

Swine influenza viruses from Hong Kong and Viet Nam

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Swine samples

Hong Kong, China

- 2021-2023
- Geographic source (Mainland provinces):
 - ✓ Guangxi
 - ✓ Guizhou
 - ✓ Guangdong
 - ✓ Hunan
 - ✓ Jiangxi

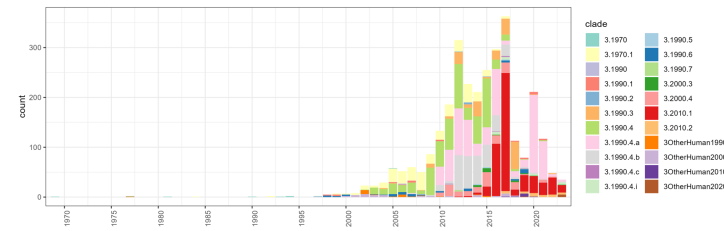
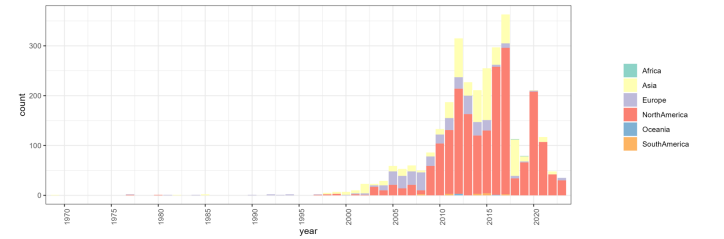
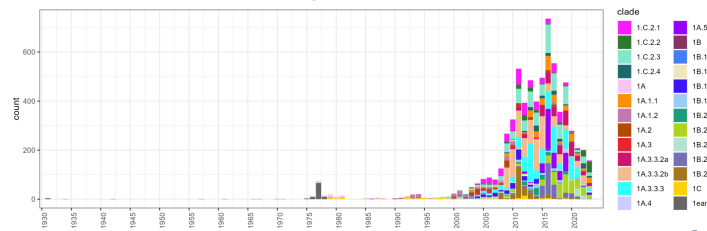
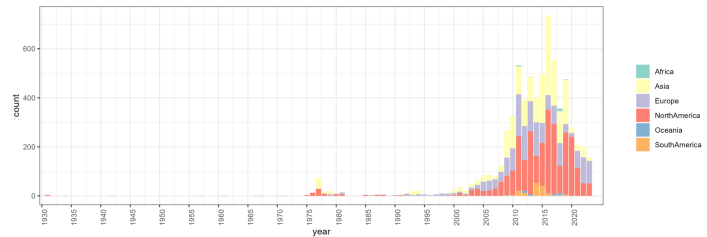
Viet Nam

- 2013-2023
- Geographical source (provinces):
 - ✓ Ha Noi
 - ✓ Bac Ninh
 - ✓ Hung Yen
 - ✓ Nghe An
 - ✓ Yen Bai
 - ✓ Ha Nam
 - ✓ Vinh Phuc
 - ✓ Thanh Hoa

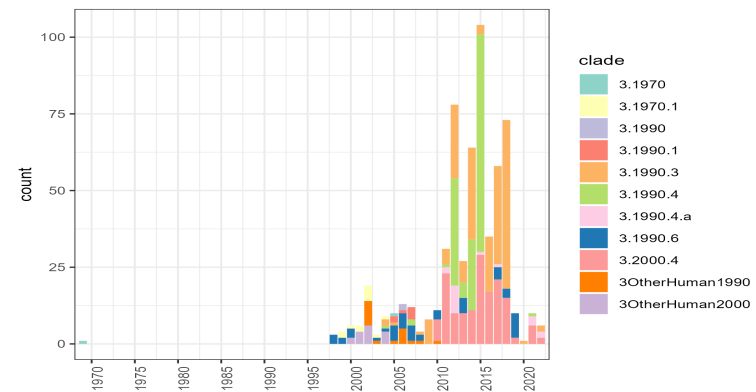
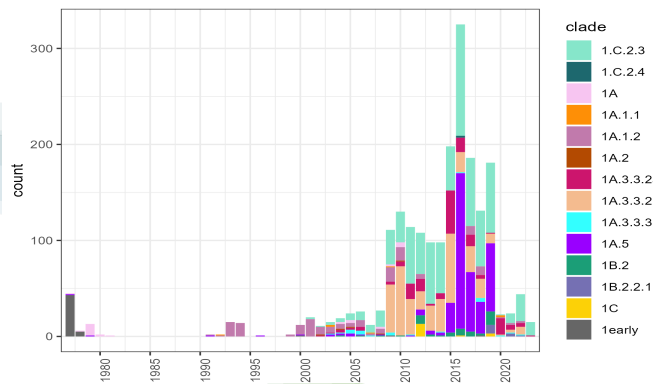
Swine samples

H1 and H3 Global epidemiology

2024 - OFFLU Swine Influenza virus Technical Meeting

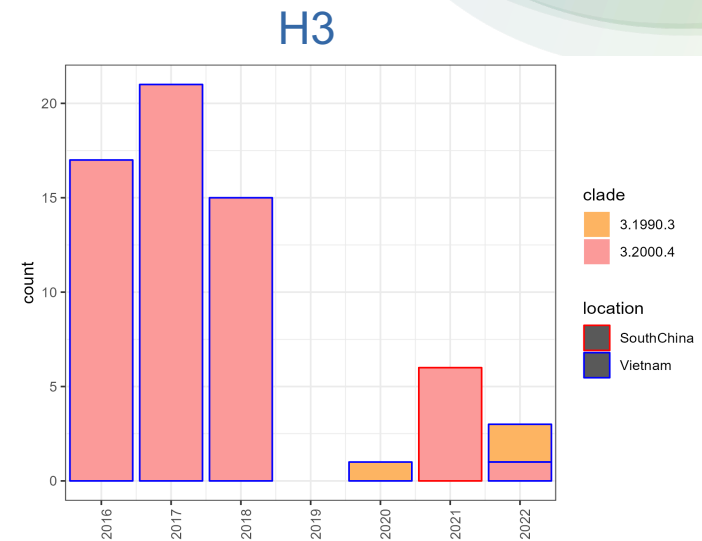
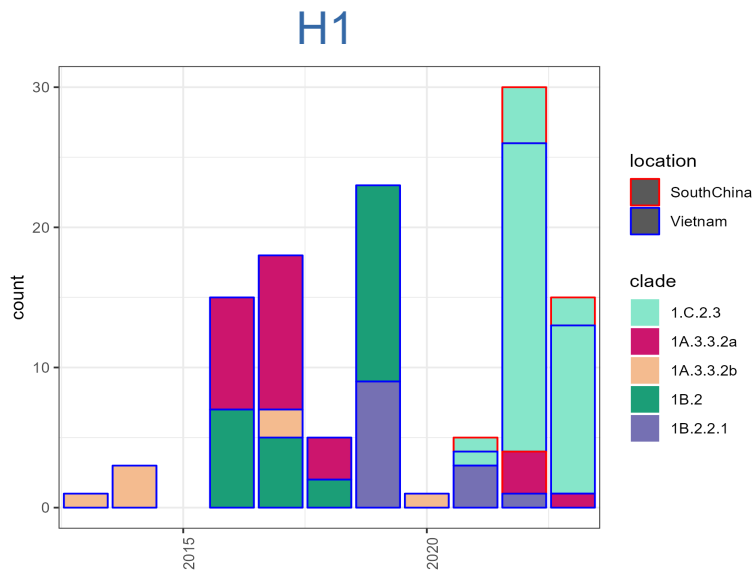


