Equine infectious anaemia: epidemiology and geographical distribution

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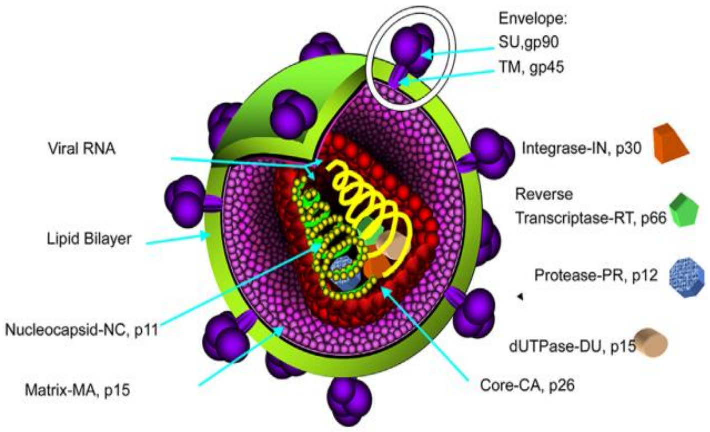
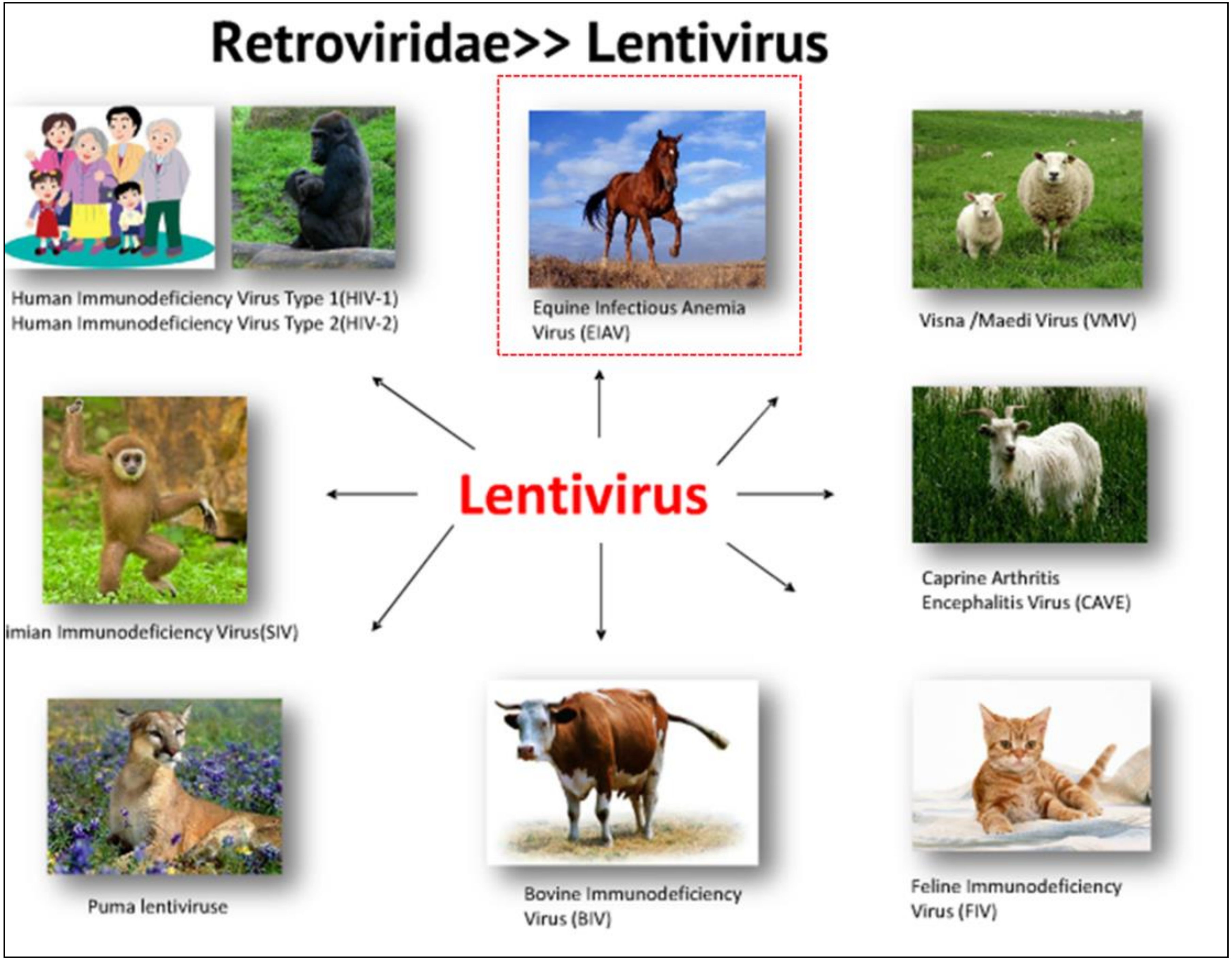
Causative agent：

Equine infectious aneamia virus (EIAV)



(Issel et al., 2014)

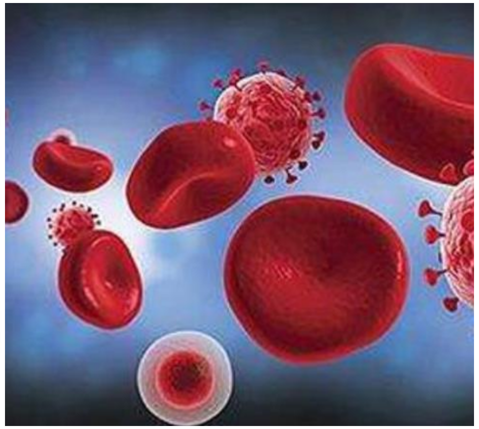


Equine infectious aneamia

- Equine infectious anemia is a worldwide disease of Equidae, including horses, donkeys, mules, and zebras.

