Trans-pool movement of two serotype A lineages: A/ASIA/G-VII AND A/AFRICA/G-IV

Kasia Bachanek-Bankowska

OS18

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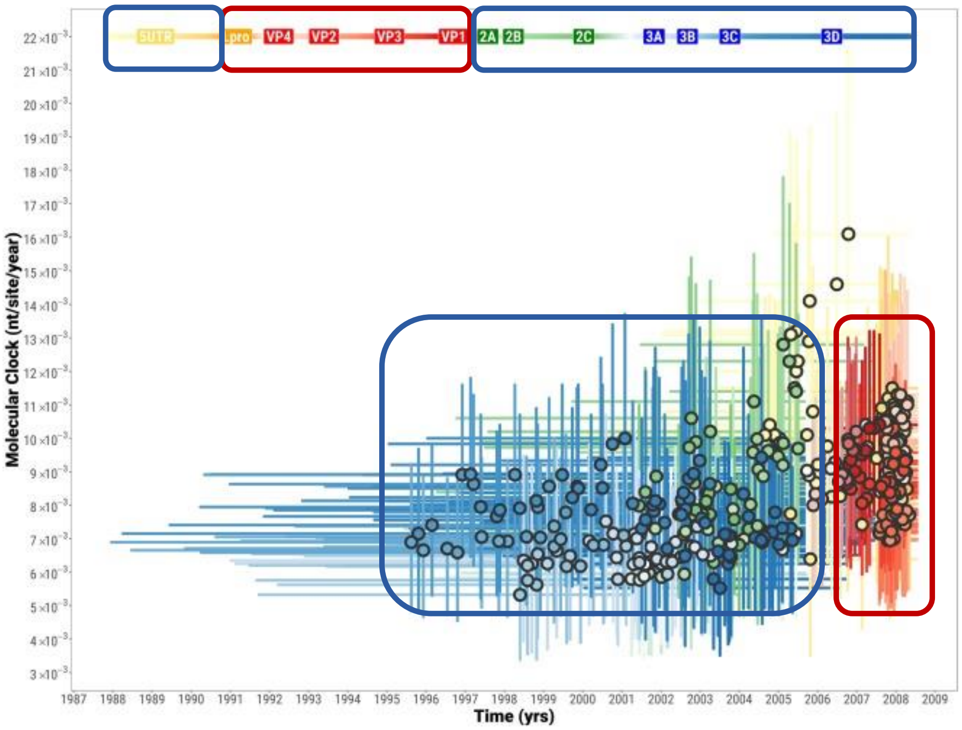
Virus movement tracing



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Bachanek-Bankowska K., Di Nardo A. et al., 2018

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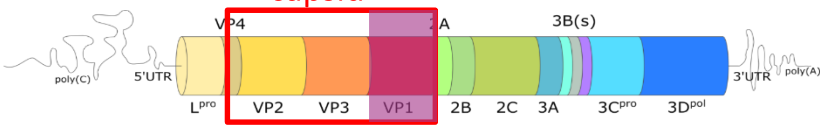
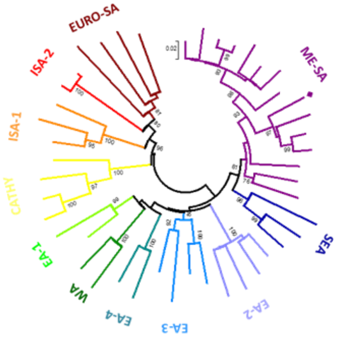
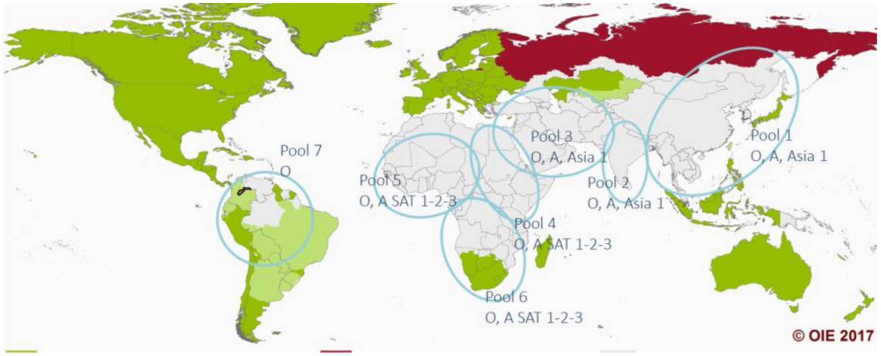
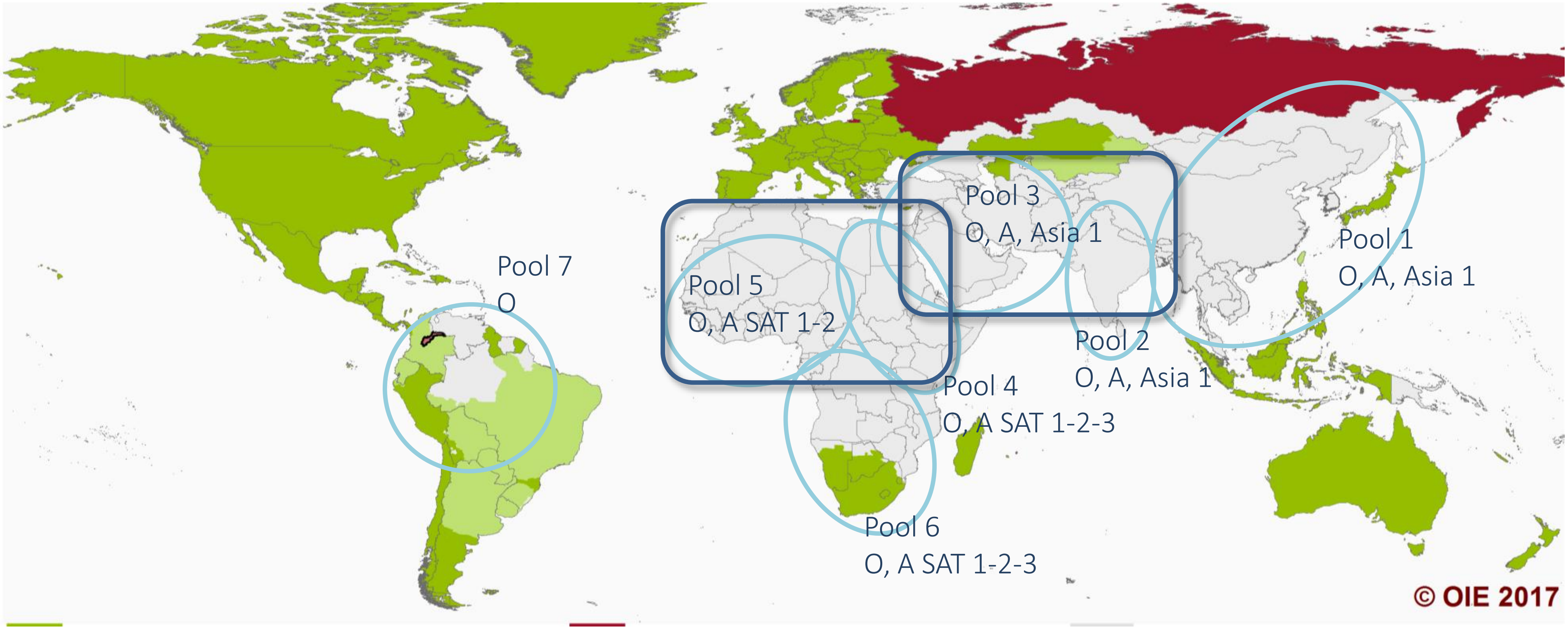