Asia epidemiology



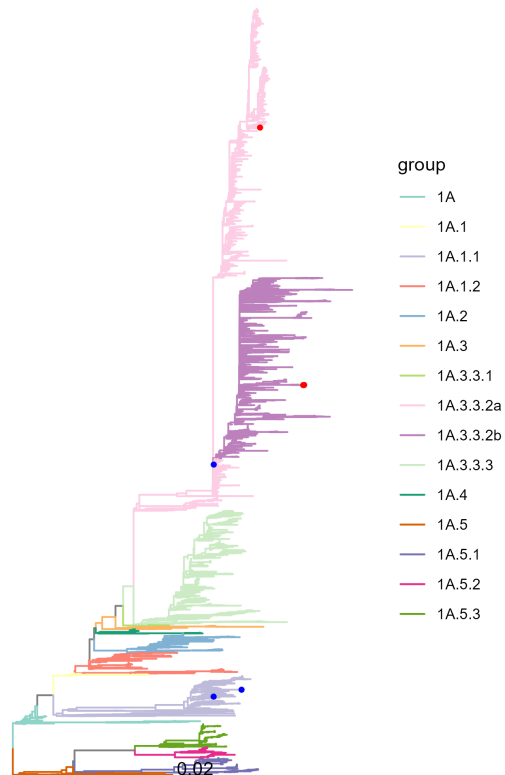
- Swine influenza virus clades did not replace as frequently as in human influenza viruses.

Swine samples

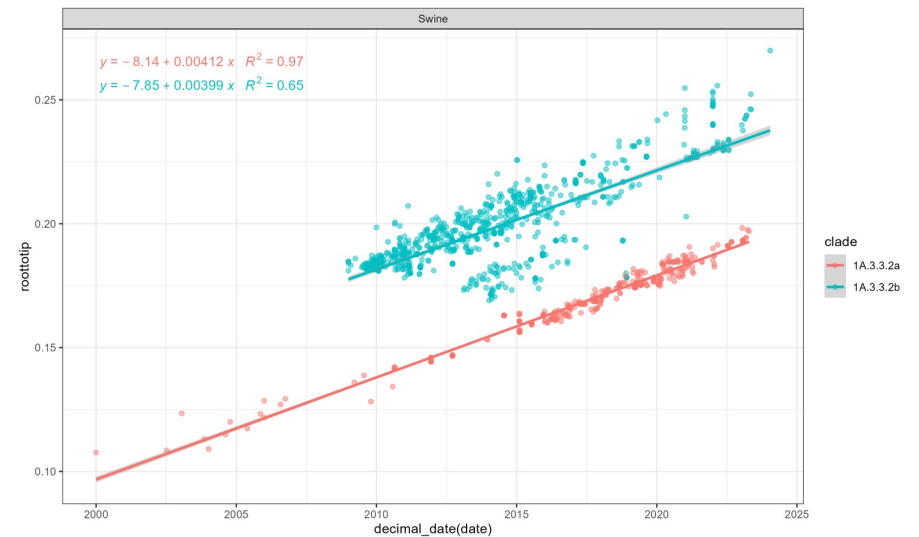


Number and clade of H1 and H3 samples from Hong Kong (southern China) and Vietnam.

