OMSA Laboratoire de référence pour la Fièvre Aphteuse

Centre de référence Organisation mondiale de la santé animale Fondée en tant qu'OIE

AHW.A.07

FMD OUTBREAKS IN EU IN 2025:

THE USE OF SEQUENCING (SANGER AND FULL GENOME)

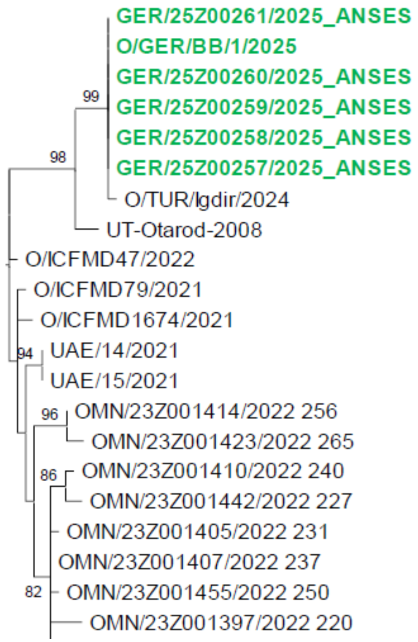
STANDING COMMITTEE ON PLANTS, ANIMALS, FOOD AND FEED (PAFF)

07 July 2025

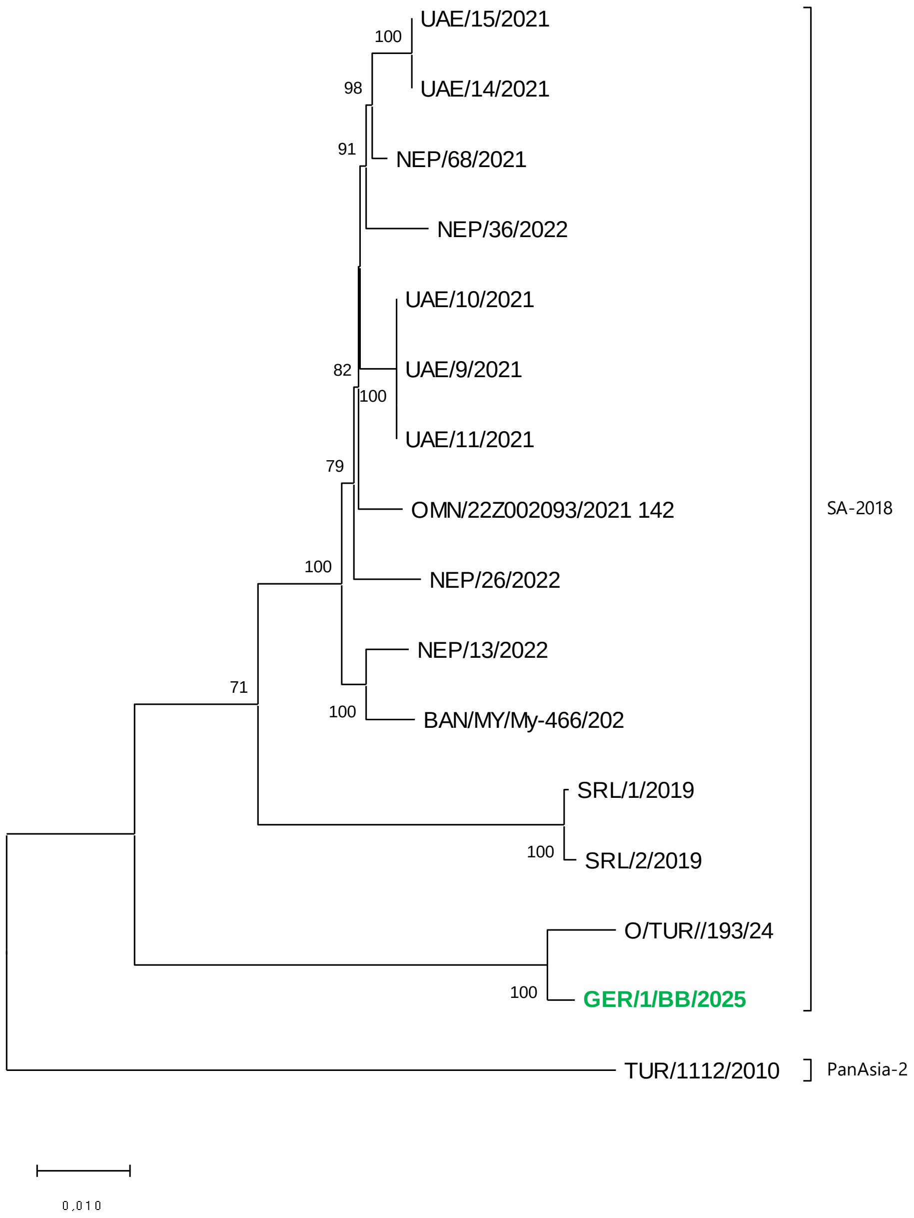
Full Genome Sequencing of EU case in Germany