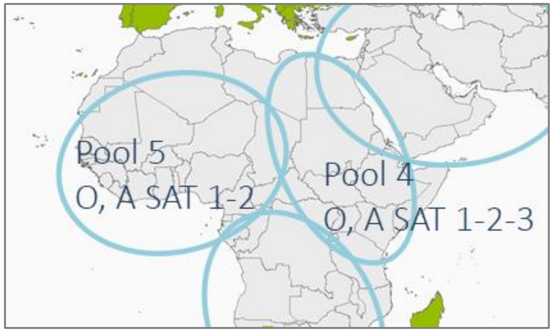


Conjectured FMD global distribution

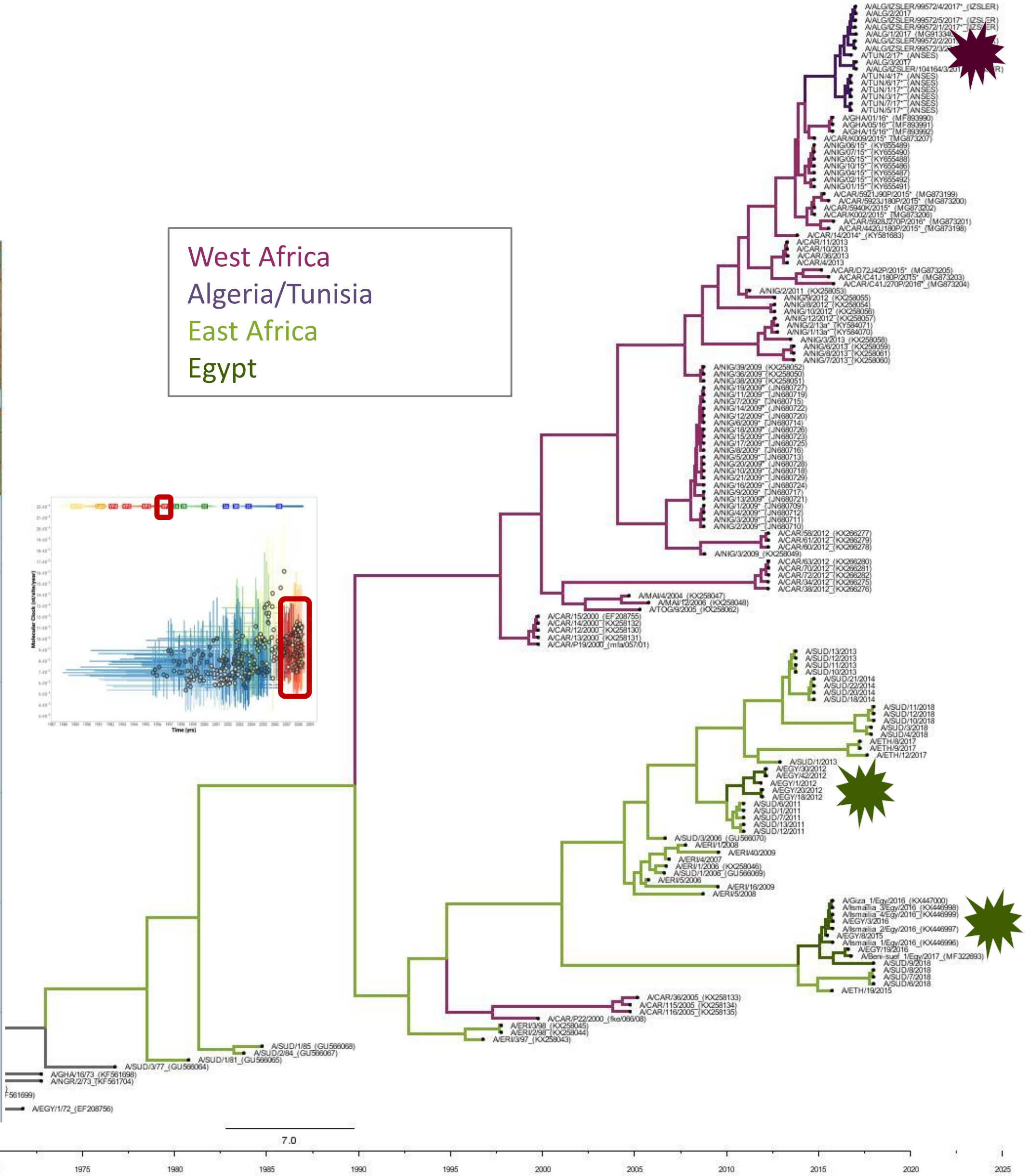


Pool 4+5: O/EA-3 SAT 2/VII **A/AFRICA/G-IV**

Pool 2+3: O/ME-SA/PanAsia-2 O/ME-SA/Ind-2001 Asia1 A/ASIA/Iran-05 **A/ASIA/G-VII**