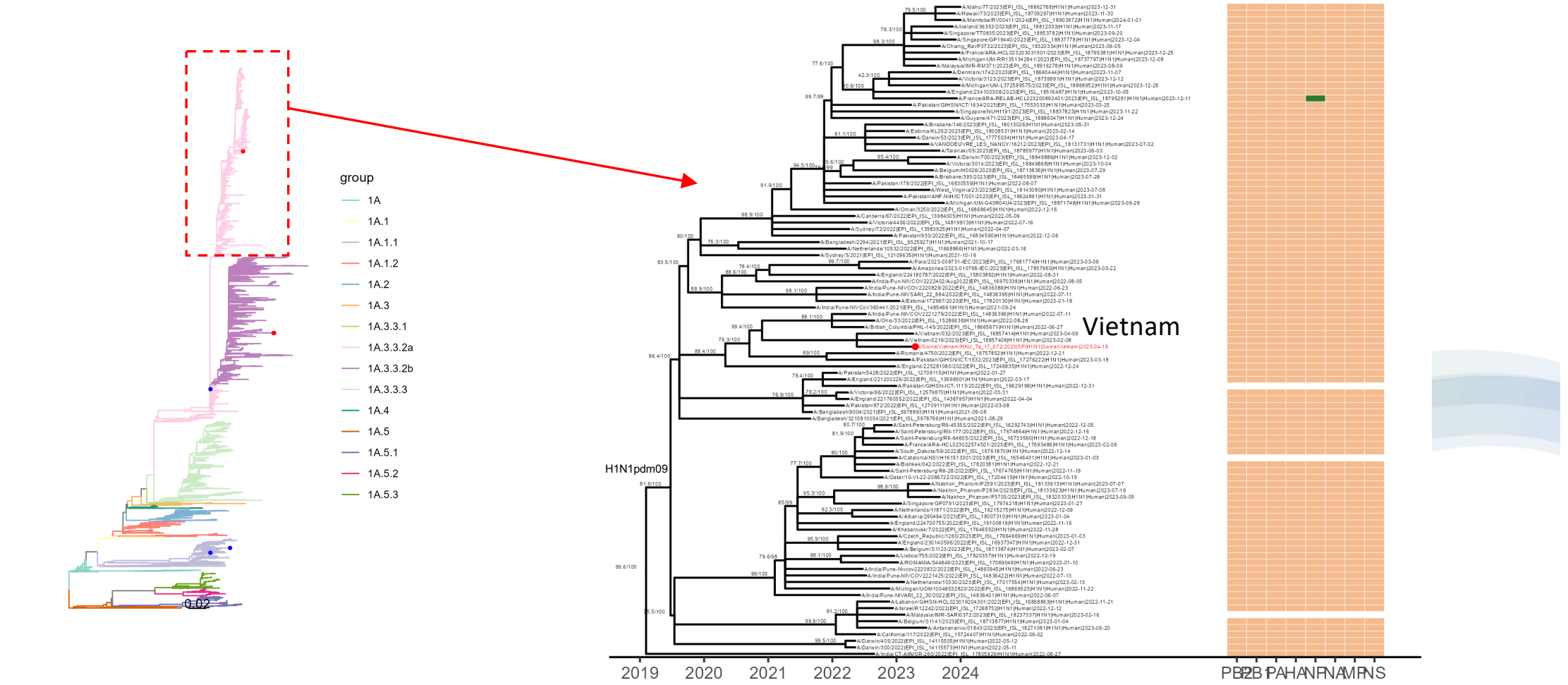
H1 classical swine lineage 1A



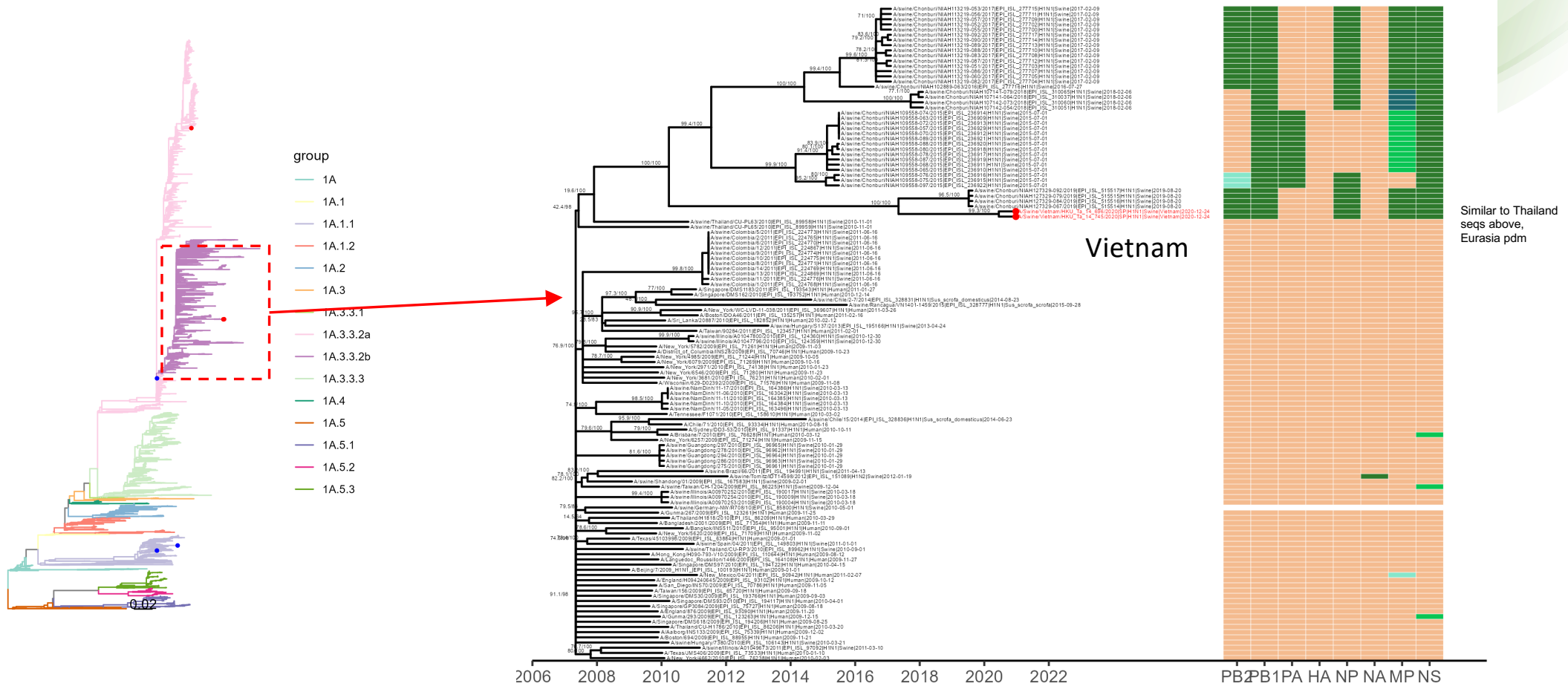
1A.3.3.2 should be split to at least two subclades (A, B) based on root-to-tip plot analysis – distinct lineages with significant mutations.



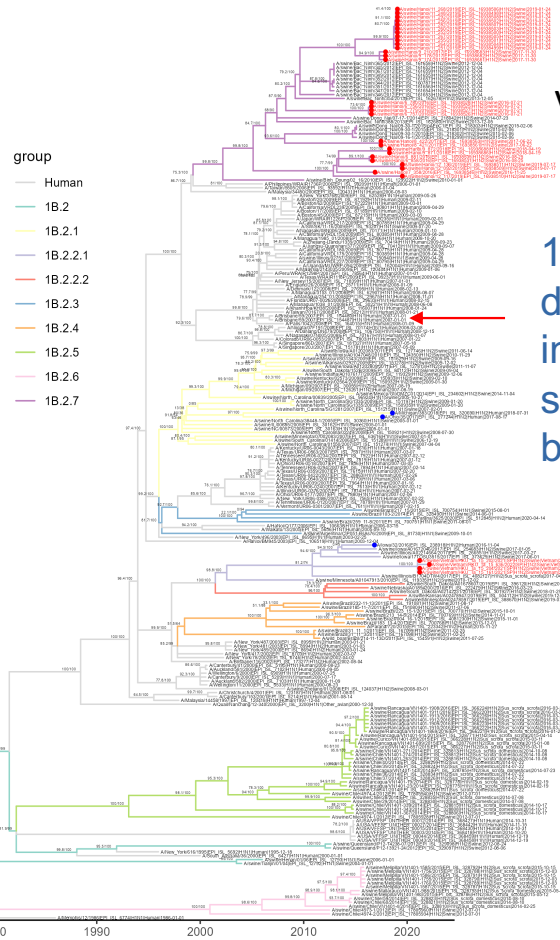
Genotype of H1 classical swine lineage 1A.3.3.2a/pdm



Genotype of H1 classical swine lineage 1A.3.3.2b/pdm



H1 Clade 1B



Vietnam

1B.2.7 has not been defined previously, including the Vietnam sequences published before

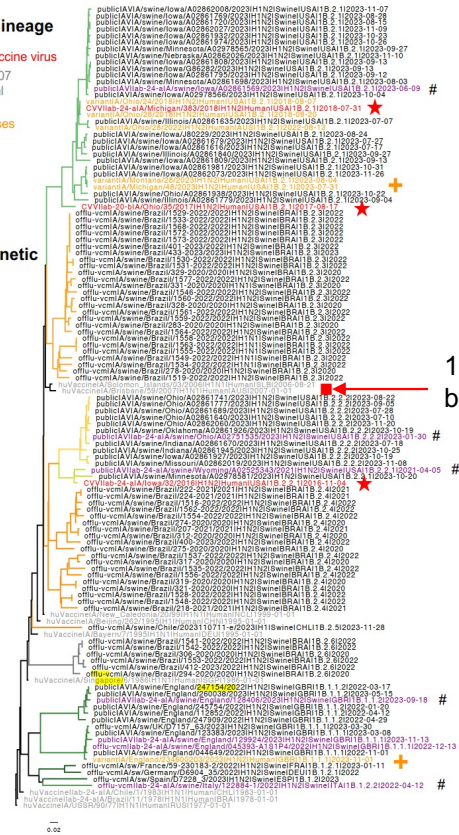
Vietnam

1B human-like lineage

- ★ H1v candidate vaccine virus
- A/Brisbane/59/2007
- Previous seasonal H1N1 vaccine
- ⊕ Reported H1v cases
- ⊕ New variant(s)
- # HI tested viruses