Phylogenetic tree of German case

- Very small number of full genomes are available for O/ME-SA/SA-2018
- As for VP1, proximity with a strain that circulated in Türkiye in 2024
- More FGS are required to have a global picture



VP1



FGS

Full Genome Sequencing of EU cases in Hungary and Slovakia

FGS for EU cases in Hungary and Slovakia (performed at EURL)

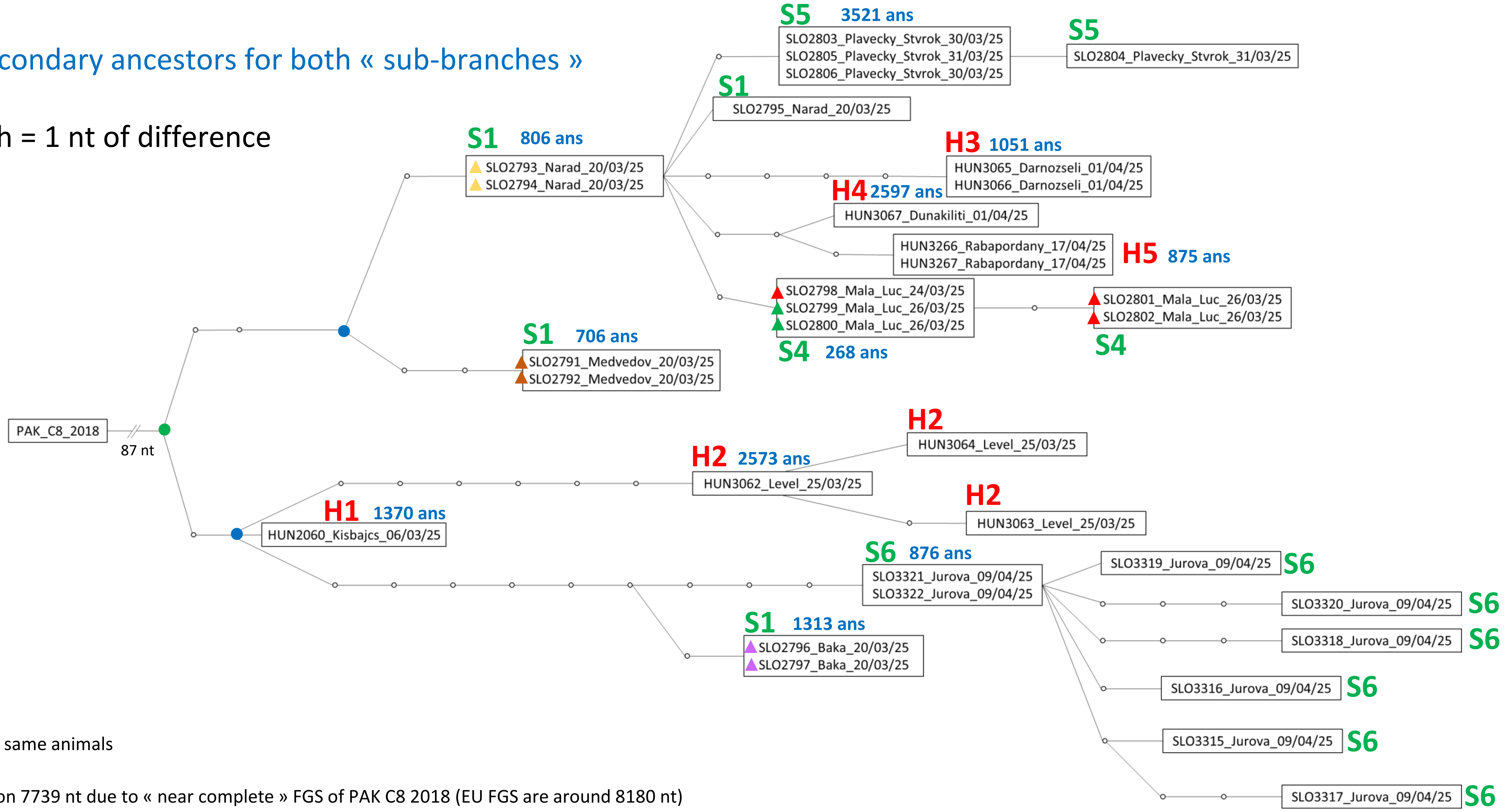
Country	Outbreak number	Date of confirmation of the outbreak	Number of animals in the farm	Nb of samples received	FGS performed
Hungary	H1 (Kisbajcs)	06/03/2025	1370	4	Yes (4/4)
Slovakia	S1 (Medvedov)	21/03/2025	706	3	Yes (2/3)
Slovakia	S2 (Narad)	21/03/2025	806	3	Yes (3/3)
Slovakia	S3 (Baka)	21/03/2025	1313	2	Yes (2/2)
Slovakia	S4 (Mala Luc)	25/03/2025	268	5	Yes (5/5)
Slovakia	S5 (Plavecky Stvrtok)	30/03/2025	3521	4	Yes (4/4)
Hungary	H2 (Levél)	26/03/2025	2573	3	Yes (3/3)
Hungary	H3 (Darnózseli)	02/04/2025	1051	2	Yes (2/2)
Hungary	H4 (Dunakiliti)	02/04/2025	2597	1	Yes (1/1)
Hungary	H5 (Rábapordány)	17/04/2025	875	2	Yes (2/2)
Slovakia	S6 (Jurova)	04/04/2025	876	8	Yes (8/8)

TCS tree (statistical parsimony analysis) – 25/05/2025

Presence of a single putative common ancestor for all the sequences recovered from infected animals provides evidence for a **single introduction of the virus**.

Putative secondary ancestors for both « sub-branches »

Each branch = 1 nt of difference



▲ Samples from same animals

Comparison based on 7739 nt due to « near complete » FGS of PAK C8 2018 (EU FGS are around 8180 nt)