A/AFRICA/G-IV

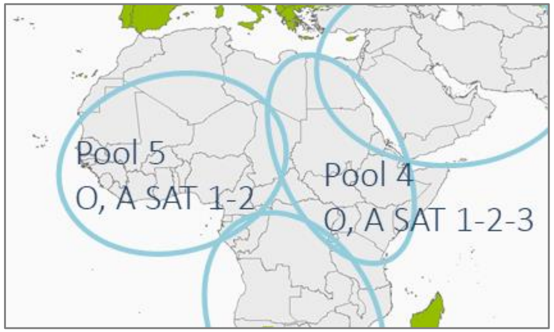


West Africa
Algeria/Tunisia
East Africa
Egypt

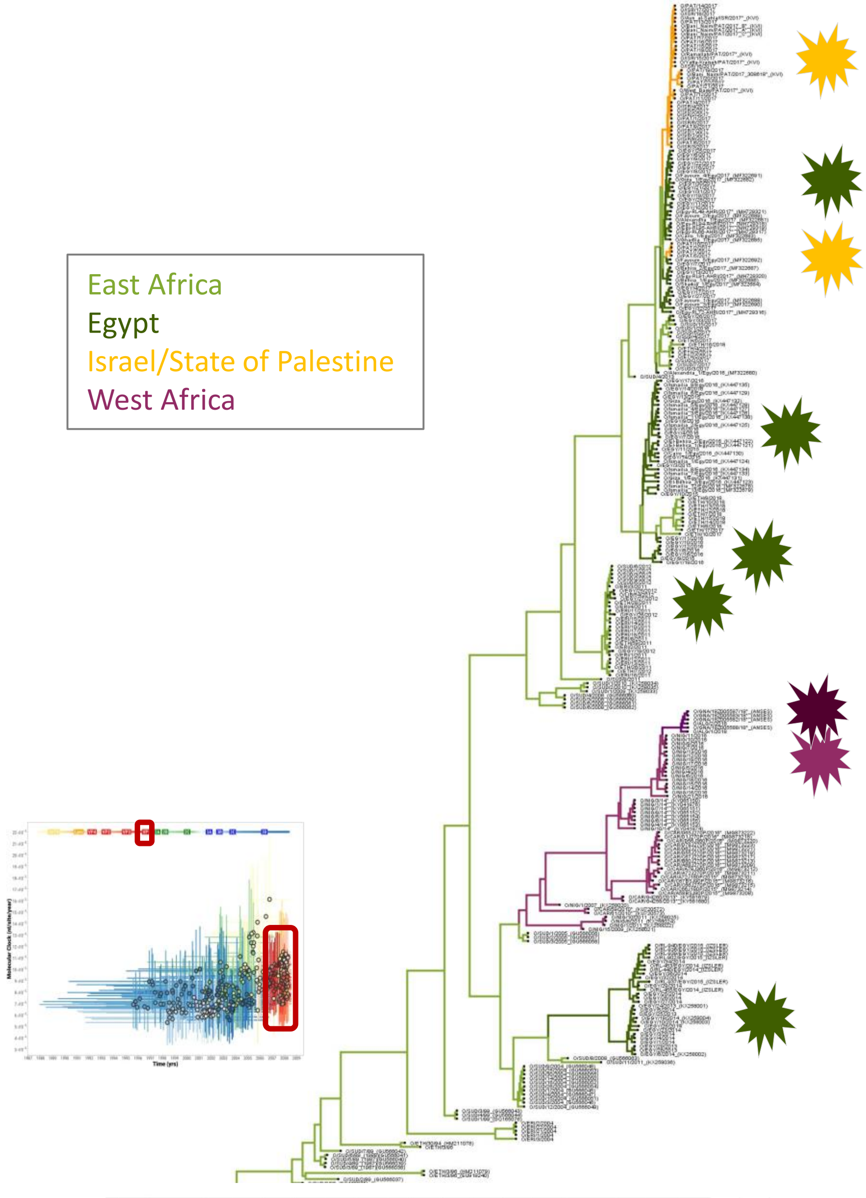
Transboundary and Emerging Diseases

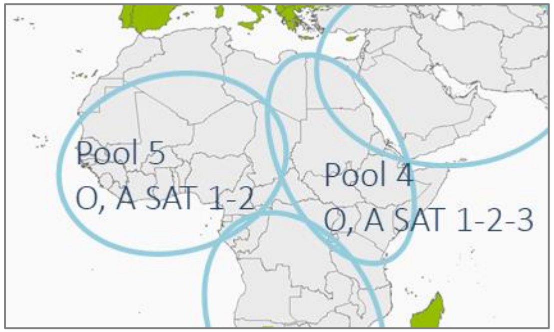
G.Pezzoni et al., 2018

O/EA-3



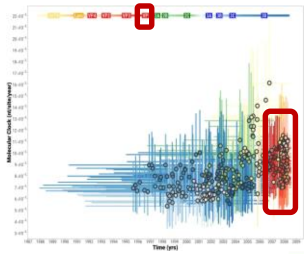
East Africa
Egypt
Israel/State of Palestine
West Africa