H1 1B swine genetic clades

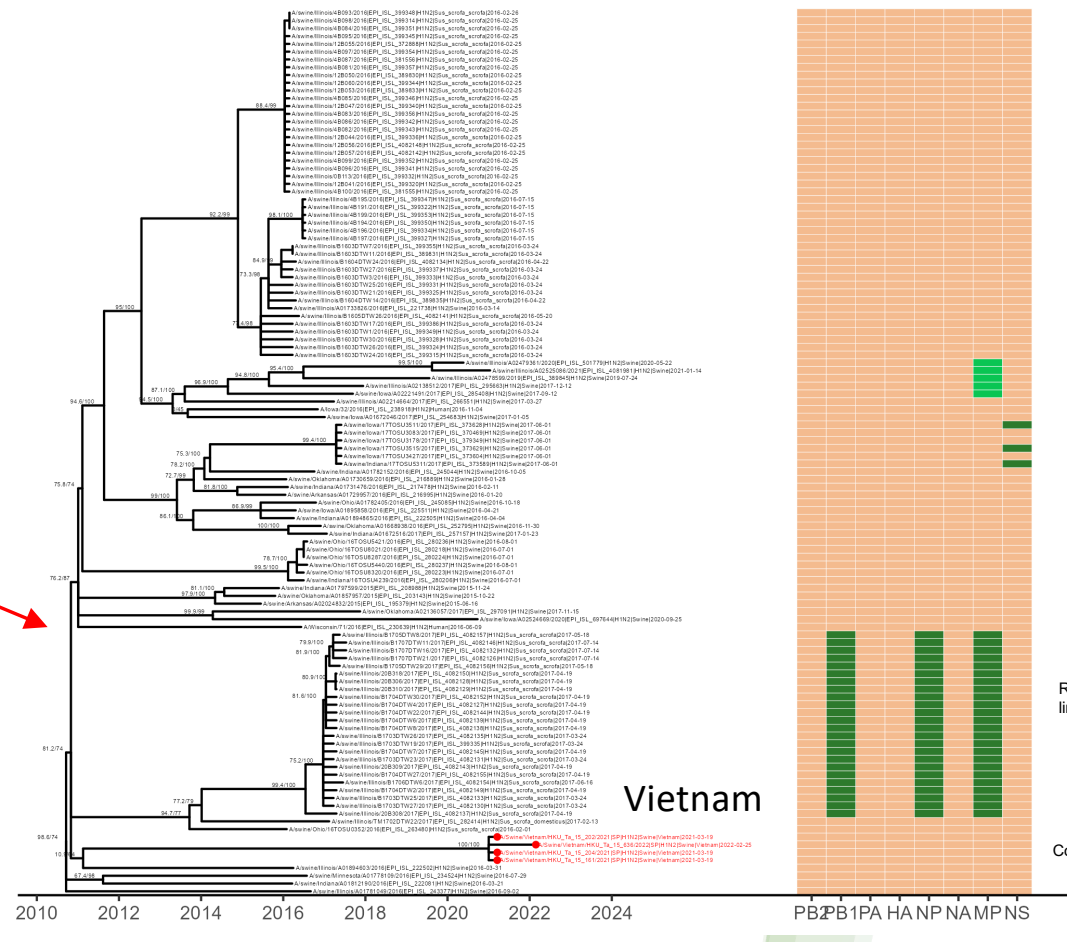
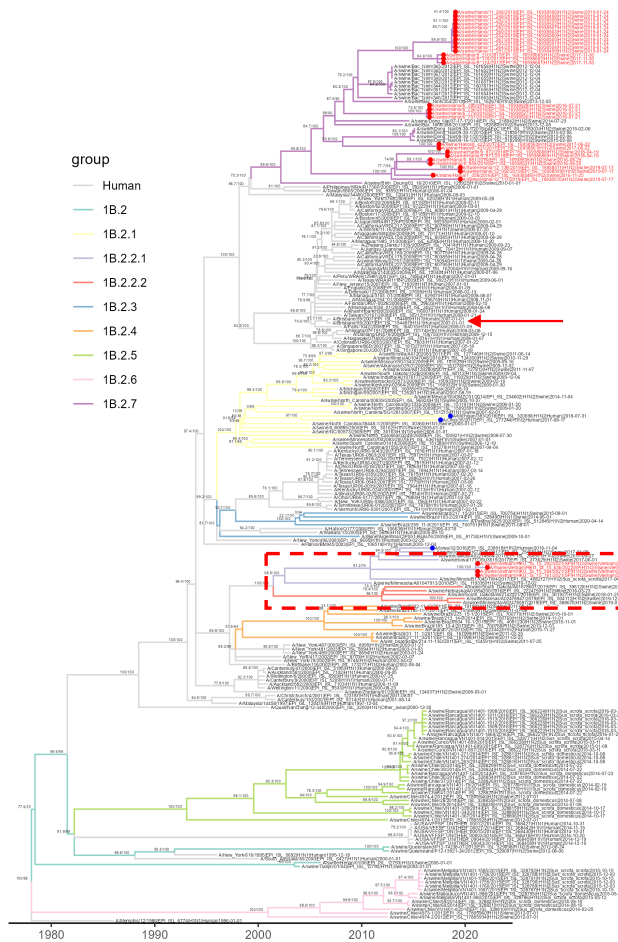
- 1B.2.1 (n=80)
- 1B.2.3 (n=26)
- 1B.2.2.2 (n=17)
- 1B.2.4 (n=19)
- 1B.2.5 (n=1)
- 1B.2.6 (n=6)
- 1B.1.1.2 (n=6)
- 1B.1.1.1 (n=4)
- 1B.1.2 (n=4)



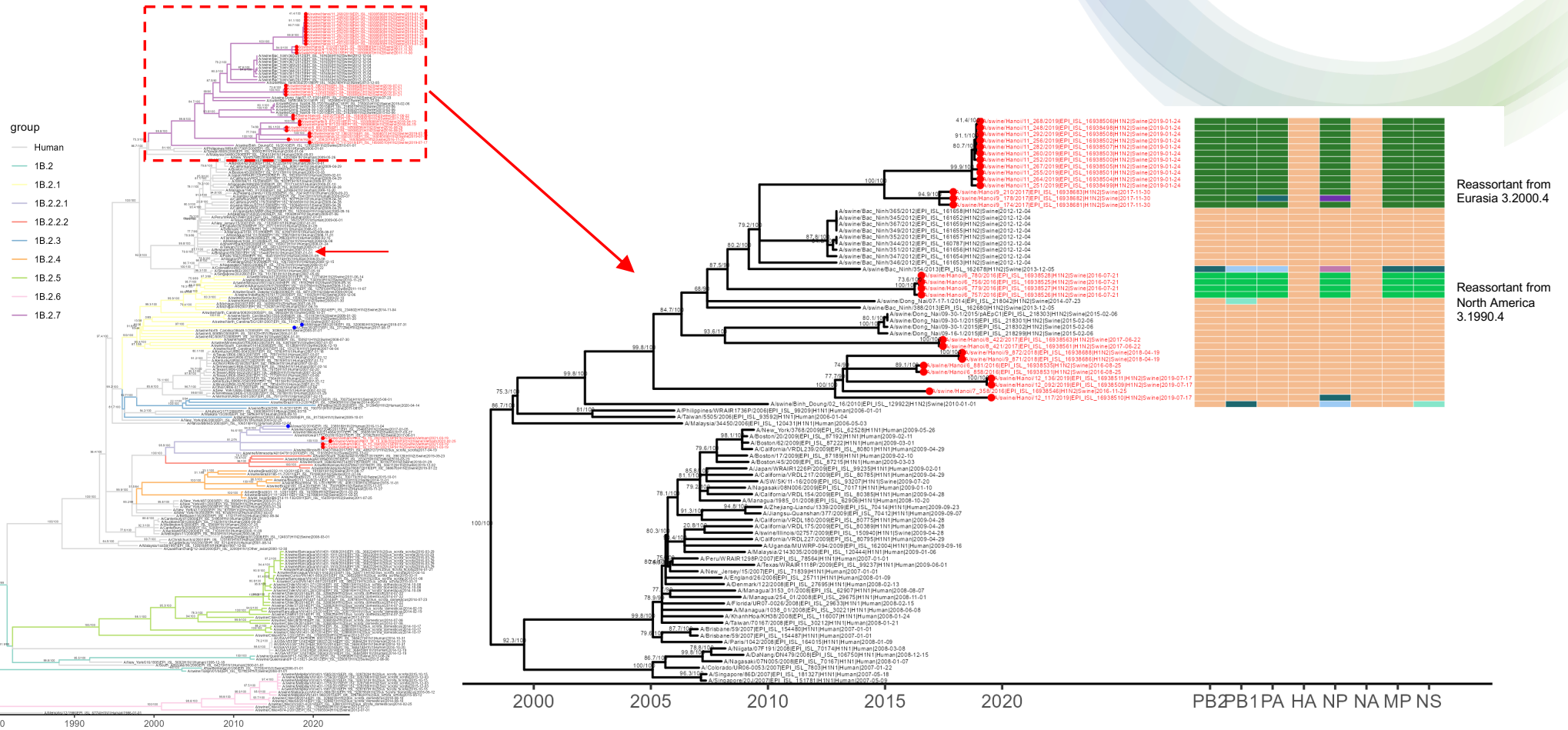
1B.2.7 should be a branch here

Figure 8. Swine H1 HA genes of the 1B lineage (tree was proportionally down sampled to 104 swine HA genes, excluding references). Number of detections of each clade from data deposited between July 1 - December 31, 2023 are presented adjacent to the clade name in the figure key.