TCS tree (statistical parsimony analysis) – update 07/07/2025

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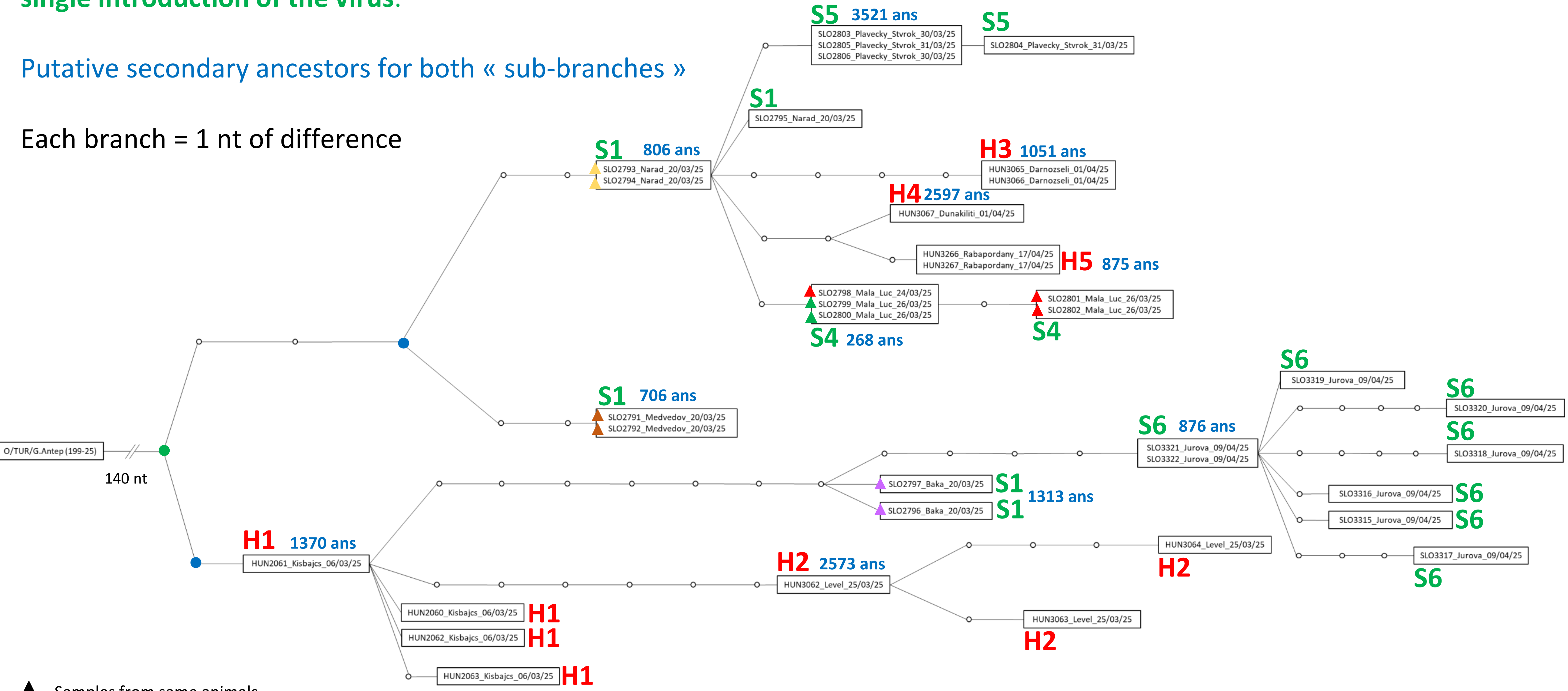

▲ Samples from same animals

Comparison based on 8180 nt

Conclusions

Take-home messages

- **FGS give a picture of the outbreaks related to available data** (Not all samples have been retrieved from all animals, and differences between apparition of clinical signs on animals and sampling lead to virus replication, and to mutations **: Full genome analyses of 36 samples** (12 from Hungary and 24 from Slovakia) **was performed at EURL**

- Single introduction of the virus

- “Real” ancestor of the outbreak not sampled (probably originated from Hungary few days before the sampling of the first animal; date of first infection was estimated 27-28 February 2025 (EUVET report))

- The Turkish strain identified in the VP1 phylogenetic tree (for HUN and SK: TUR/Gaziantep/2024) has been sequenced and confirm that a similar virus has circulated in West Asia, but as for the VP1 analysis (98,58% of nt identity), it is not a “perfect match” (98,26 % of identity with HUN2061)

- **More information is required on strains circulating in West Asia**

Thank you for your attention