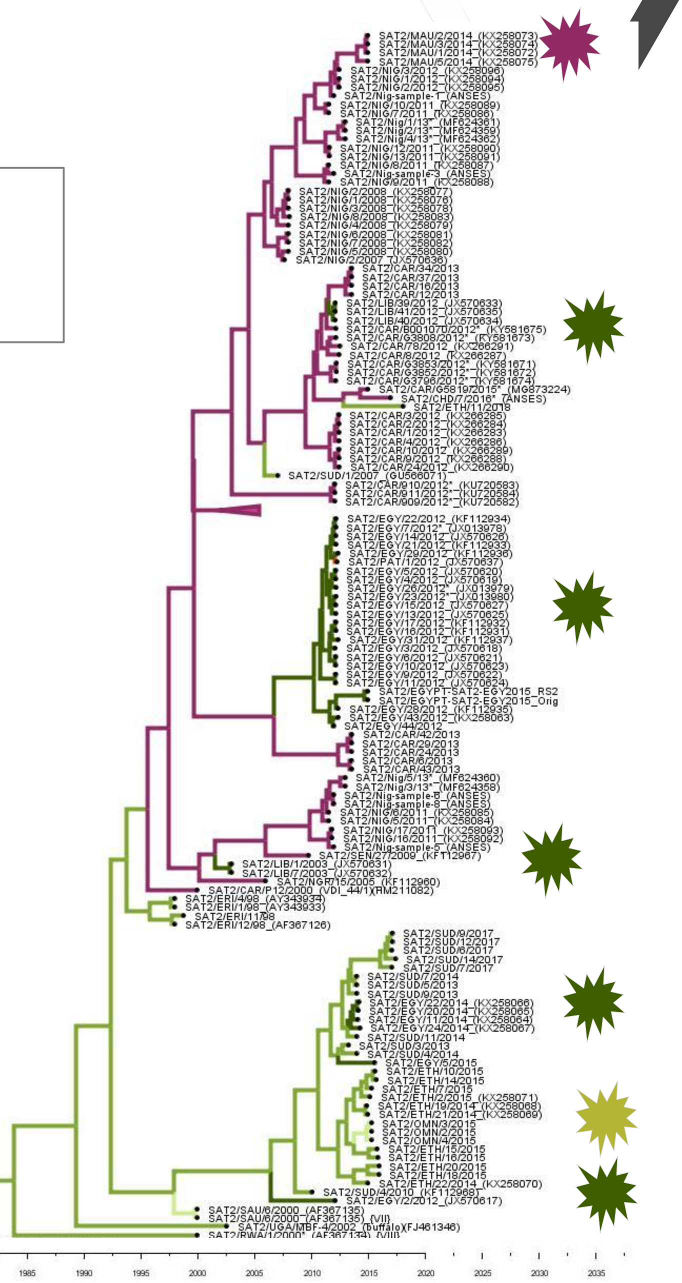




SAT 2/VII

West Africa
East Africa
Egypt/Libya
Oman/Saudi Arabia

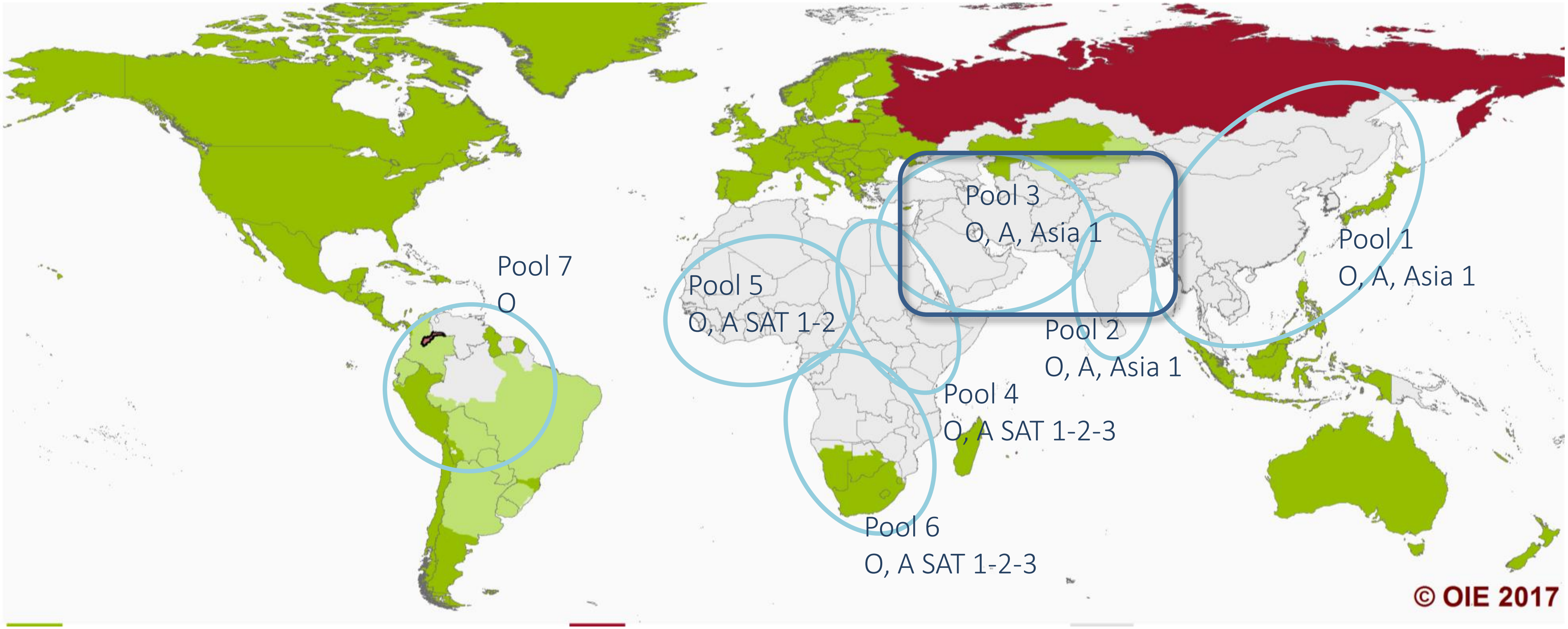




A/AFRICA/G-VII: key points

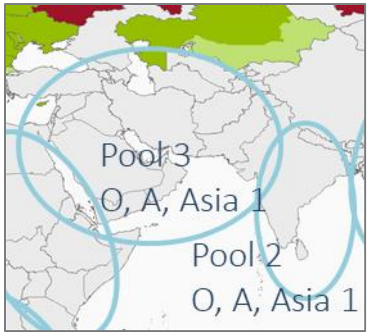
- Three main lineages O/EA-3, SAT 2/VII and A/AFRICA/G-IV dominate the FMDV ecological landscape in Northern part of Africa.
- Precise movement of viruses is not possible to be established due to scarce sample/sequence availability but there is a strong evidence of East to West movement.
- Multiple outbreaks due to the dominant serotypes/lineages occurred in North Africa. There is evidence that outbreaks in Egypt and Libya are caused by viruses of East African origin, while outbreaks in the Maghreb region are related to viruses of West Africa origin.
