vaccine matching data for field isolates from regions where this lineage is present
- WRLFMFD data now includes O-Campos (from Biogenesis Bago)
- Data supported by *in vivo* studies with O-3039, O-Manisa and combination (Boehringer-Ingelheim)
 - Fishbourne et al., (2017) Vaccine 35: 2761-2765
 - Singanallur et al., (2021) Vaccines 9: 1110



A novel O/ME-SA/PanAsia-2^{ANT-10} lineage in the Eastern Mediterranean

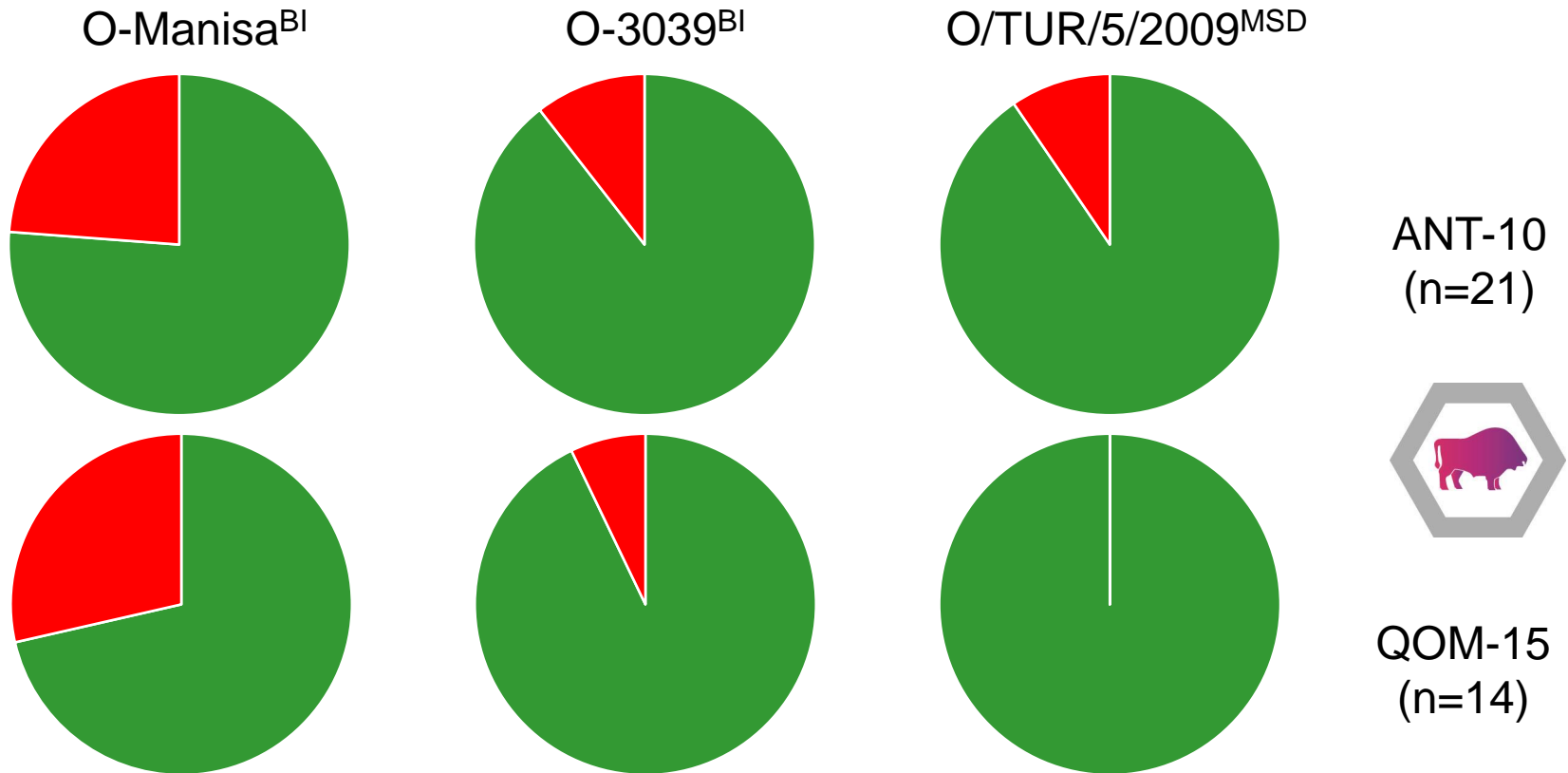
- FMD cases in Jordan and Palestine (West Bank) during Dec 2021 and Israel in 2022
- Samples submitted to WRLFMD and sequences shared by JUST, Jordan and KVI, Israel*
- Reports of severe clinical FMD signs associated with infection
- Most closely related to FMDV from Pakistan (2019 and 2021)
- Poor vaccine-matching data for O/Manisa
- Other cases reported in the Gaza Strip due to O/EA-3