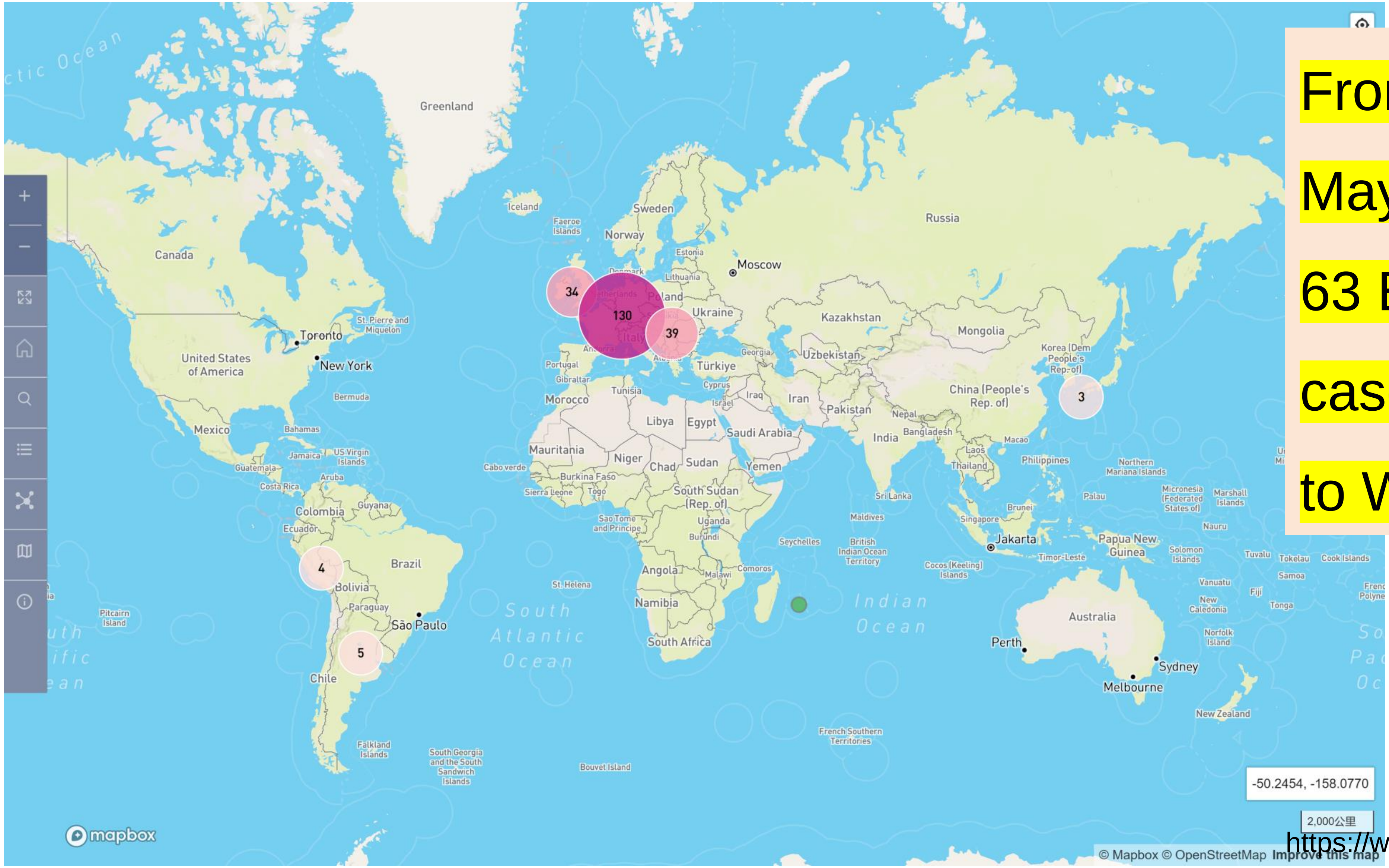
Transmission of the virus

horse flies, Tabanus spp. (Diptera: Tabanidae) - 5549600



- mechanically transmitted mainly by insect vectors
- contaminated needles, teeth rasps, stomach tubes and any other instrument that may cause abrasion.
- contaminated serum or other biological products for horses
- Transplacental/ venereal

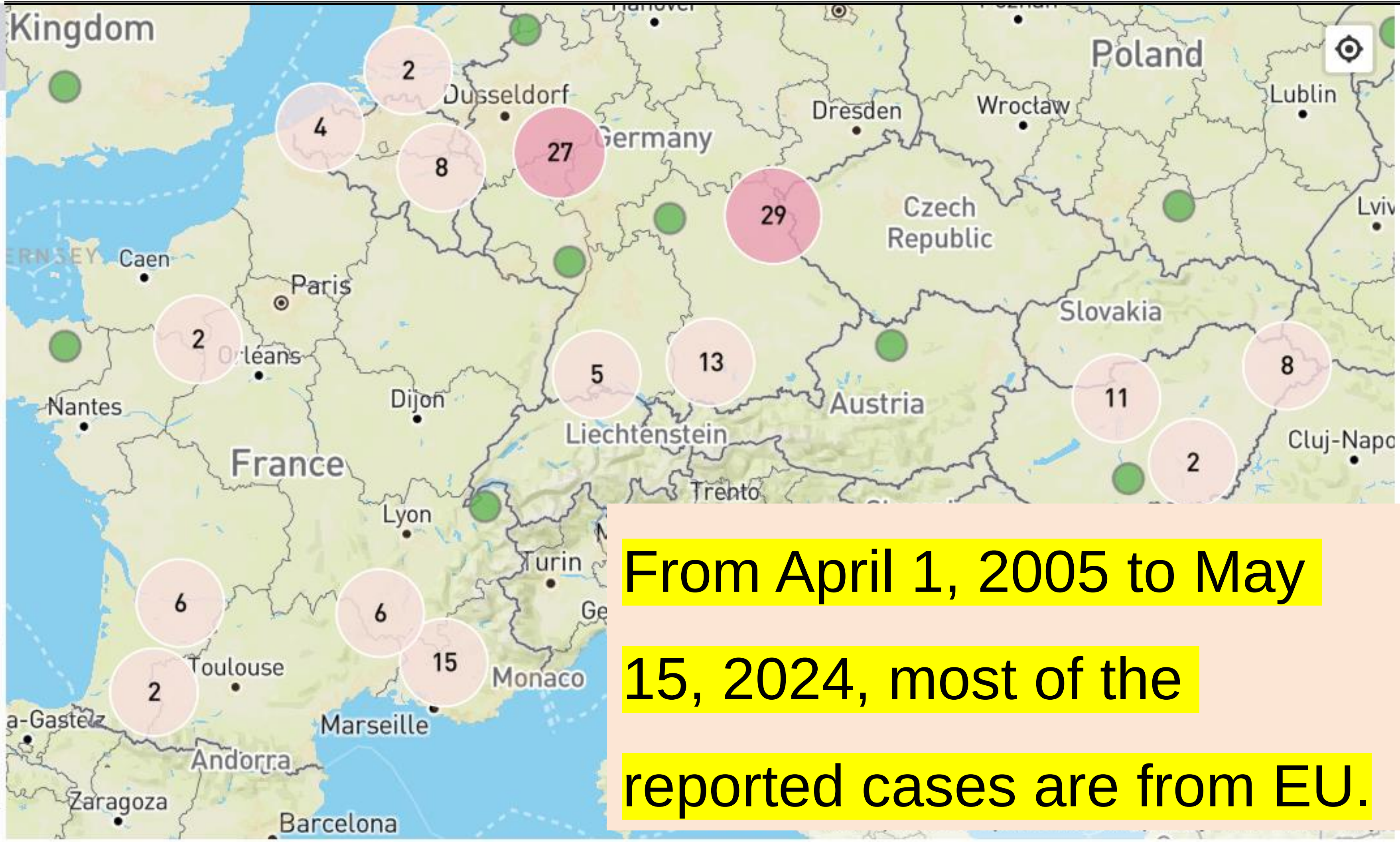
Global Epidemiology of EIA



From April 1, 2005 to May 15, 2024, a total of 63 EIA outbreaks (363 cases) were reported to WOAH.