- Due to similarities in movement patterns of the dominant viruses, it is highly likely that outbreaks due to multiple serotypes/lineages may occur.

Conjectured FMD global distribution



Pool 2+3: O/ME-SA/PanAsia-2 O/ME-SA/Ind-2001 Asia1 A/ASIA/Iran-05 **A/ASIA/G-VII**

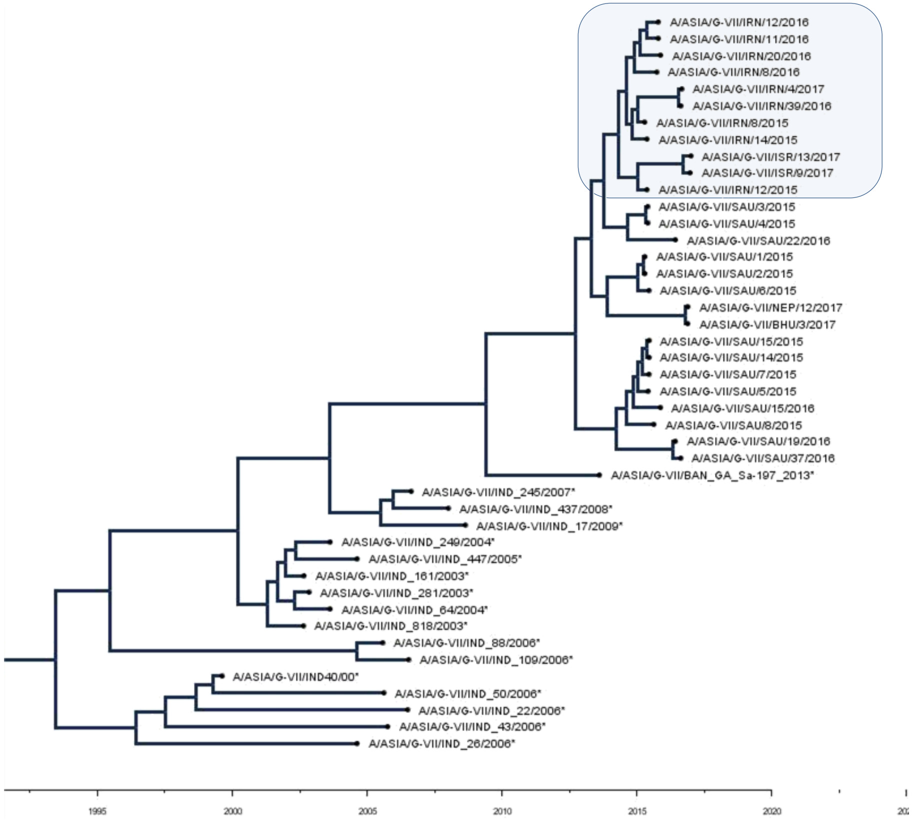
A/ASIA/G-VII: background



EMERGING INFECTIOUS DISEASES®

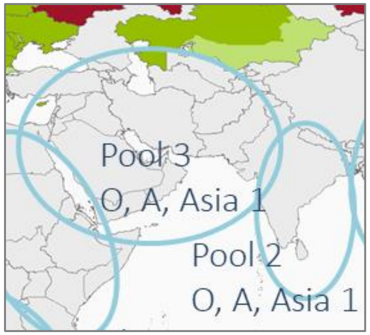
Bachanek-Bankowska K. et al., 2018

- Outbreaks in Saudi Arabia, Armenia, Iran, Turkey between 2015-2016
- Evidence of at least two independent introductions to the region
- **2017: detection in Israel**