* Thanks to Dr Iyad Adra, Dr Sharon Karniely (KVI), Dr Mustafa Ababbeh, Dr Majed Hawaasha and scientists at JUST



O/ME-SA/PanAsia-2 : vaccine matching (2014-2021)

- Quick and cost-effective laboratory assessment of the antigenic relationship between **field** and **vaccine** viruses



Matched
Not matched



PA-2 vaccines from ŞAP (QOM-15) and ARRIAH (ANT-10) also show good match

A/ASIA/Iran-05: vaccine matching (2014-2021)

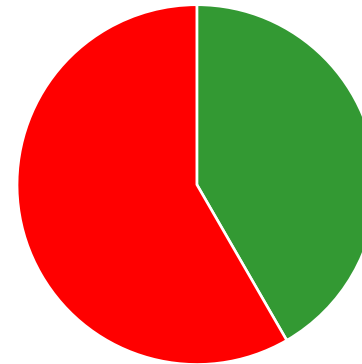
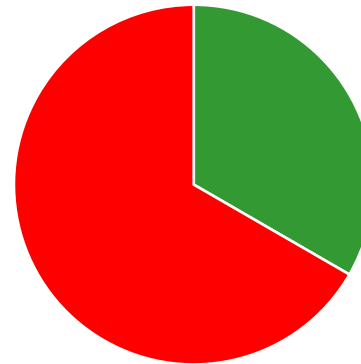
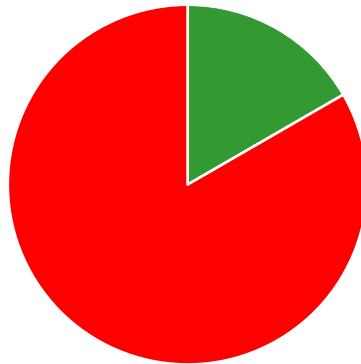
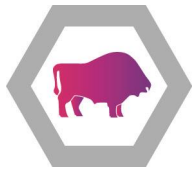


A/IRAN-05^{BI}

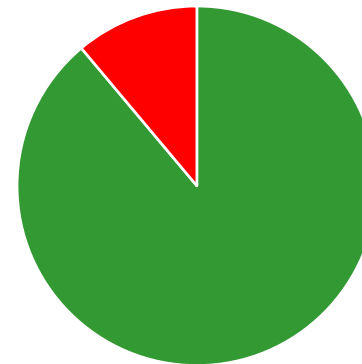
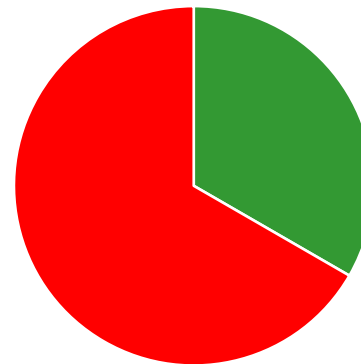
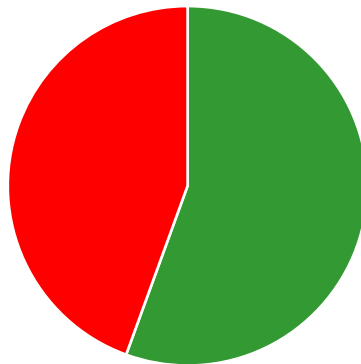
A/TUR/20/2006^{MSD}



A22 IRAQ^{BI}

FAR-11
(n=12)



SIS-13
(n=9)



 Matched
 Not matched



ARRIAH – 50%
match to isolates
from Pakistan

Poor match of
Turkish vaccines
for FAR-11
viruses from Iran
[update;
WRLFMD data
1/2 isolates
matched for
these 3 vaccines]

*As a result of
vaccine
matching, A
new vaccine
strain has
been Adapted
at Şap
Institute for
Serotype A:
A/IRAN05/FAR
-11(ATUR21)*

- Reinforces the importance of good quality vaccines,
booster regime with good coverage in target host populations