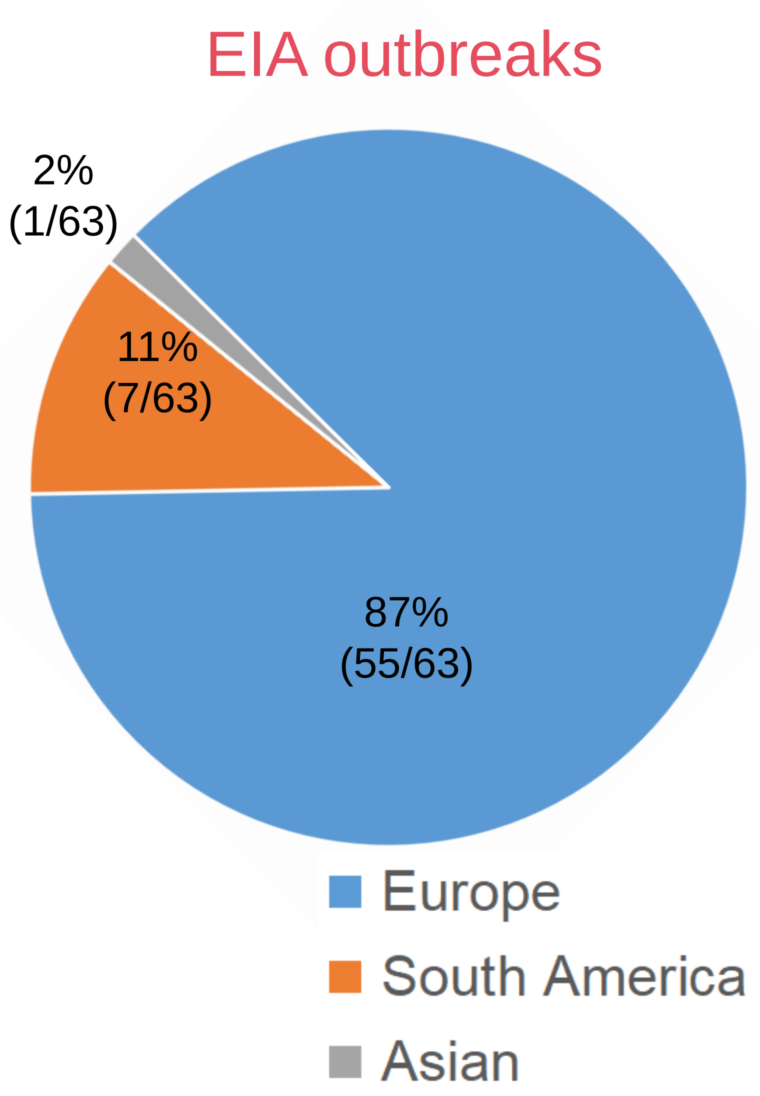
https://wahis.woah.org/#/event-management

Geographical distribution of global prevalence of EIA

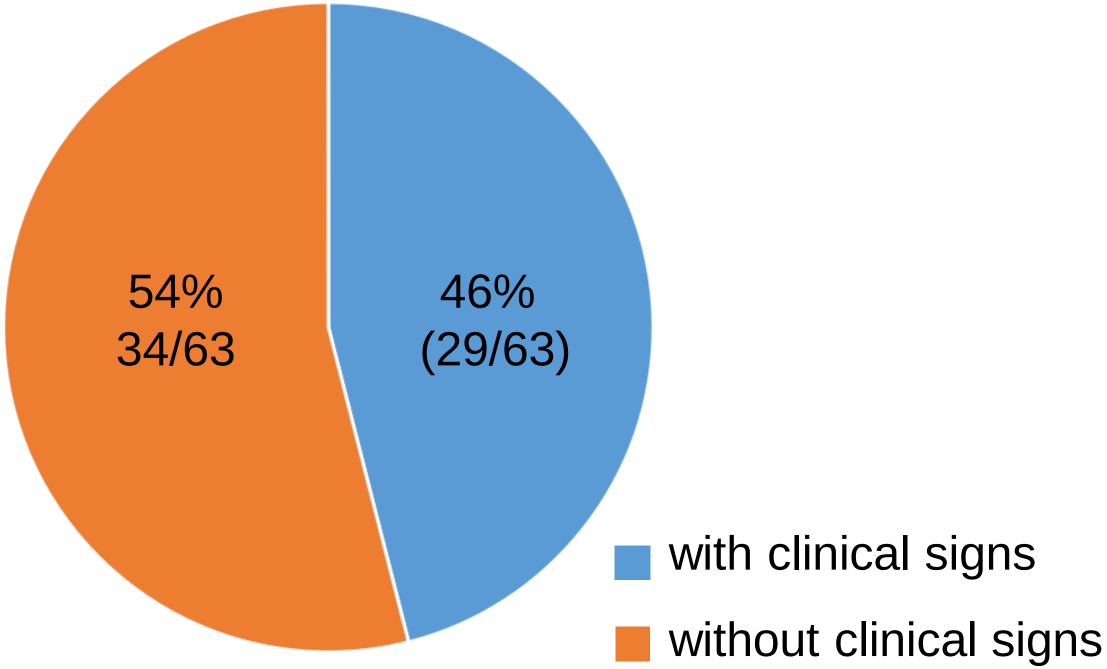


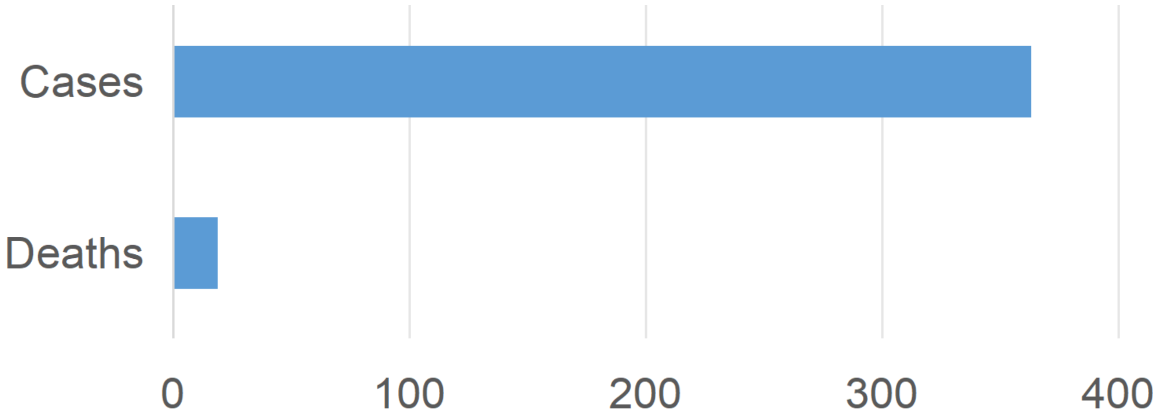
From April 1, 2005 to May 15, 2024, most of the reported cases are from EU.

