

Influenza A Virus in Swine in Brazil

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Embrapa Swine and Poultry

OFFLU SWINE INFLUENZA EXPERTS TECHNICAL MEETING
28 – 29 April 2026
WOAH Headquarters, Paris

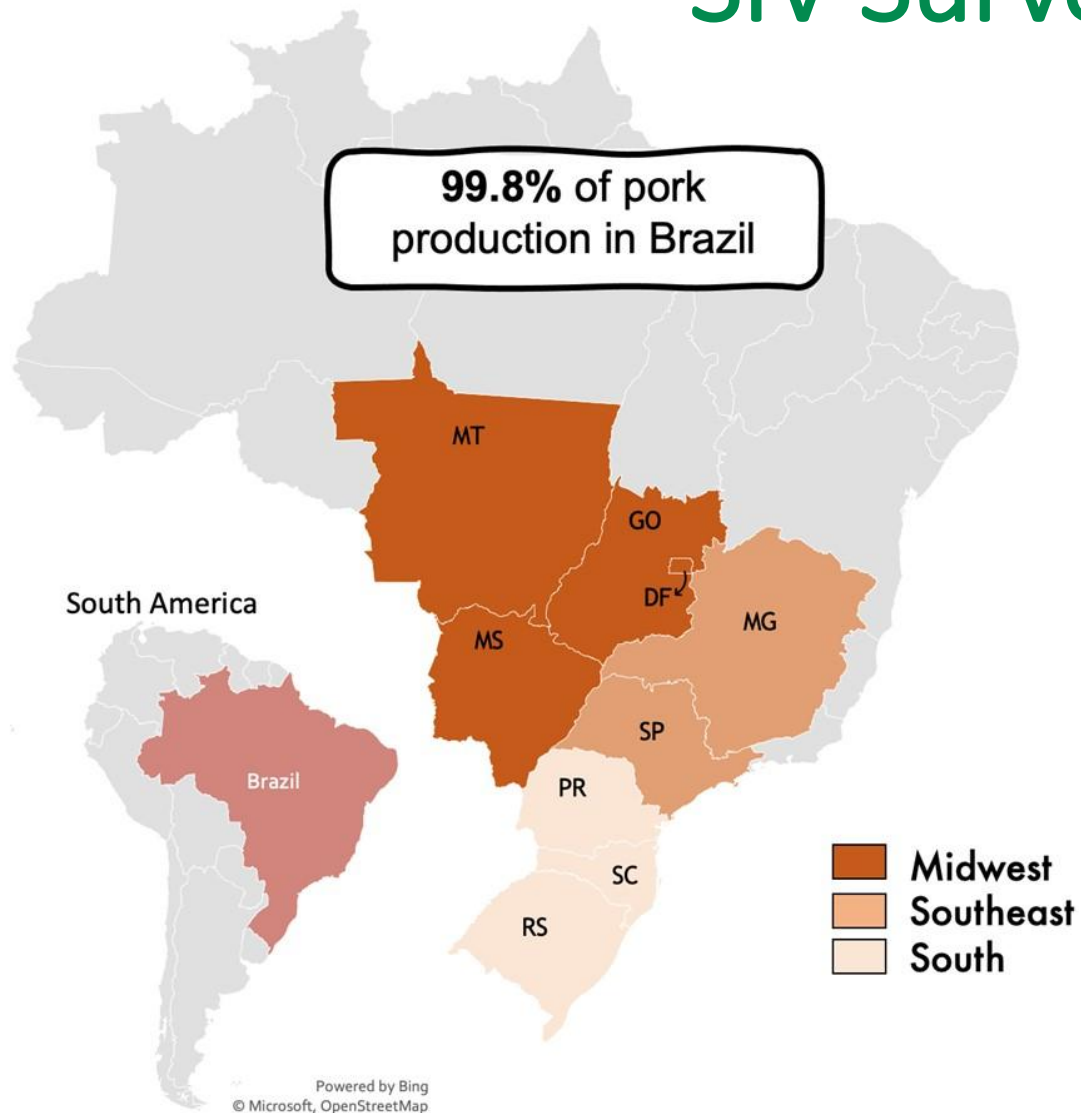


SIV Surveillance – Brazil



Suínos e Aves

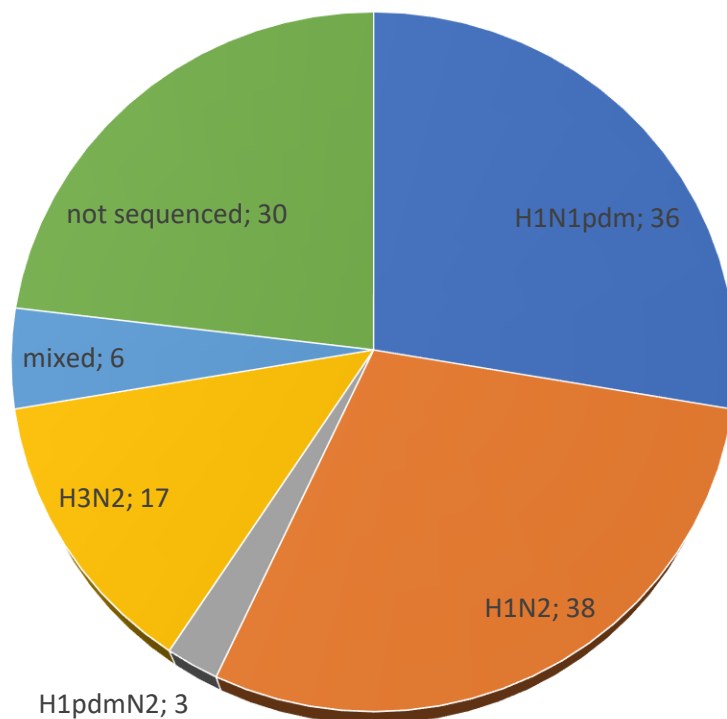
Brazilian Agricultural
Research Corporation



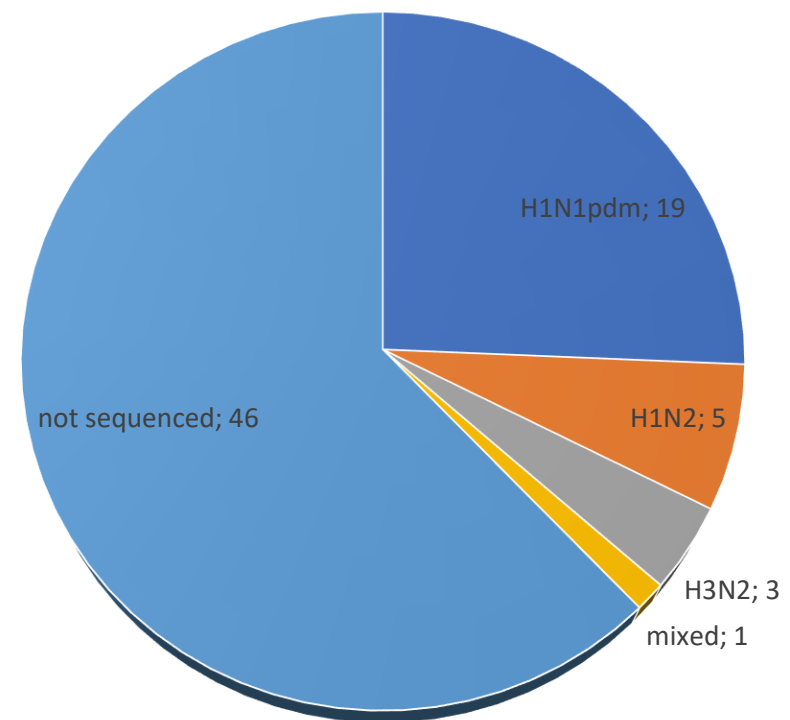
- Passive virological surveillance established in late 2009;
- Nasal swabs and lung tissue from clinically affected herds submitted by veterinary diagnostic laboratories; Sanger and/or Illumina-based NGS for subtype characterization and phylogenetic inference.
- Sampling network expanded to nine states (SC, RS, PR, SP, MG, MS, MT, GO, DF) across South, Southeast, and Midwest regions.