A/ASIA/Iran-05 and A/ASIA/G-VII






- These are antigenically distinct lineages (demonstrated by vaccine matching and cross-protection studies)
- New paper demonstrates low-levels of cross-protection provided by A/G-VII vaccine (homologous potency 6.5 PD₅₀) to challenge by an A/ASIA/Iran-05 isolate
- Measured heterologous potency was 2.0 PD₅₀ and heterologous titres were $\leq \log_{10} 0.9$



Brief Report

A Vaccine Based on the A/ASIA/G-VII Lineage of Foot-and-Mouth Disease Virus Offers Low Levels of Protection against Circulating Viruses from the A/ASIA/Iran-05 lineage

Nagendrakumar Balasubramanian Singanallur ¹, Phaedra Lydia Eblé ², Anna Barbara Ludi ³, Bob Statham ³, Abdelghani Bin-Tarif ³, Donald P. King ³, Aldo Dekker ² and Wilna Vosloo ^{1,*}

WELNET FMD (LAB NETWORK) ACTIVITIES

1. Participate in annual proficiency test scheme (PTS)

- WRL and ANSES currently organize PTS regularly.
- Currently EuFMD supports PT panels for four countries/Türkiye participates ANSES
- Funding can be made available to FAO to cover the cost of preparing the panels and shipping.
- This year Panels have already delivered and testing ongoing.

2. Assess the capacity/capability and performance of the national veterinary diagnostic labs.

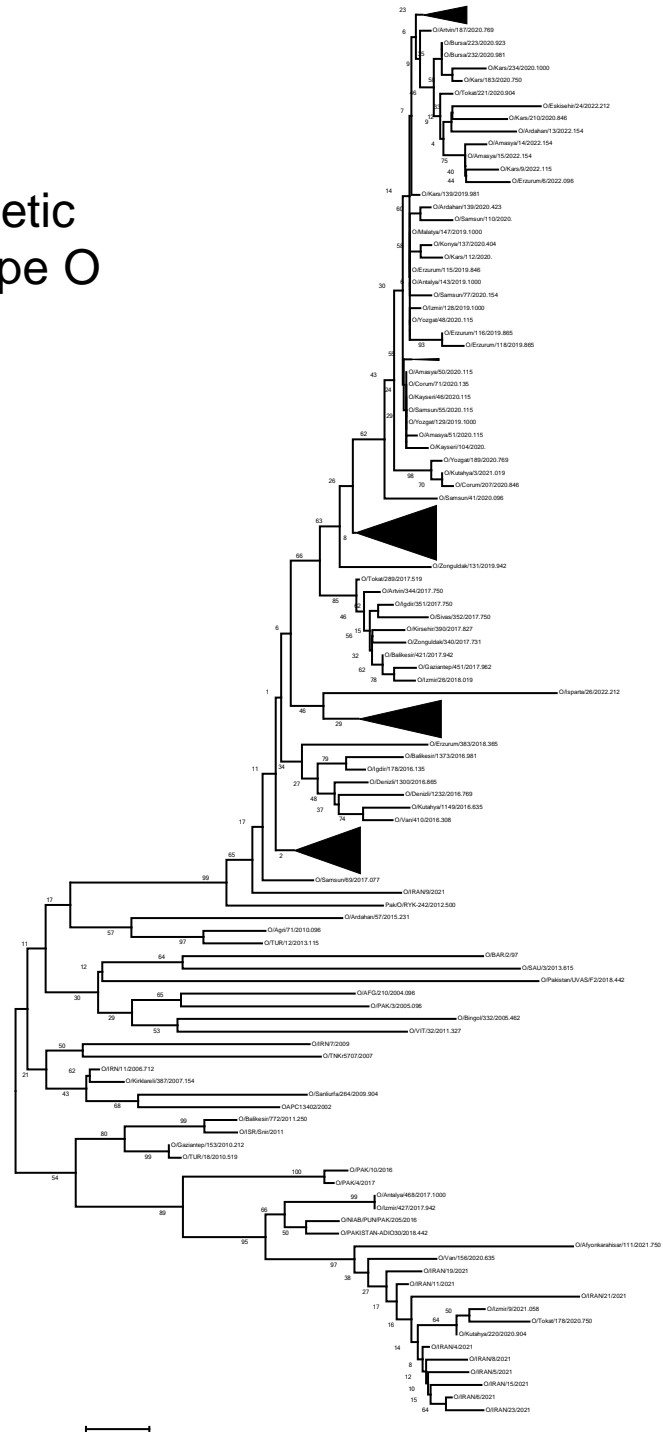
- ANSES performed a questionnaire
- Based on outputs, training activities will be conducted for labs in the region
- Online training/workshop/webinar have been done by EuFMD
- e-learning platform is available on diagnosis of FMD conducted by EuFMD
- Lab training opportunity is available at Şap Institute for lab in the region