https://wahis.woah.org/#/event-management



Characteristics of the global prevalence of EIA



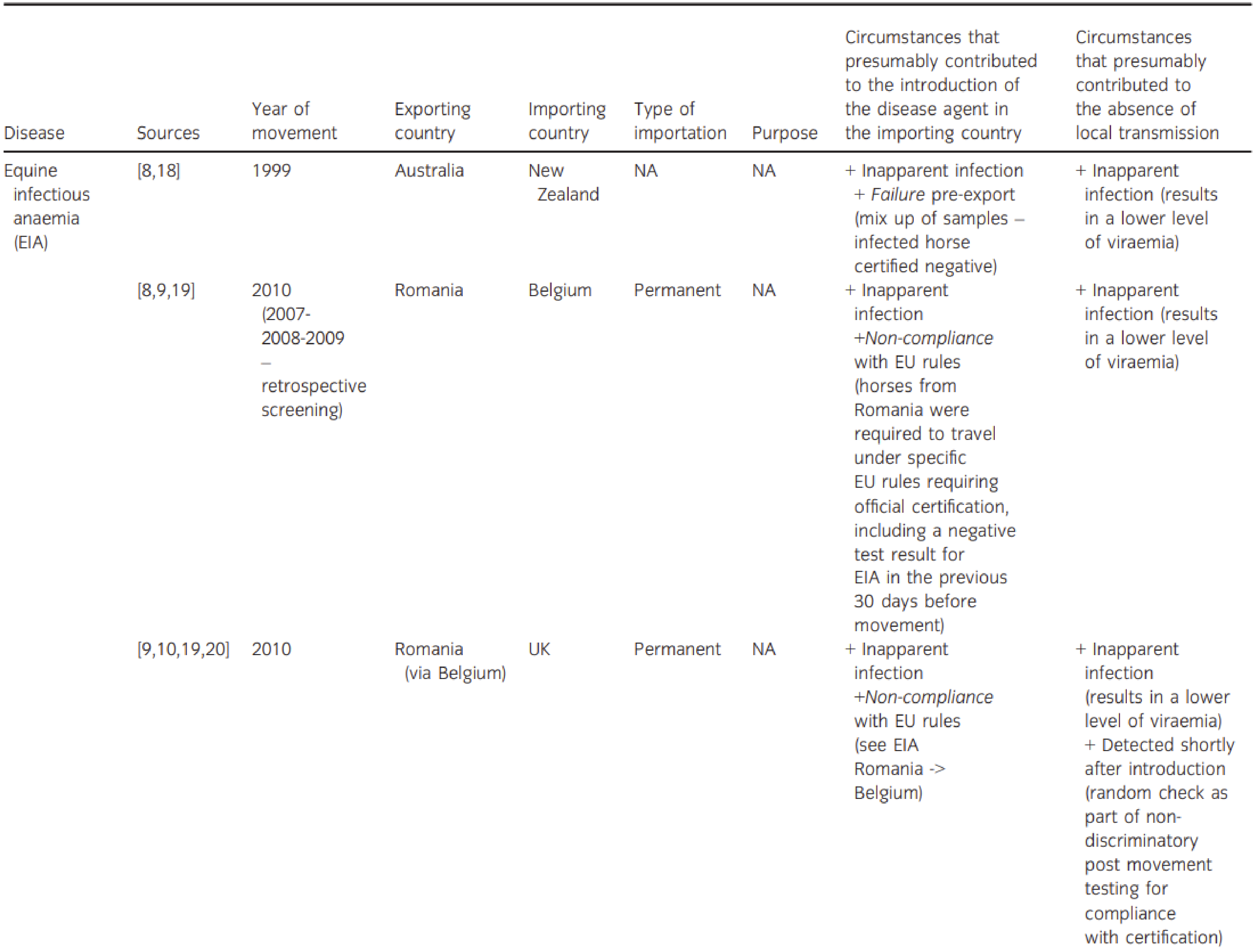


From 2005 to 2024, 63 EIA outbreaks were reported, of which 29 had clinical signs and 34 had no clinical signs.

From 2005 to 2024, 63 EIA outbreaks were reported, with a total of 363 cases and 17 deaths.

https://wahis.woah.org/#/event-management

EIA events that led to the introduction of a pathogen into the importing country without subsequent local transmission, 1995 –2014 (n = 23)*

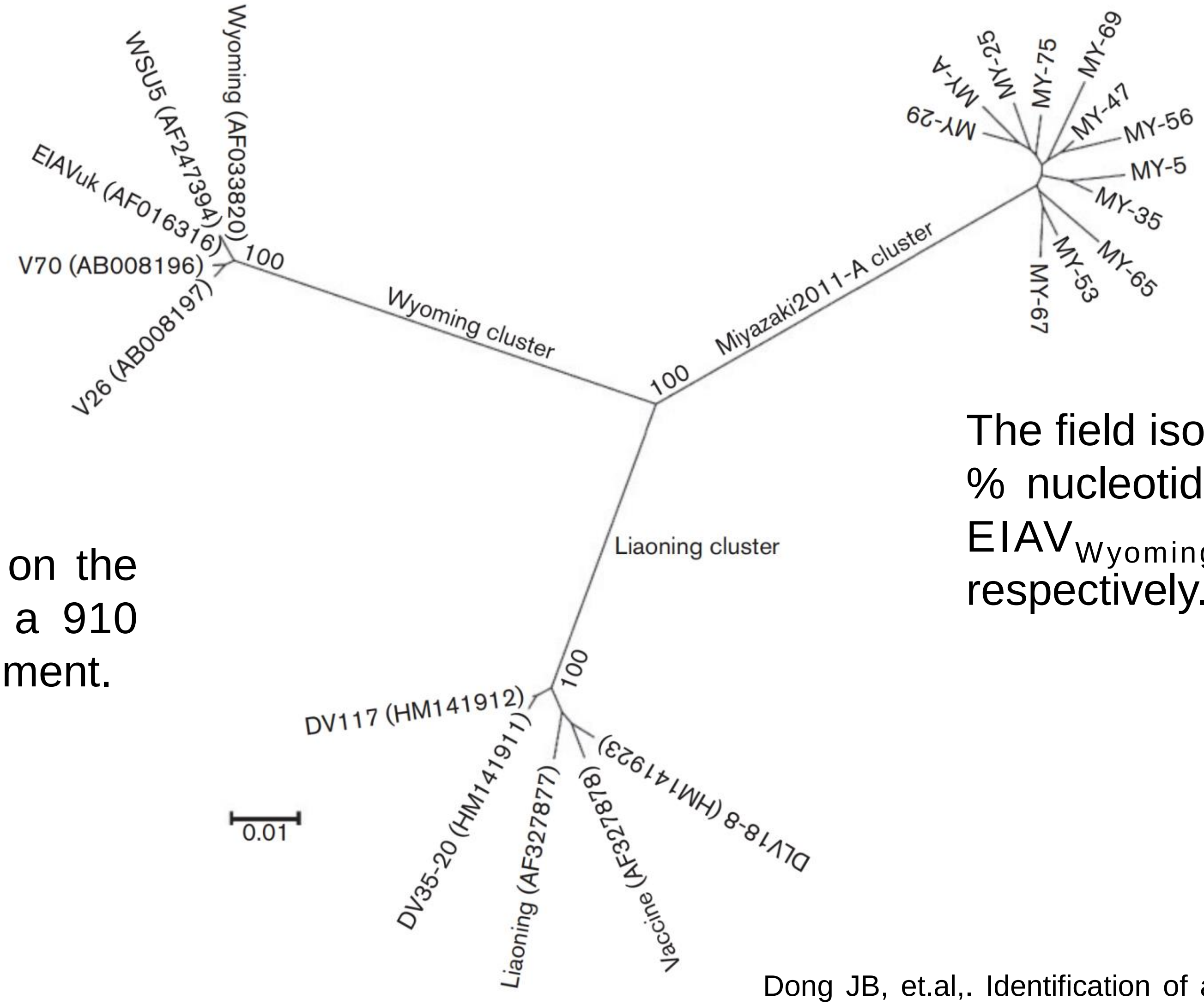


Disease	Sources	Year of movement	Exporting country	Importing country	Type of importation	Purpose	Circumstances that presumably contributed to the introduction of the disease agent in the importing country	Circumstances that presumably contributed to the absence of local transmission
Equine infectious anaemia (EIA)	[8,18]	1999	Australia	New Zealand	NA	NA	+ Inapparent infection + *Failure* pre-export (mix up of samples – infected horse certified negative)	+ Inapparent infection (results in a lower level of viraemia)
	[8,9,19]	2010 (2007-2008-2009 – retrospective screening)	Romania	Belgium	Permanent	NA	+ Inapparent infection +*Non-compliance* with EU rules (horses from Romania were required to travel under specific EU rules requiring official certification, including a negative test result for EIA in the previous 30 days before movement)	+ Inapparent infection (results in a lower level of viraemia)
	[9,10,19,20]	2010	Romania (via Belgium)	UK	Permanent	NA	+ Inapparent infection +*Non-compliance* with EU rules (see EIA Romania -> Belgium)	+ Inapparent infection (results in a lower level of viraemia) + Detected shortly after introduction (random check as part of non-discriminatory post movement testing for compliance with certification)