Bases on VP1 analyses only, it is difficult to conclude the direction of virus movement in the region.

“Melting pot” of viruses?
FMDV lineages circulating in Pools 2 and 3



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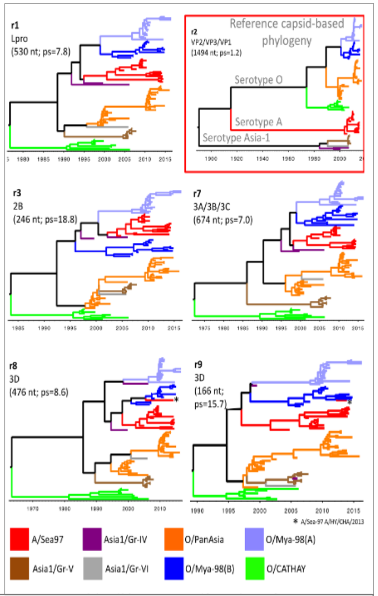
B. Brito at al., 2018

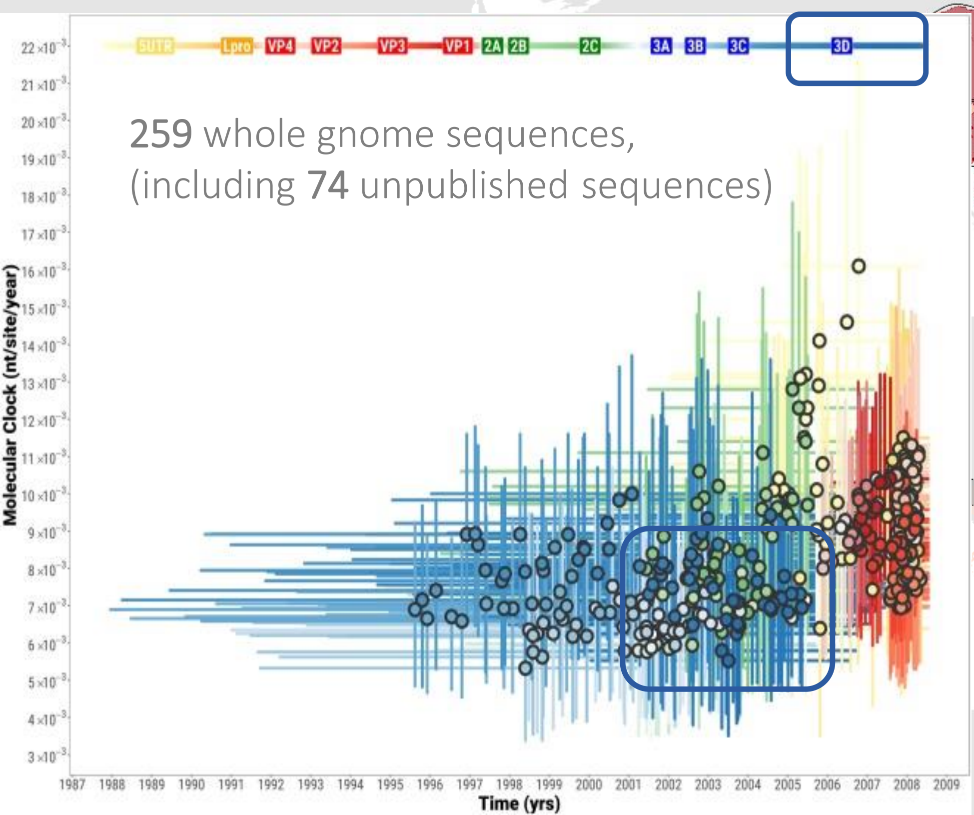


Evidence of intra-linage recombination in Southeast Asia

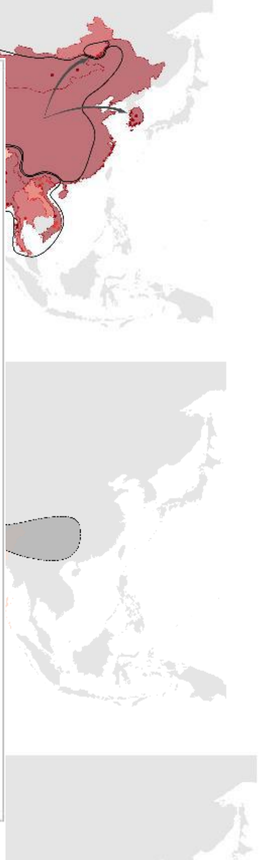
A/ASIA/G-VII (genotype 18)