2024



2025

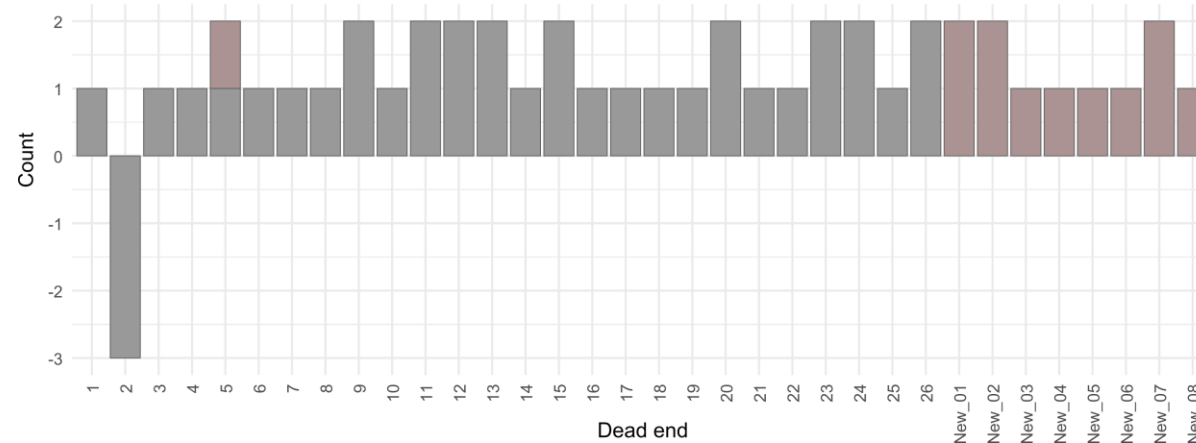
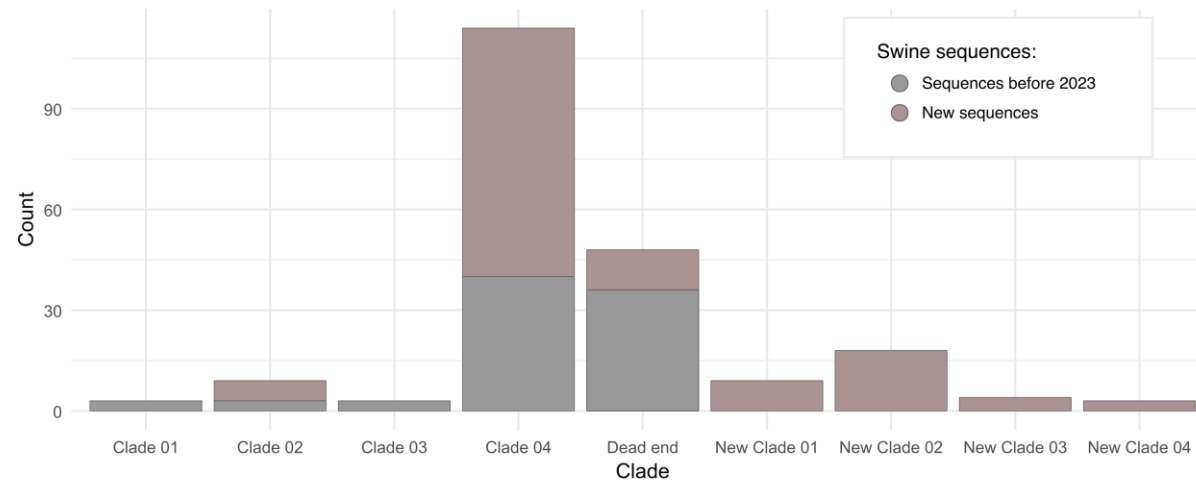