WELNET FMD (LAB NETWORK) ACTIVITIES

3. ACTIVITIES in FAVOUR OF EARLY WARNING SYSTEM

- **The Şap Institute** continues accepting FMD sample submission from countries in WE
 - Samples are tested by serotyping, genetic analysis and vaccine matching and reported in time
 - Iran submitted FMD samples (two times)
 - Iraq will send FMD samples
- A regional and collaborative initiative, Statement of Intention (SoI)
- Participation to the Group for Vaccination Advice, Guidance and Consultation for SEEN countries
- Small scale immunogenicity studies (SSIS) to assess FMD vaccines
- Regional cooperation for the prevention and control of Foot-and-mouth And Similar Transboundary (FAST) animal diseases, between Turkey, Islamic Republic of Iran, Pakistan and the EuFM

Latest phylogenetic trees for serotype O



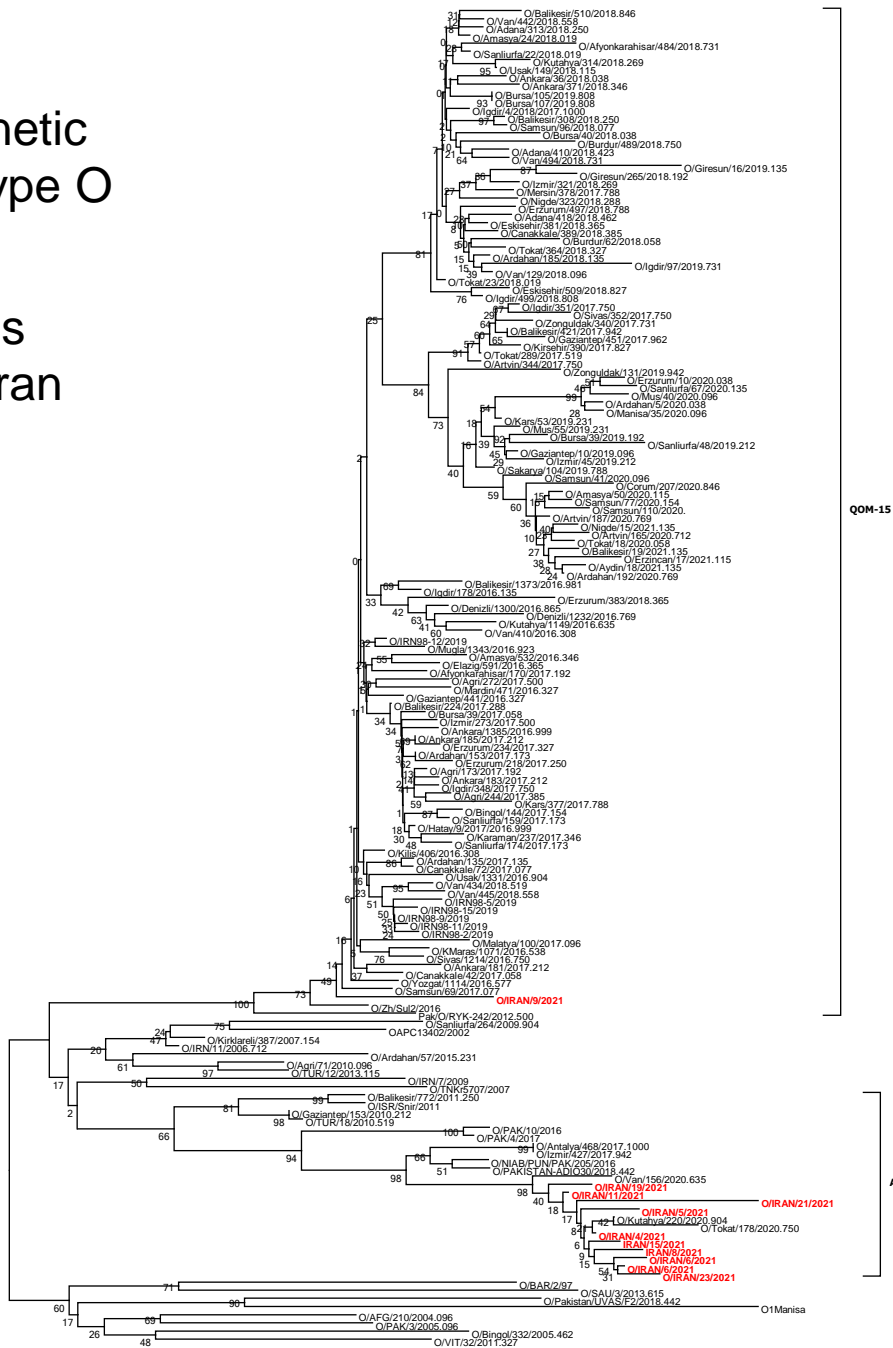
QOM-15

ANT-10

0.01

Latest phylogenetic trees for serotype O