EIA events that led to the introduction of a pathogen into the importing country without subsequent local transmission, 1995–2014 (n = 23)*

[9,11,21]	2008	Romania	France	Permanent	NA	+ Inapparent infection +*Non-compliance* with EU rules (see EIA Romania -> Belgium)	+ Inapparent infection (results in a lower level of viraemia)
[9–11,22]	2010	The Netherlands (possible origin Romania)	UK	Permanent	NA	+ Inapparent infection + *Non-compliance* with EU rules (identification irregularities)	+ Inapparent infection (results in a lower level of viraemia) + Detected shortly after introduction (following investigation of health certification irregularities)

Phylogenetic analysis of EIAV isolates from Miyazaki,Japan



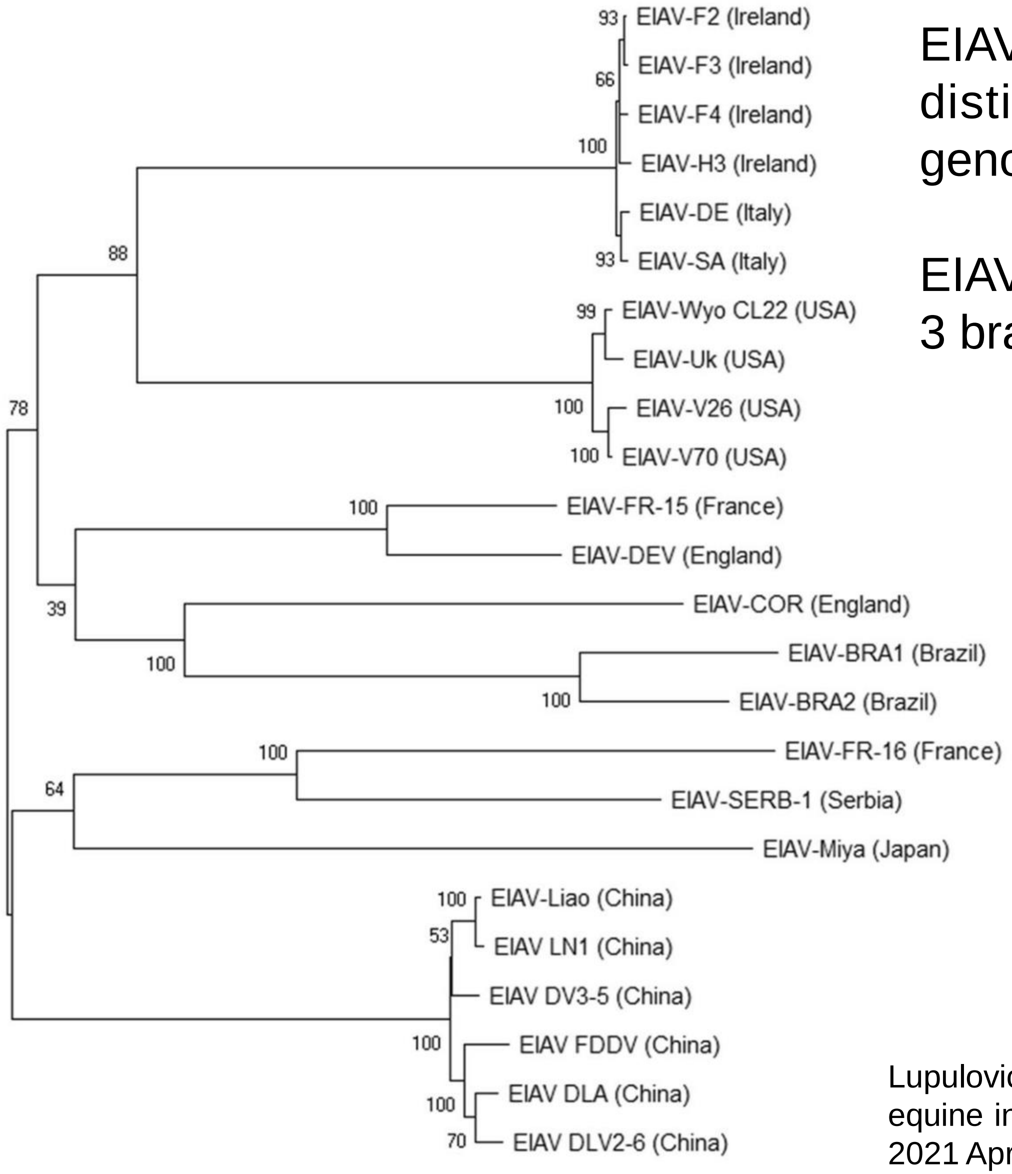
Phylogenetic tree based on the nucleotide sequence of a 910 bp of 5’-end genomic fragment.

The field isolate possesses 77.2 and 78.7 % nucleotide sequence identity with the $\text{EIAV}_{\text{Wyoming}}$ and $\text{EIAV}_{\text{Liaoning}}$ strains, respectively.

Dong JB, et.al,. Identification of a novel equine infectious anemia virus field strain isolated from feral horses in southern Japan. J Gen Virol. 2013 Feb;94(Pt 2):360-365.