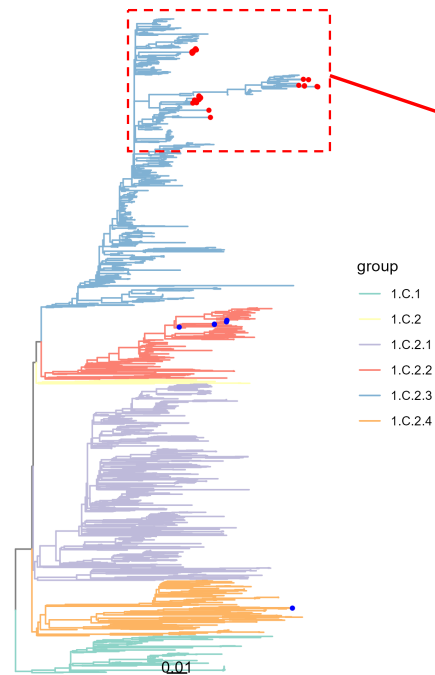
Genotype of H1 Eurasian avian lineage 1B.2.2.1



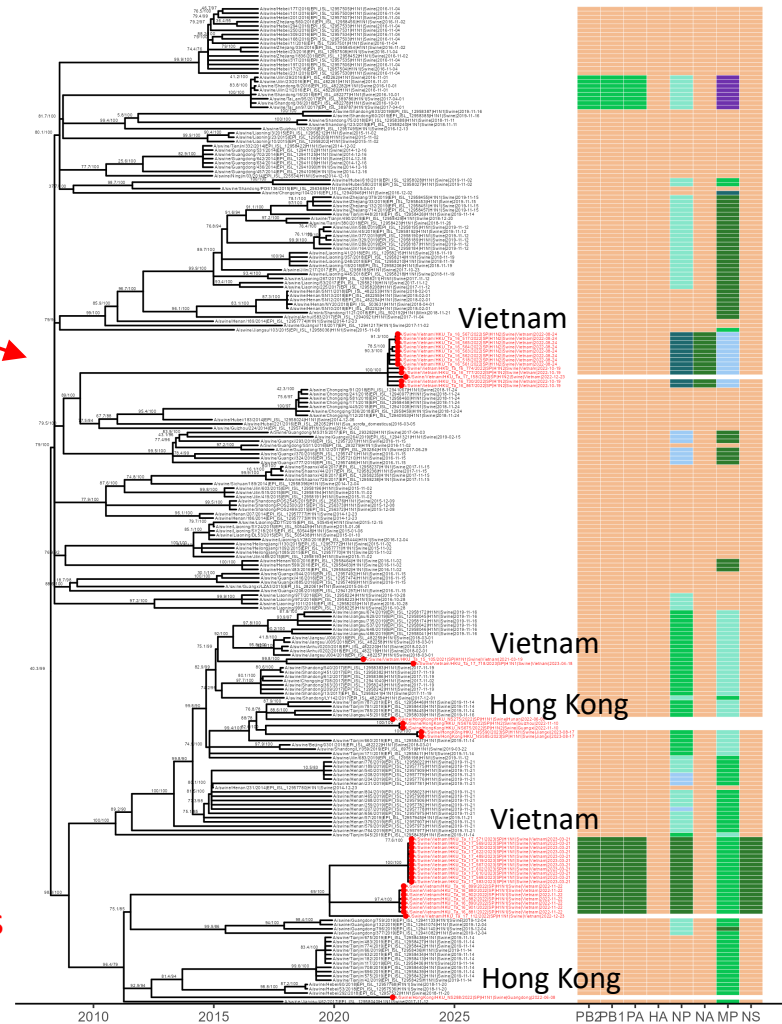
Genotype of H1 Eurasian avian lineage 1B.2.7



Clade and Genotype of H1 Eurasian avian lineage 1C.2.3



- Hong Kong and Vietnam samples
- CVV



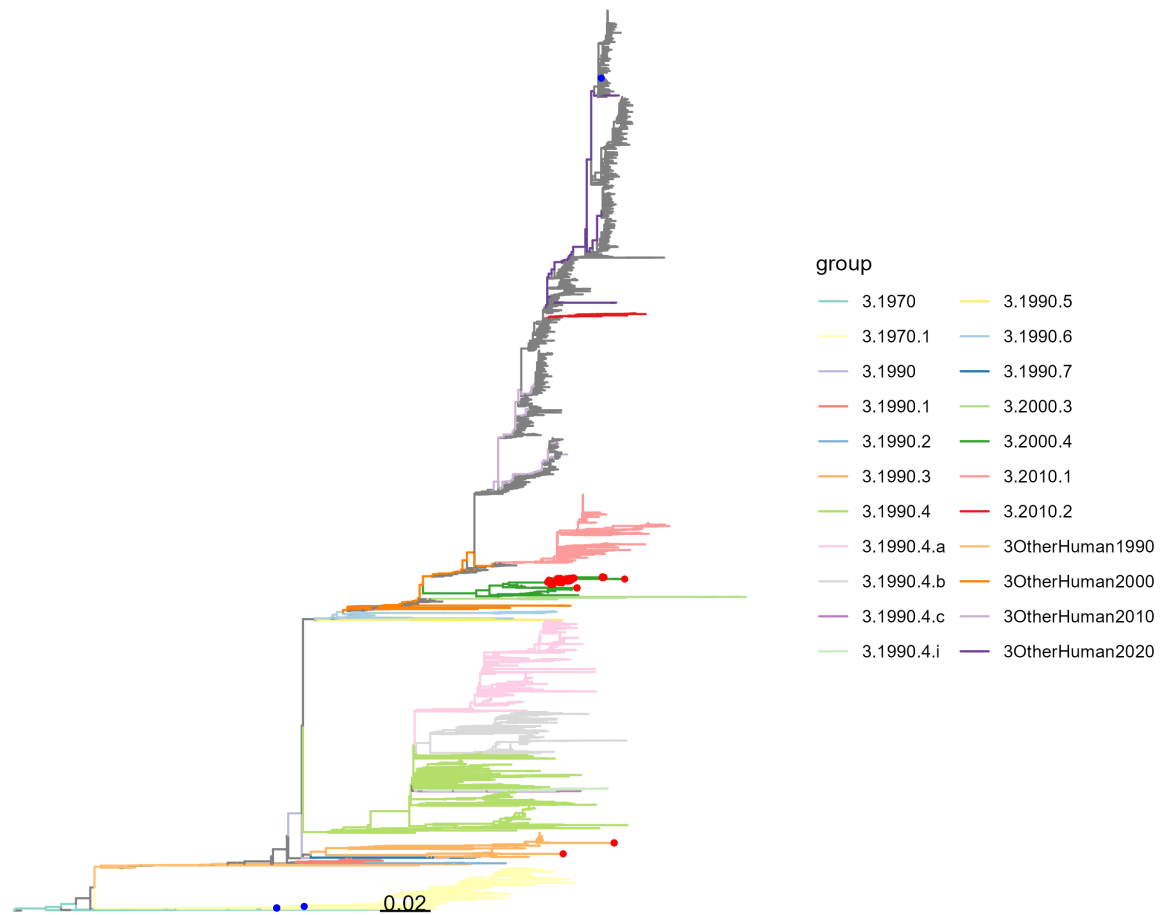
Reassortant from Asia 1A.3.3.2a(pd) NP, N2, 1B.2.7 M