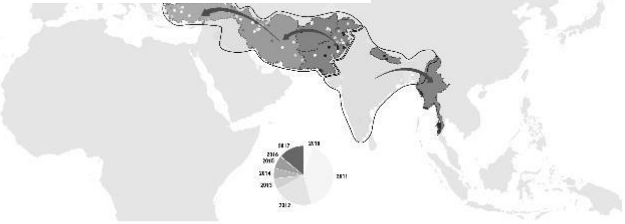
O/ME-SA/Ind-2001

A/ASIA/



259 whole gnome sequences,
(including **74** unpublished sequences)





Maps credits: A. Di Nardo

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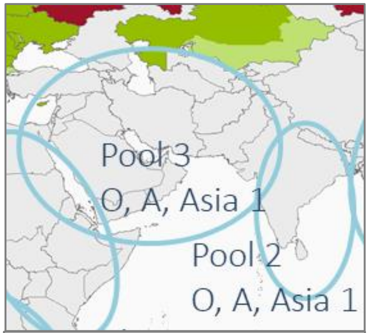
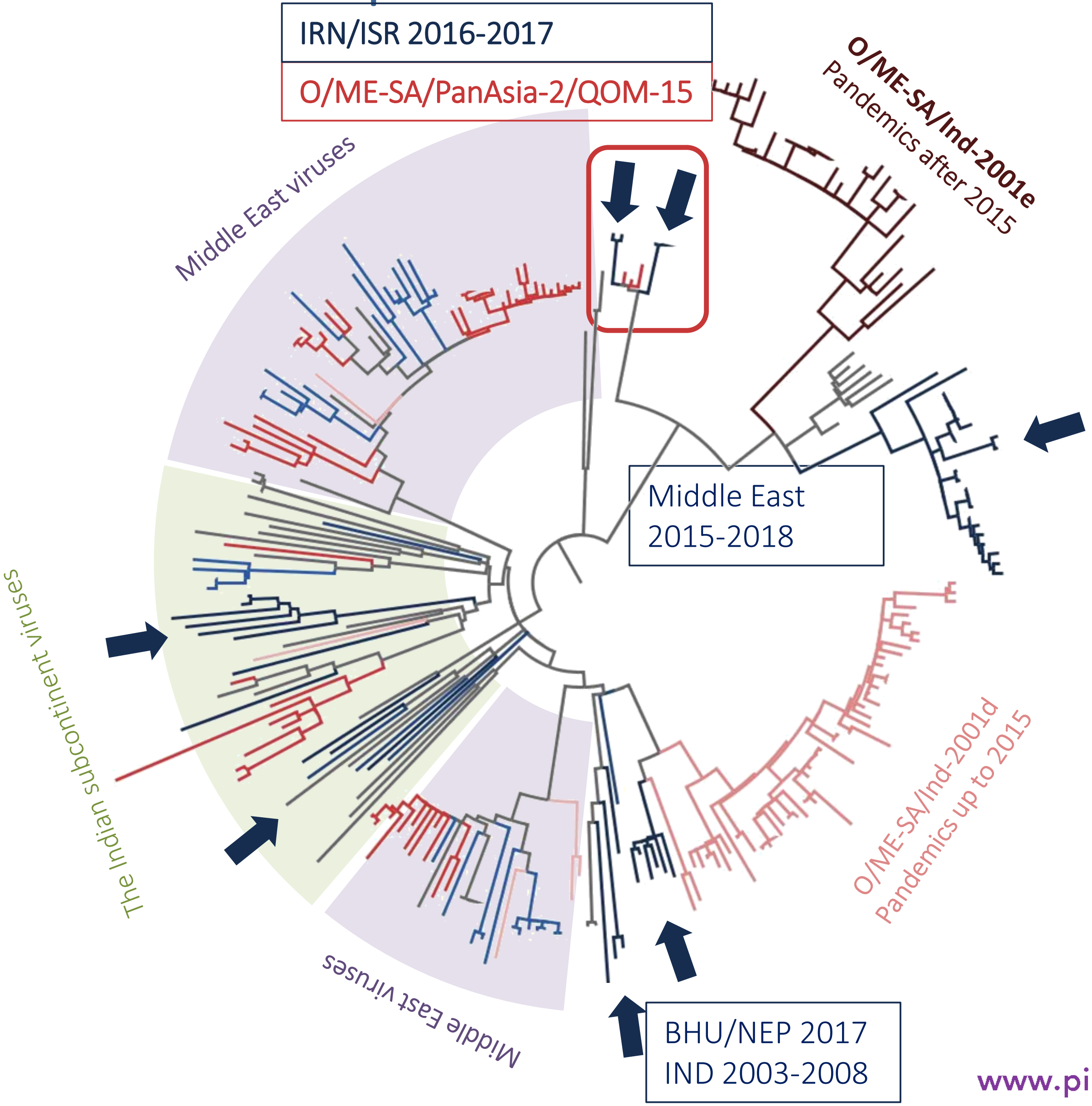
Reference Laboratories
Network

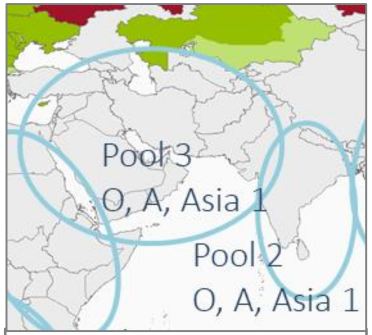
A/ASIA/G-VII:
non-structural components have different ancestral origin