Phylogenetic analysis of EIAV isolates from Europe

Phylogenetic tree based on 24 complete EIAV genome sequences

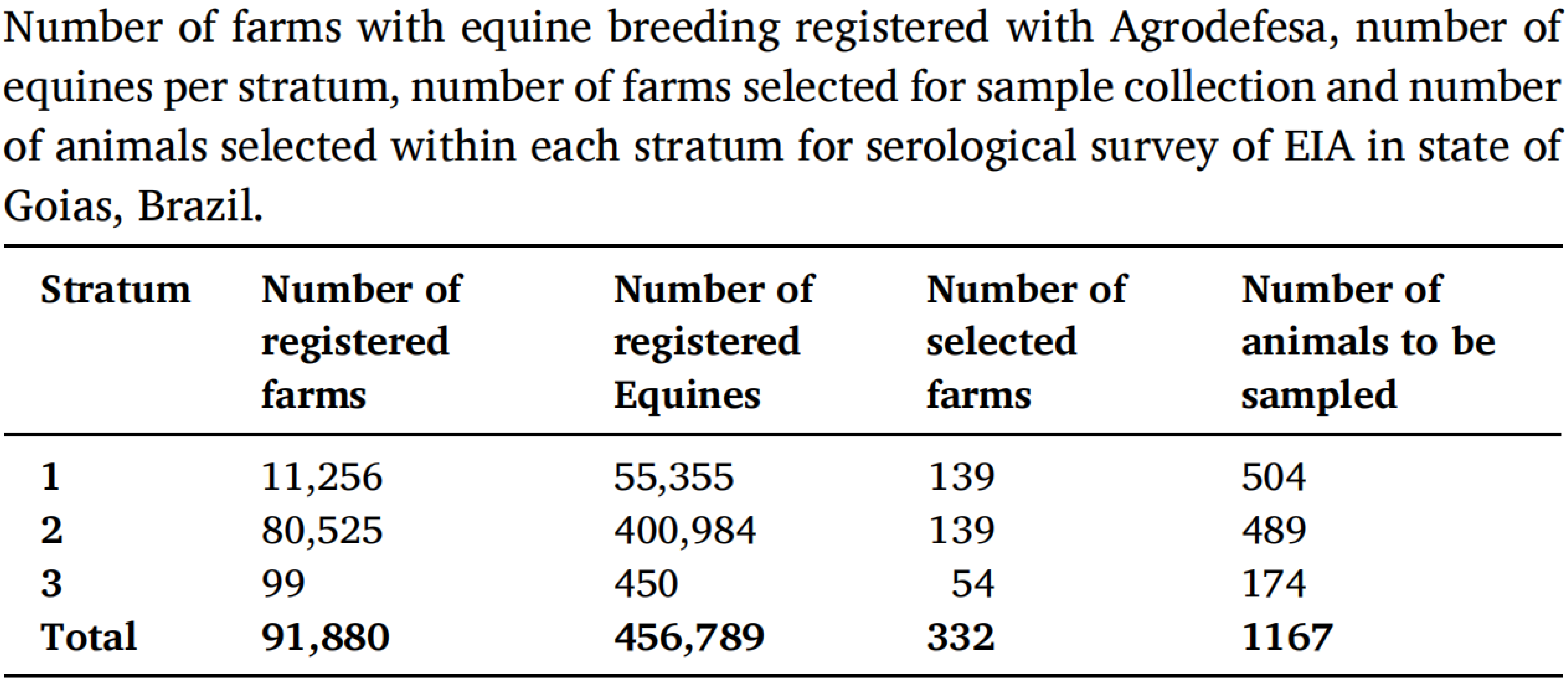


EIAV isolates can be divided, at least, in 6 distinct clades, based on the full EIAV genome sequences.

EIAV isolates from Europe are divided into 3 branches

Lupulovic D, et al., Identification and genetic characterization of equine infectious anemia virus in Western Balkans. BMC Vet Res. 2021 Apr 15;17(1):168.

Seroprevalence of EIA in the state of Goiás, Brazil

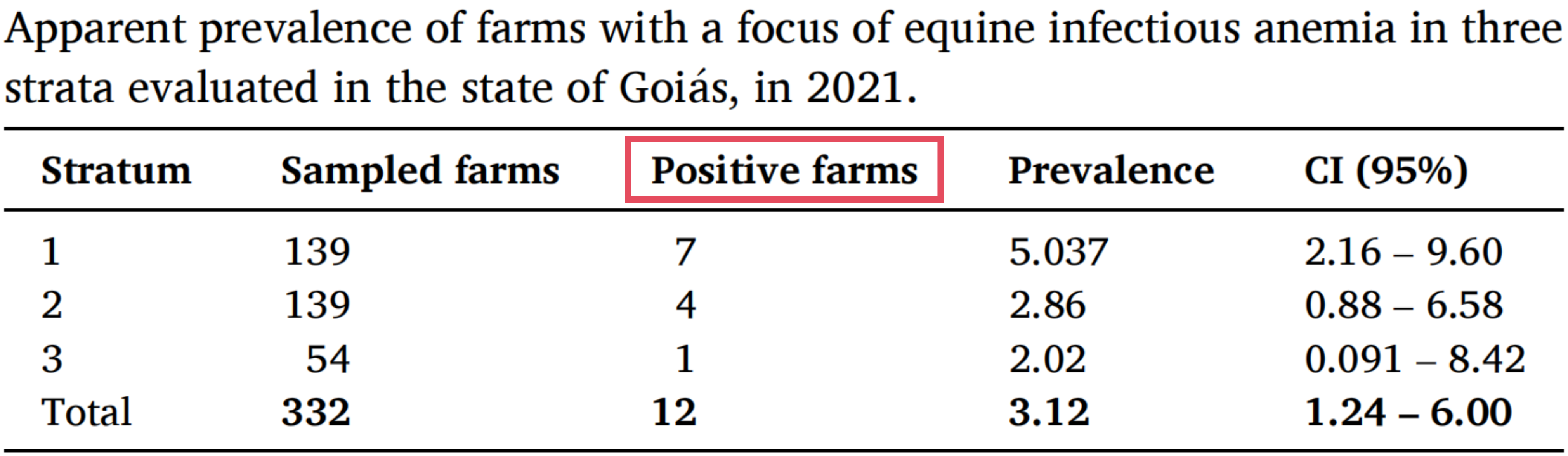


Number of farms with equine breeding registered with Agrodefesa, number of equines per stratum, number of farms selected for sample collection and number of animals selected within each stratum for serological survey of EIA in state of Goias, Brazil.

Stratum	Number of registered farms	Number of registered Equines	Number of selected farms	Number of animals to be sampled
1	11,256	55,355	139	504
2	80,525	400,984	139	489
3	99	450	54	174
Total	**91,880**	**456,789**	**332**	**1167**

de Pádua BR, et al,. Seroprevalence and risk factors associated with equine infectious anemia in the state of Goiás, Brazil. Prev Vet Med. 2022 Dec;209:105781.

Seroprevalence of EIA in the state of Goiás, Brazil

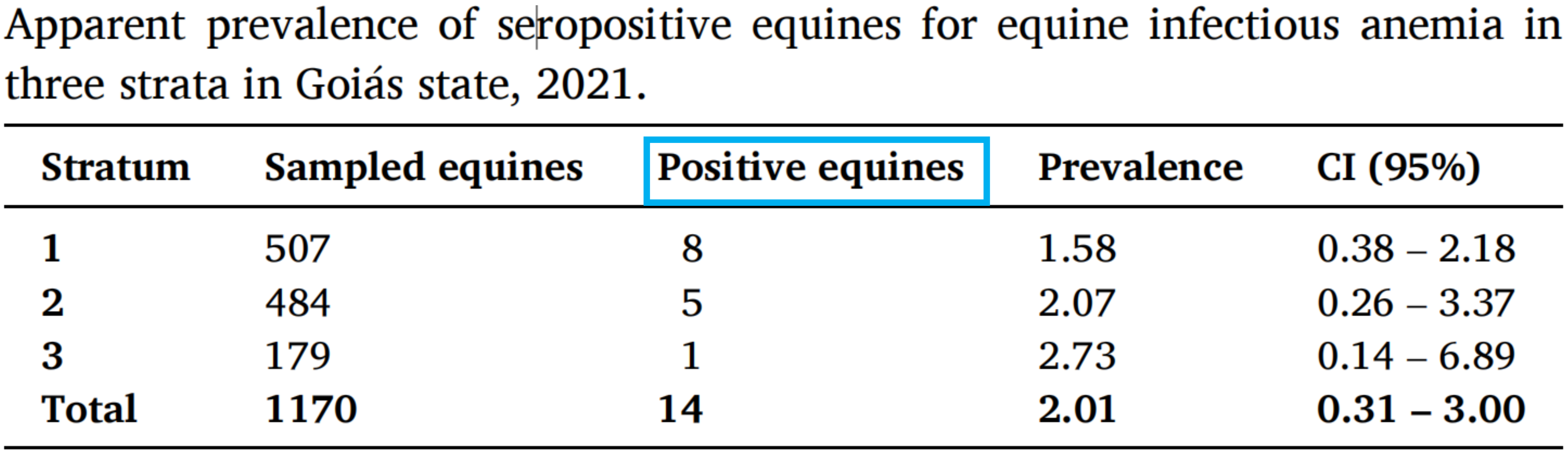


Apparent prevalence of farms with a focus of equine infectious anemia in three strata evaluated in the state of Goiás, in 2021.