Reassortant from Asia 1A.3.3.2b(pd) NP, M

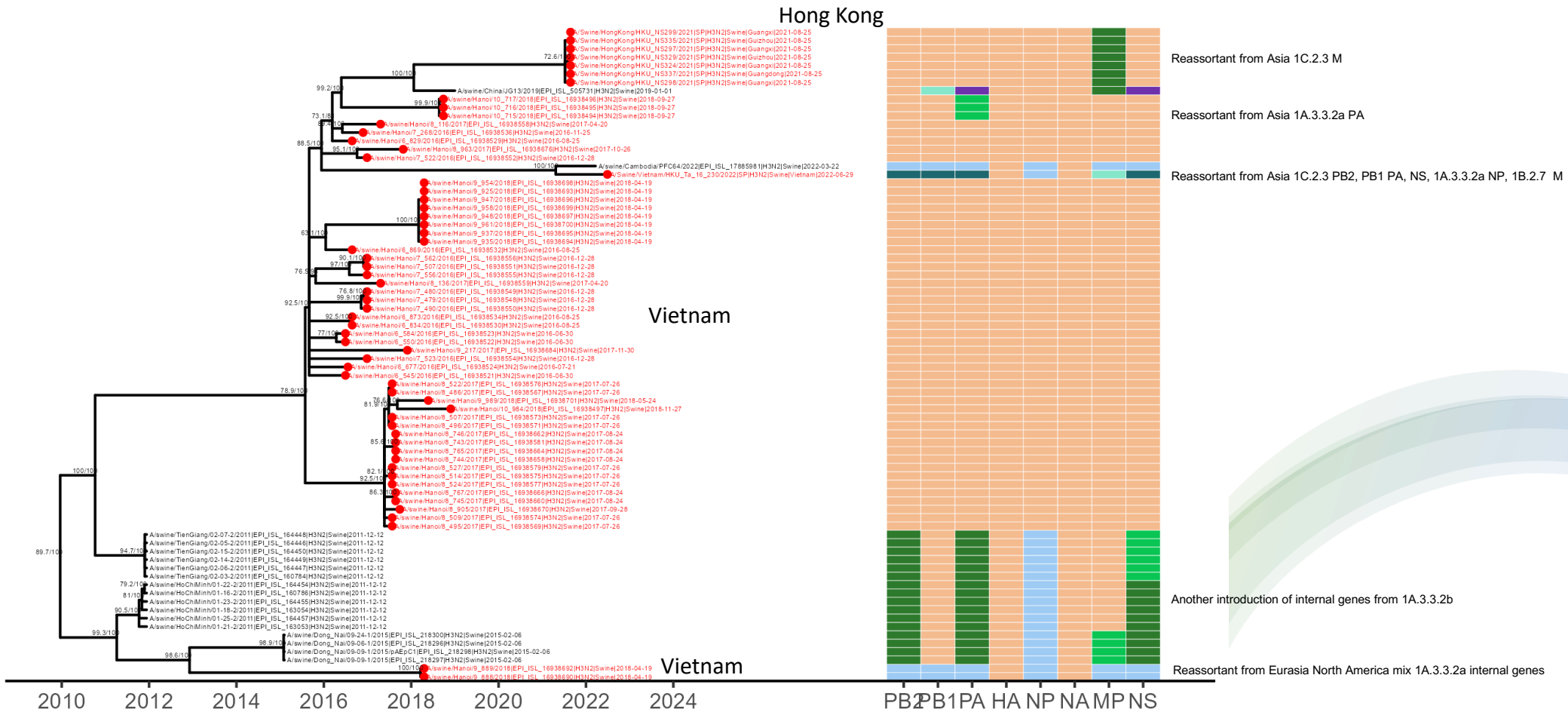
Reassortant from 1B.2.2.1 North America PB2, PB1, PA, NP, NS