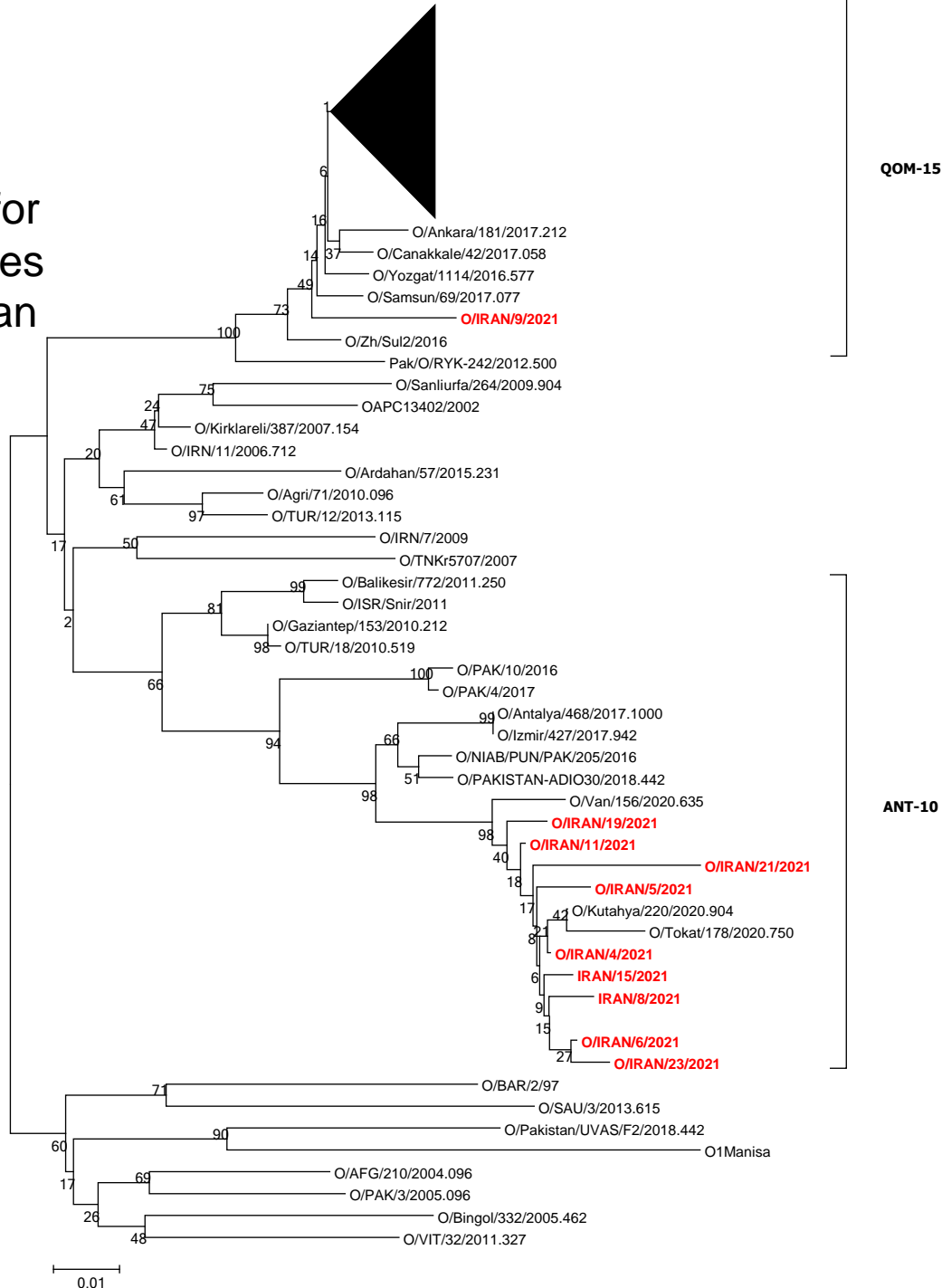
Including viruses collected from Iran



QOM-15

ANT-10

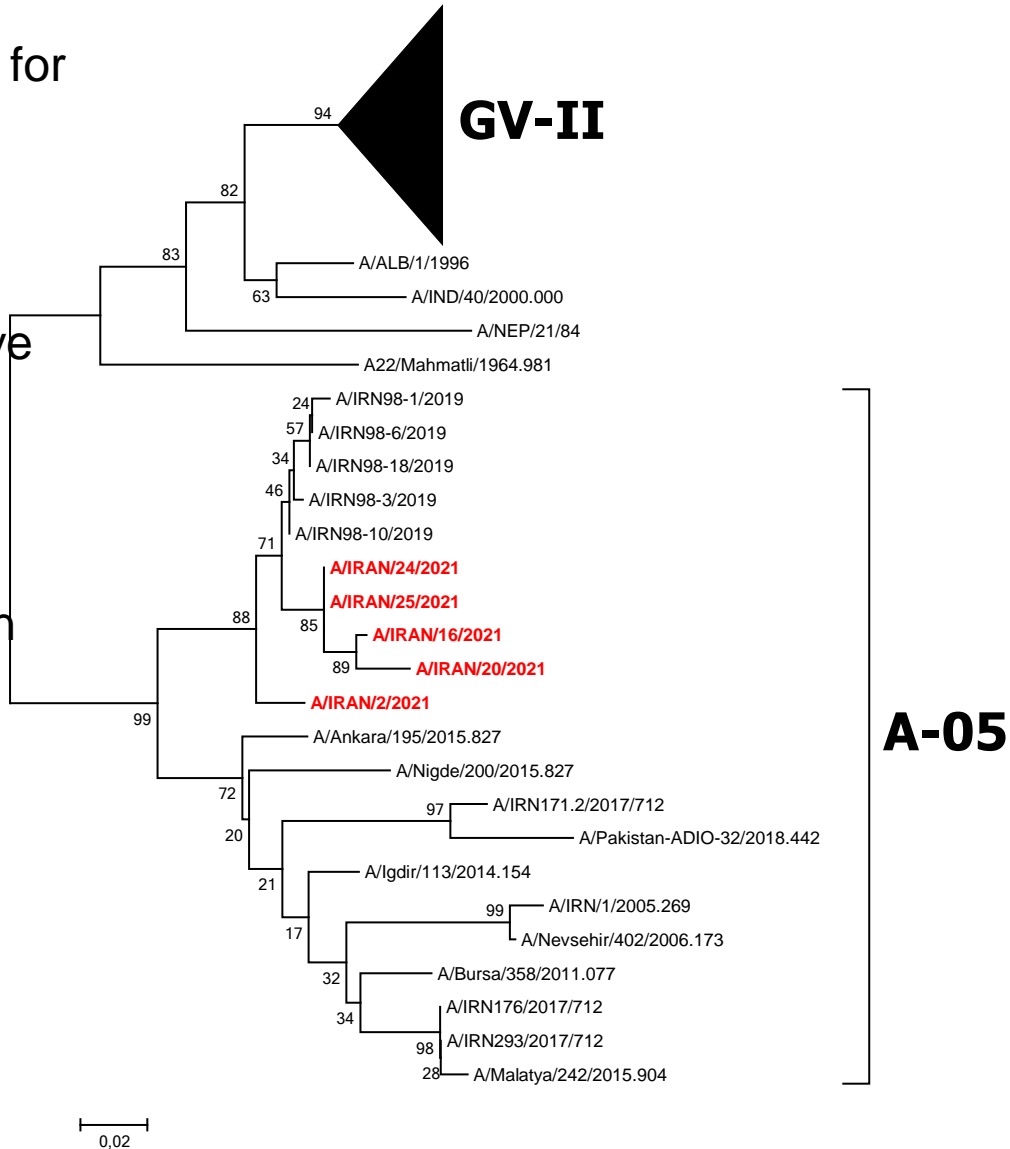
Filogenetic tree for Particularly viruses collected from Iran



phylogenetic trees for serotype A

Related Viruses circulated in Türkiye before 2018

Including viruses collected from Iran





Thank you very much for your attention!

- Acknowledges
- The Şap Institute
- Colleagues from The Pirbright Institute



Discover
the potential