Stratum	Sampled farms	Positive farms	Prevalence	CI (95%)
1	139	7	5.037	2.16 – 9.60
2	139	4	2.86	0.88 – 6.58
3	54	1	2.02	0.091 – 8.42
Total	**332**	**12**	**3.12**	**1.24 – 6.00**

de Pádua BR, et al,. Seroprevalence and risk factors associated with equine infectious anemia in the state of Goiás, Brazil. Prev Vet Med. 2022 Dec;209:105781.

Seroprevalence of EIA in the state of Goiás, Brazil



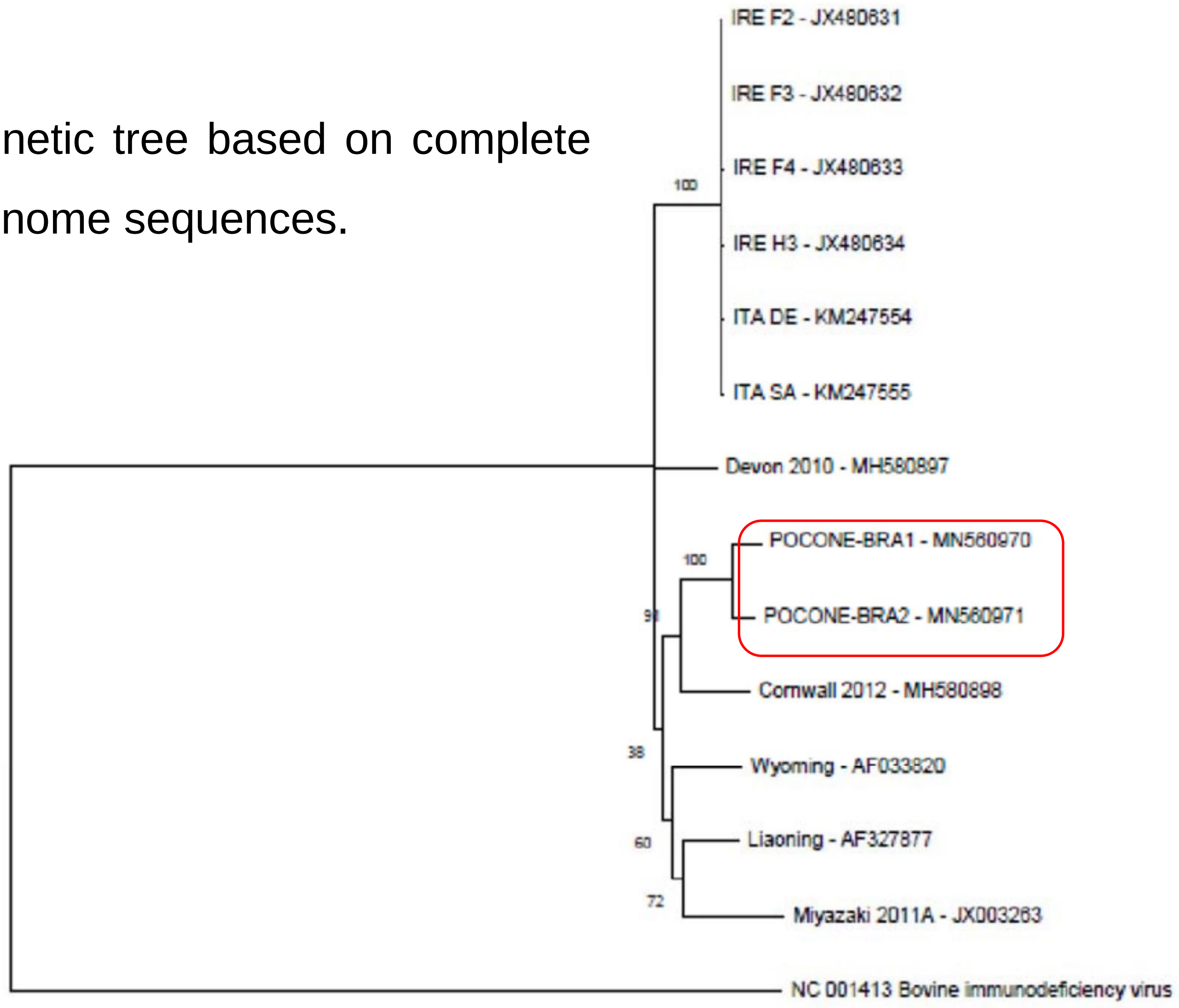
Apparent prevalence of seropositive equines for equine infectious anemia in three strata in Goiás state, 2021.

Stratum	Sampled equines	Positive equines	Prevalence	CI (95%)
1	507	8	1.58	0.38 – 2.18
2	484	5	2.07	0.26 – 3.37
3	179	1	2.73	0.14 – 6.89
Total	**1170**	**14**	**2.01**	**0.31 – 3.00**

de Pádua BR, et al,. Seroprevalence and risk factors associated with equine infectious anemia in the state of Goiás, Brazil. Prev Vet Med. 2022 Dec;209:105781.

High genomic variability of EIAV isolates from Pantanal, Brazil

Phylogenetic tree based on complete EIAV genome sequences.