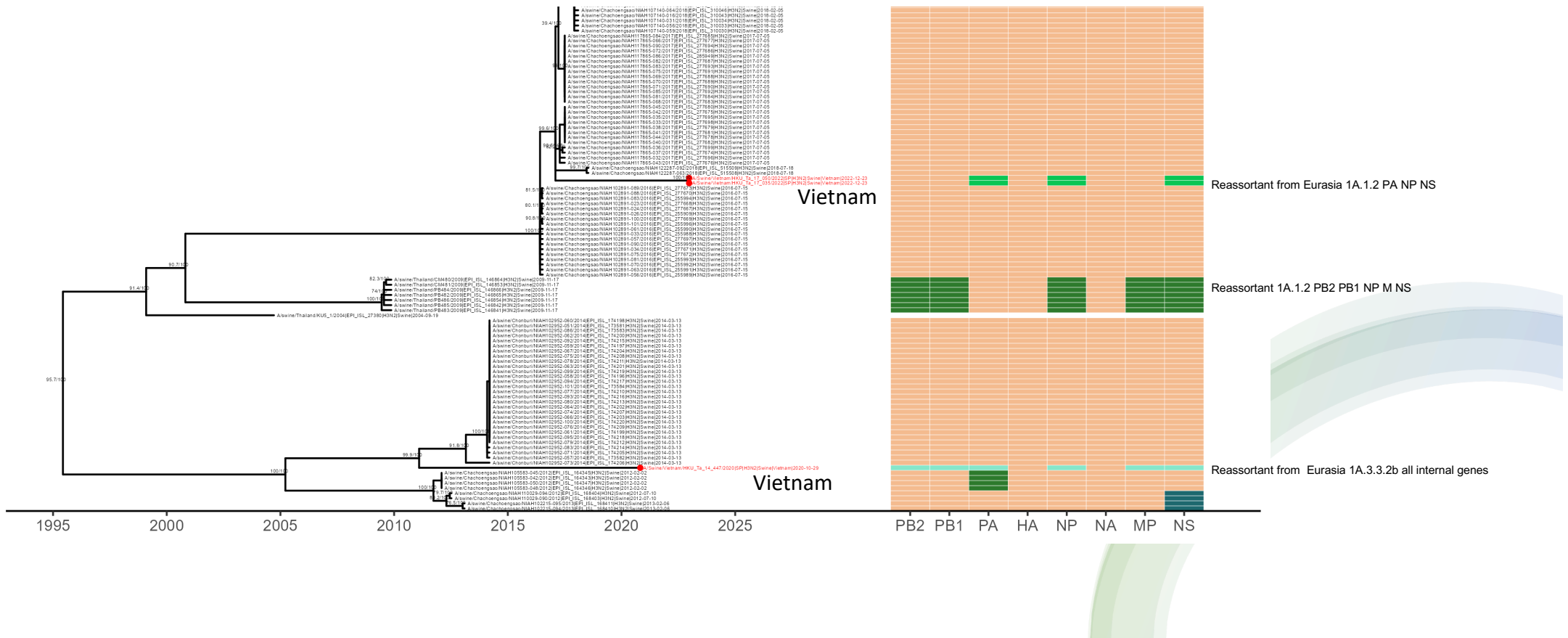
H3 swine viruses



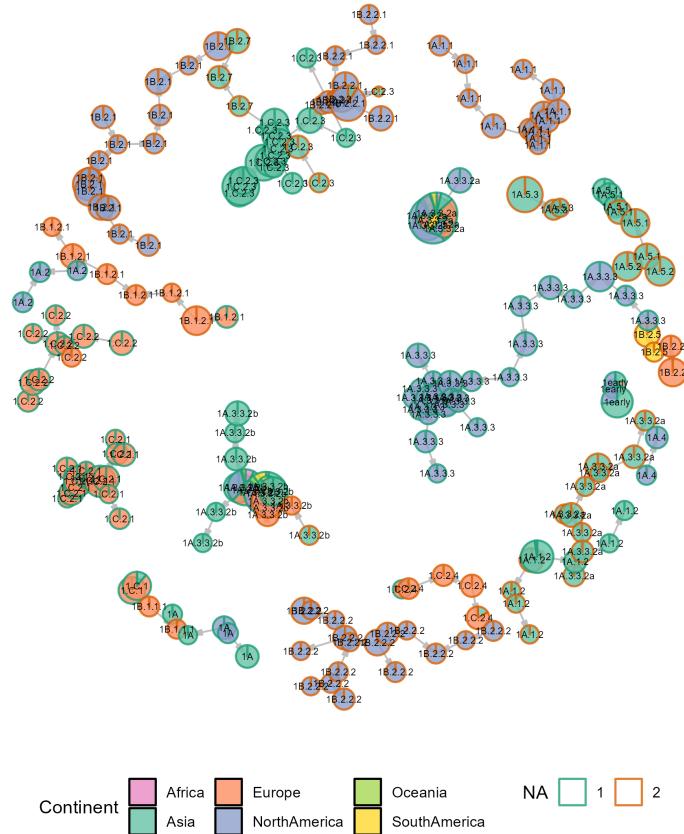
Genotype of H3 swine lineage 3.2000.4



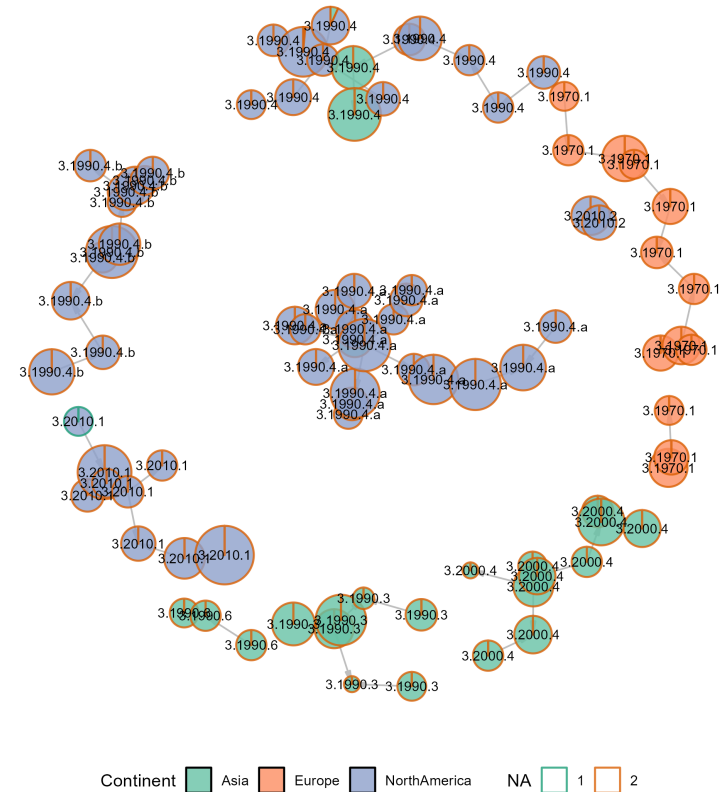
Genotype of H3 swine lineage 3.1990.3



Genotype network



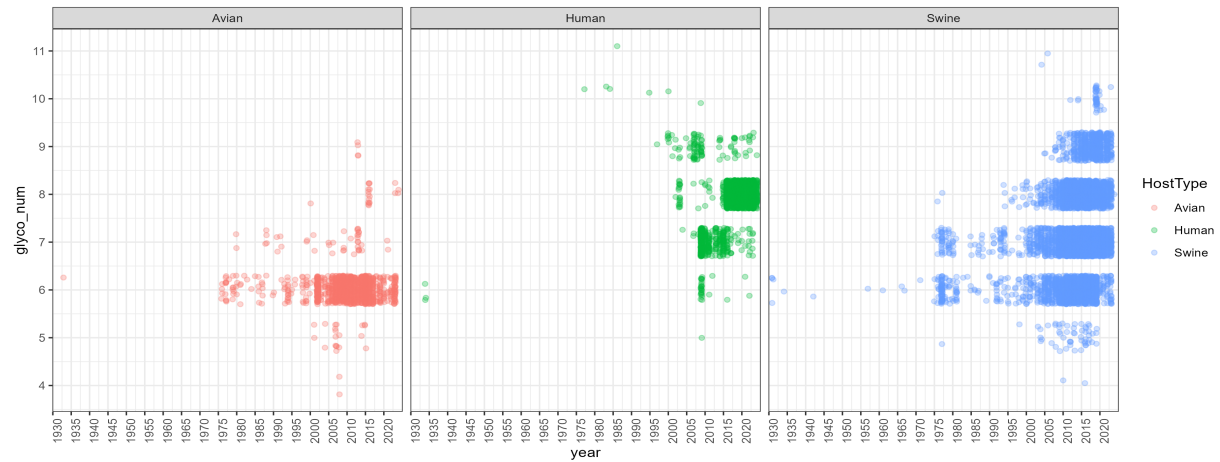
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H1 swine influenza exchanged between continents more than H3.