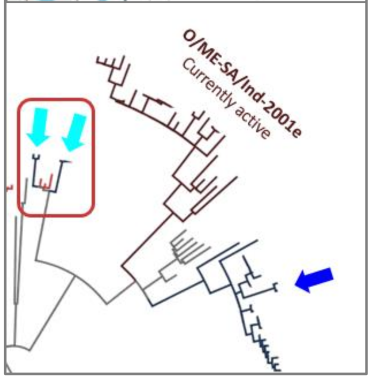


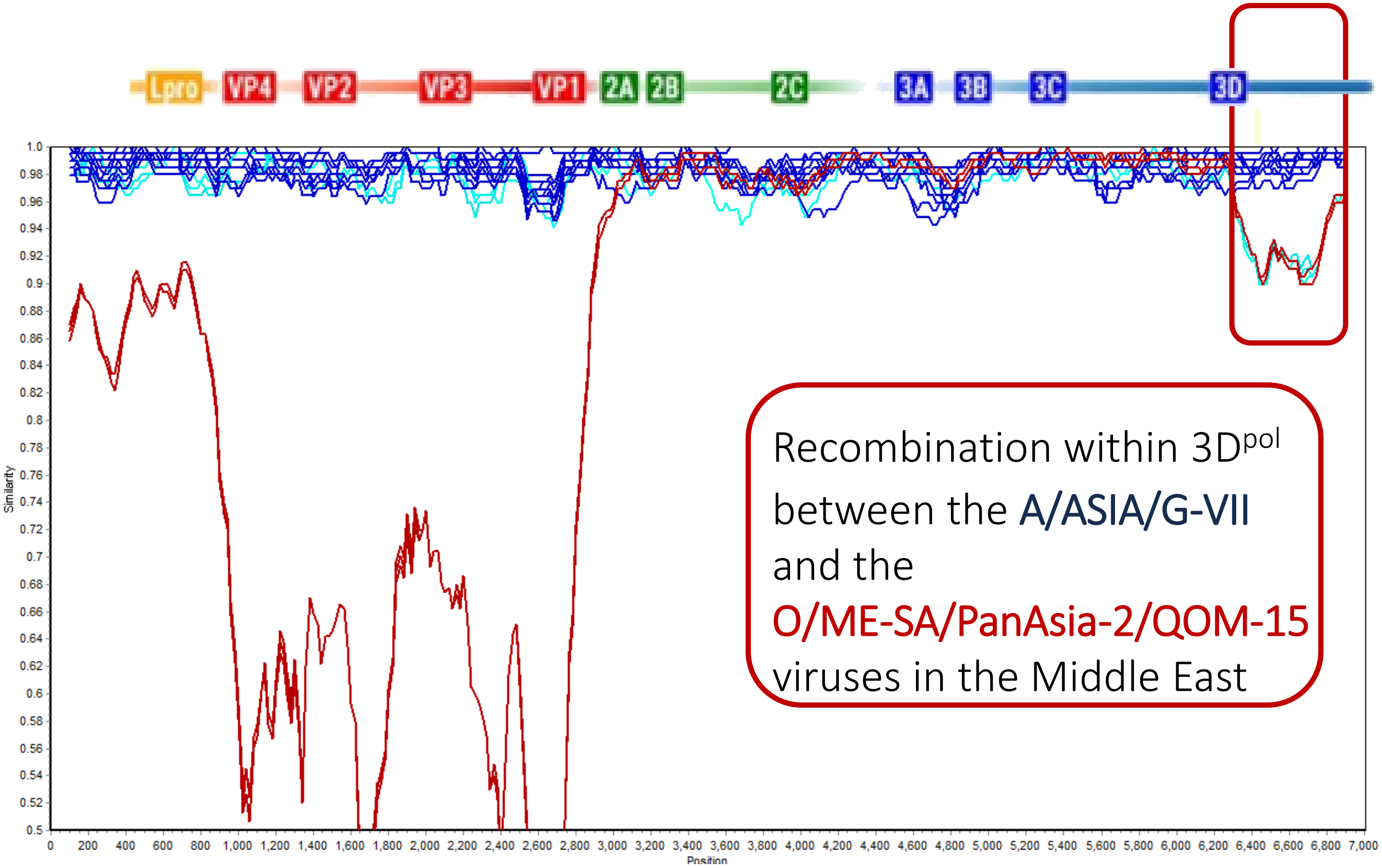
- A/ASIA/G-VII ⬅
- A/ASIA/Iran-05
- A/ASIA/Iran-96
- A/ASIA/unnamed
- Asia 1
- O/ME-SA/Ind-2001d
- O/ME-SA/Ind-2001e
- O/ME-SA/PanAsia
- O/ME-SA/PanAsia-2
- O/ME-SA/unnamed



Recombination analyses: SimPlot







Recombination within 3D^{pol} between the **A/ASIA/G-VII** and the **O/ME-SA/PanAsia-2/QOM-15** viruses in the Middle East

A/ASIA/G-VII: The Middle East 2015-2016

A/ASIA/G-VII: ISR/IRN 2016-2017

O/ME-SA/PanAsia-2/QOM-15

A/ASIA/G-VII: key points

- There is evidence that in A/ASIA/G-VII viruses, the regions encoding non-structural protein has different ancestral origin.
- Viruses of the A/ASIA/G-VII and O/ME-SA/PanAsia-2/QOM-15 can exchange genetic material. The direction of the exchange is not established yet.
- Further analyses are on the way to understand the mosaic structure of FMDV genomes which might lead to better understanding of emergence and spread of new and upcoming lineages.

FMD viruses exist in complex ecological niches where multiple serotypes and lineages co-exist and evolve.

Continued monitoring and vigilance is necessary.

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