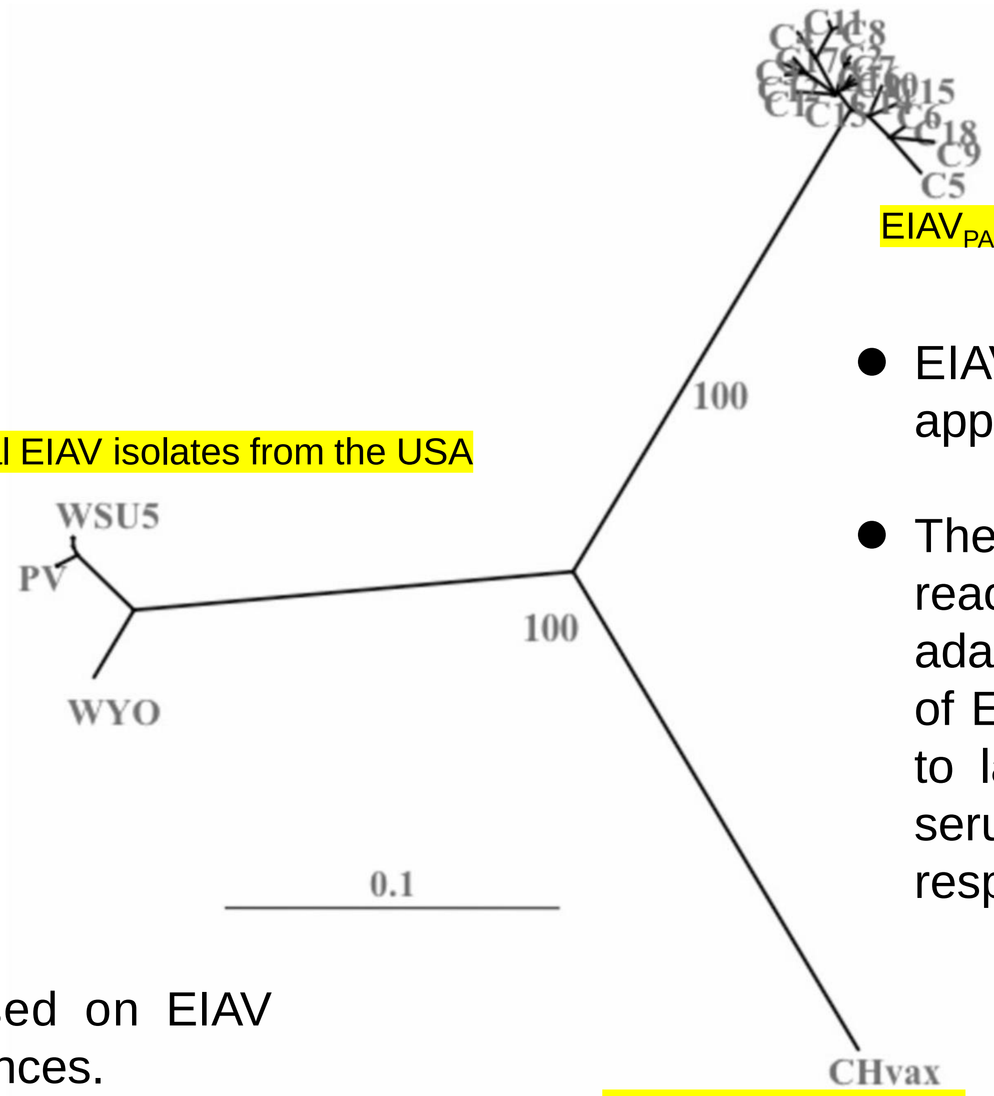


Brazilian genome sequences presented 75.8 to 77.3% with main field strains, such as EIAV Liaoning, Wyoming, Ireland, and Italy isolates.

This Brazilian strain comprises a separate monophyletic group

Malossi CD, et al., High Genomic Variability in Equine Infectious Anemia Virus Obtained from Naturally Infected Horses in Pantanal, Brazil: An Endemic Region Case. Viruses. 2020 Feb 12;12(2):207.

Phylogenetic analysis of an EIAV field isolates from Pennsylvania, USA



EIAV$_{PA}$, a natural primary isolate from Pennsylvania, USA

Published reports of natural EIAV isolates from the USA

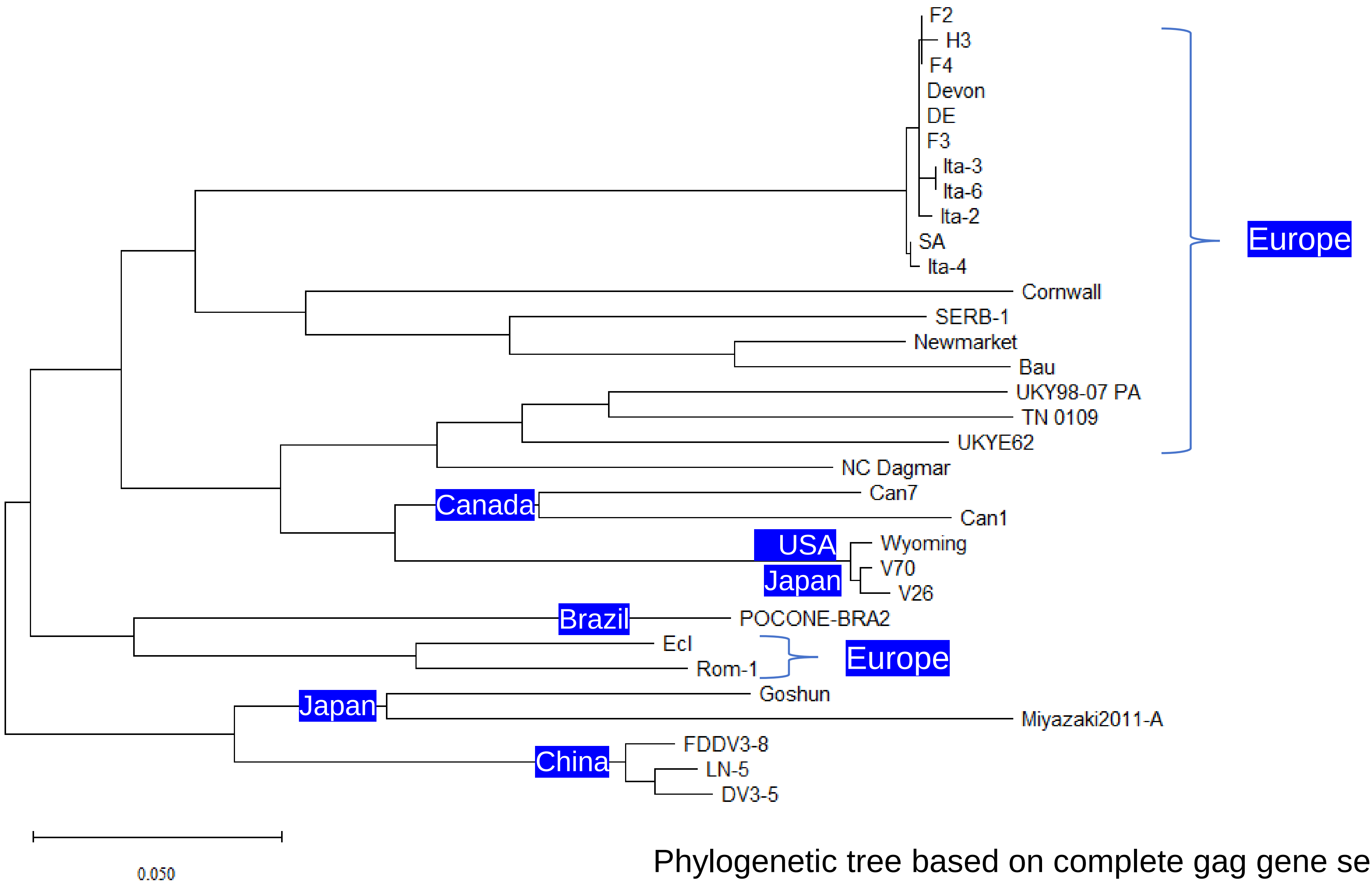
Chinese vaccine stain

- EIAV$_{PA}$ Env amino acid sequence variation, approximately 40% as compared to EIAV$_{WY}$.
- The EIAV$_{PA}$ Env was serologically cross reactive with the Env proteins of the cell-adapted reference strain, EIAV$_{PV}$ (derivative of EIAV$_{WY}$), the two variant Envs were shown to lack any cross neutralization by immune serum from horses infected with the respective virus strains.

Phylogenetic tree based on EIAV gp90 amino acid sequences.

Craigo JK, et al., An EIAV field isolate reveals much higher levels of subtype variability than currently reported for the equine lentivirus family. Retrovirology. 2009 Oct 20;6:95.

High genomic variability of EIAV



Phylogenetic tree based on complete gag gene sequences

Thank you for your attention