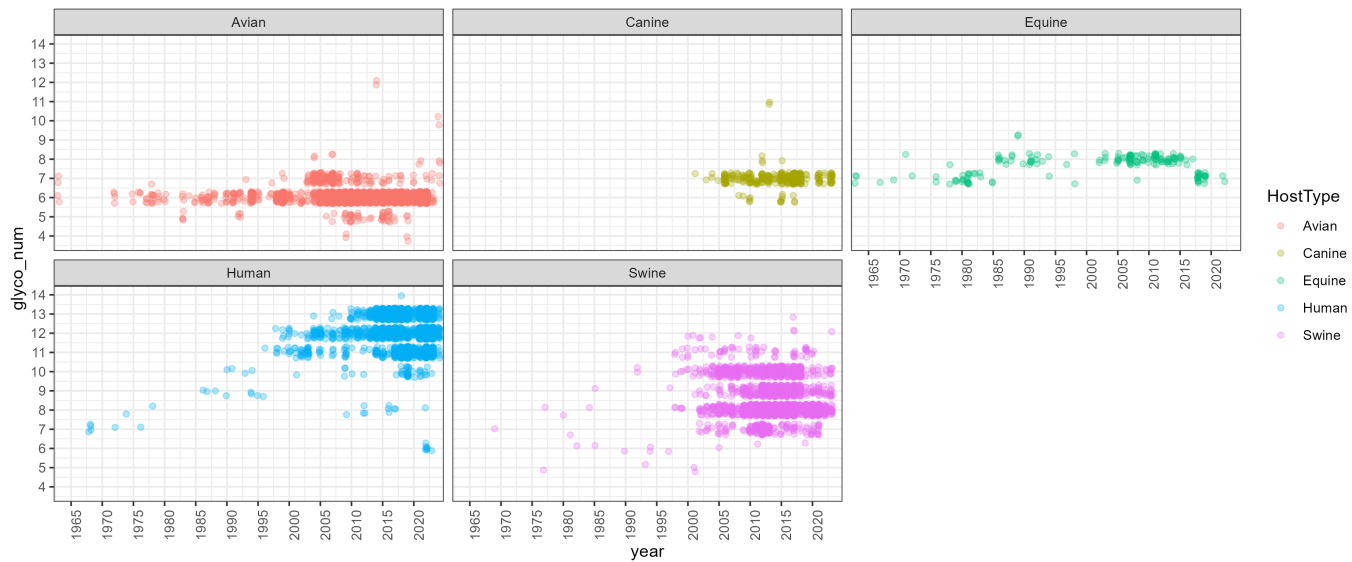
Glycosylation

H1

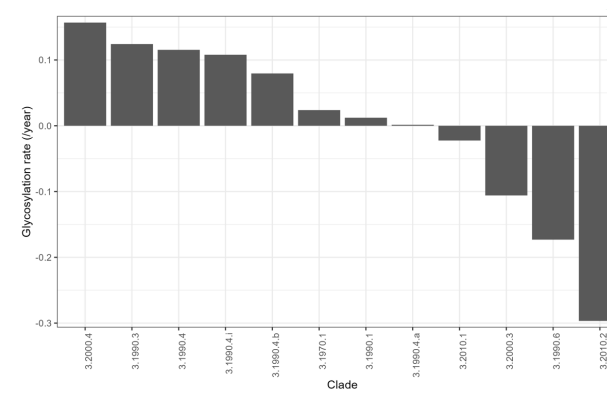
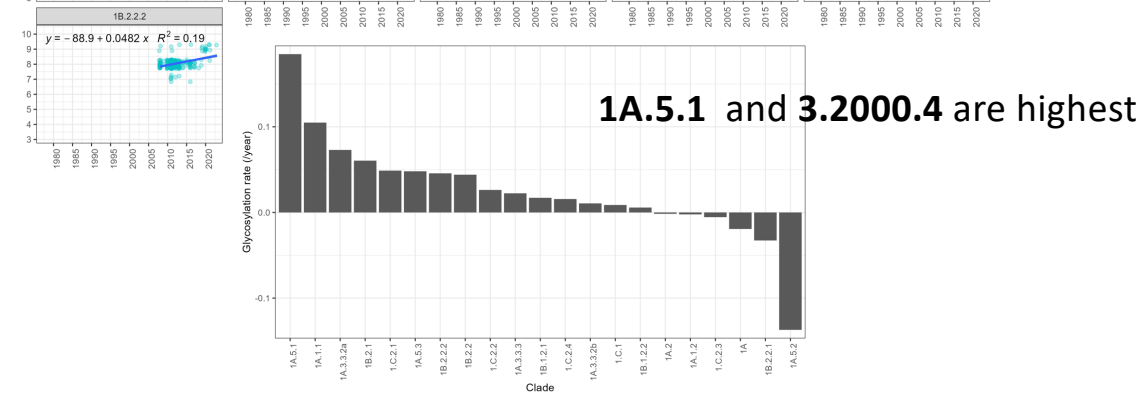
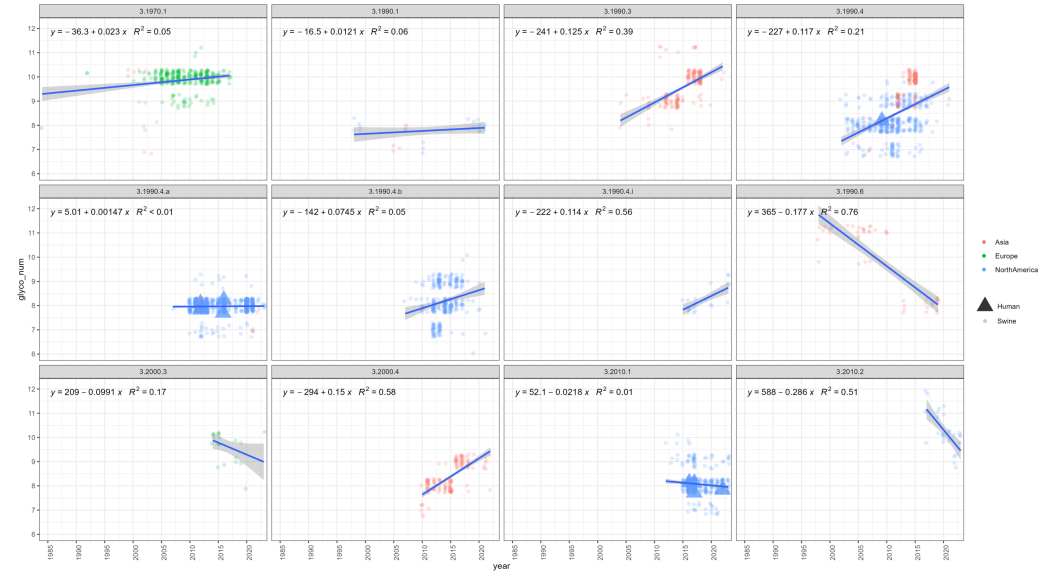
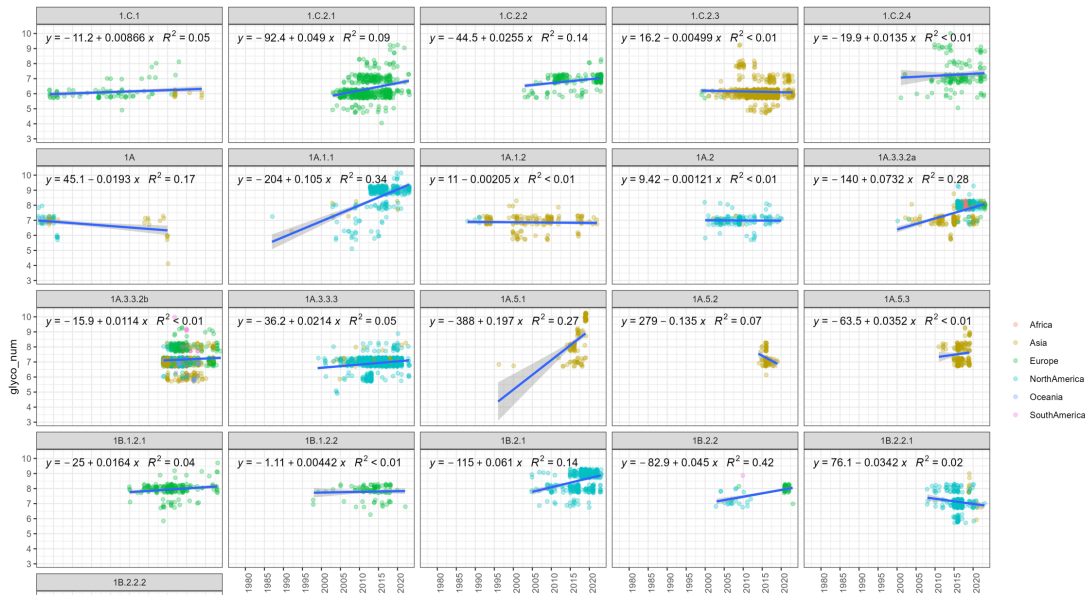


Glycosylation on swine H1 strains increased by time.

H3



H1 & H3 glycosylation of swine strains by clade



Conclusions

Hong Kong 2021-2023

- H1 – 1C.2.3
- H3 – 3.2000.4

Vietnam 2014

- H1 – 1A.3.3.2, 1B.2, 1B.2.2.1, 1C.2.3
- H3 – 3.1990.3, 3.2000.4



Acknowledgement

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 - Ngoc This Pham



Thank you