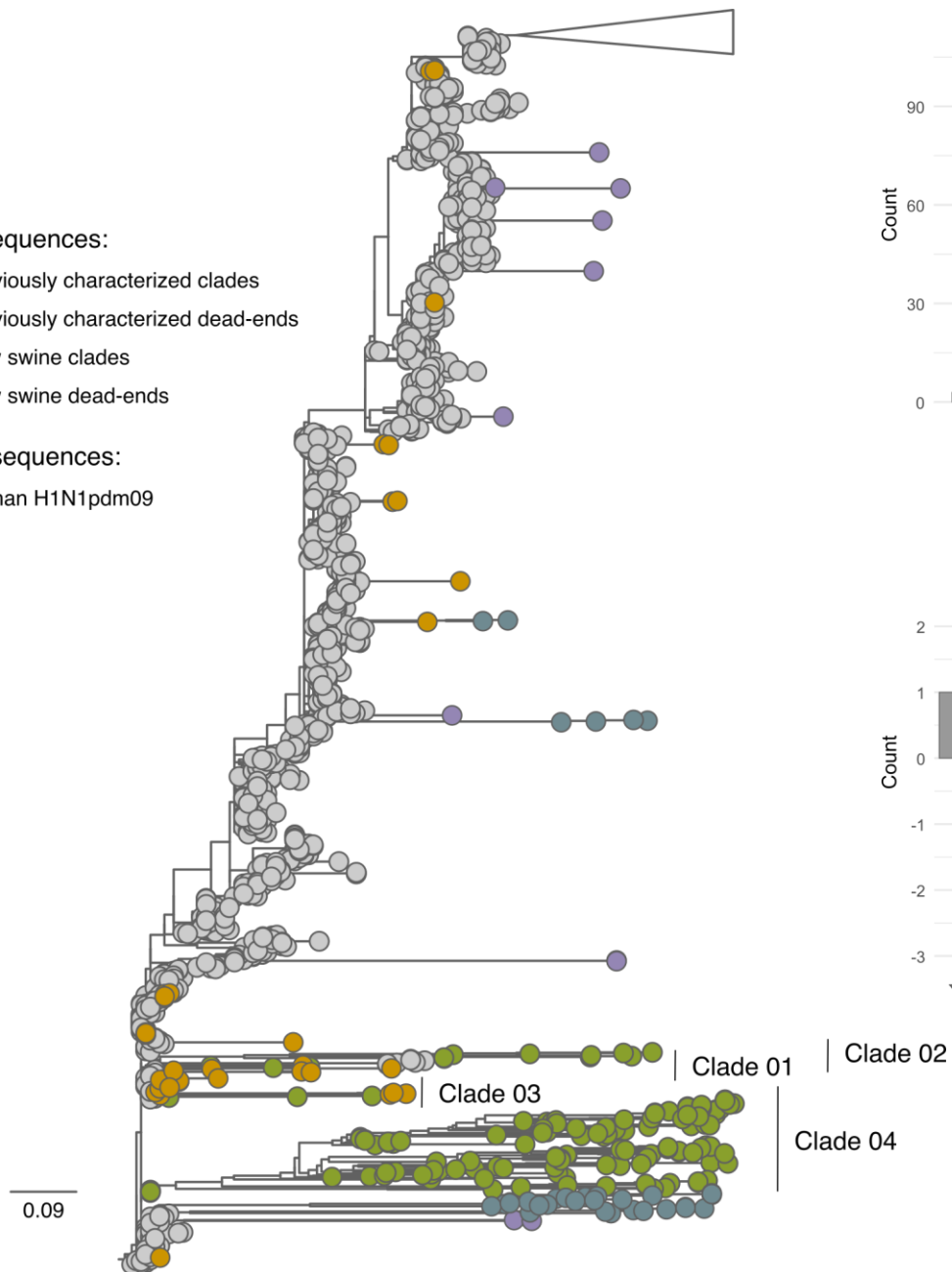


Swine sequences:

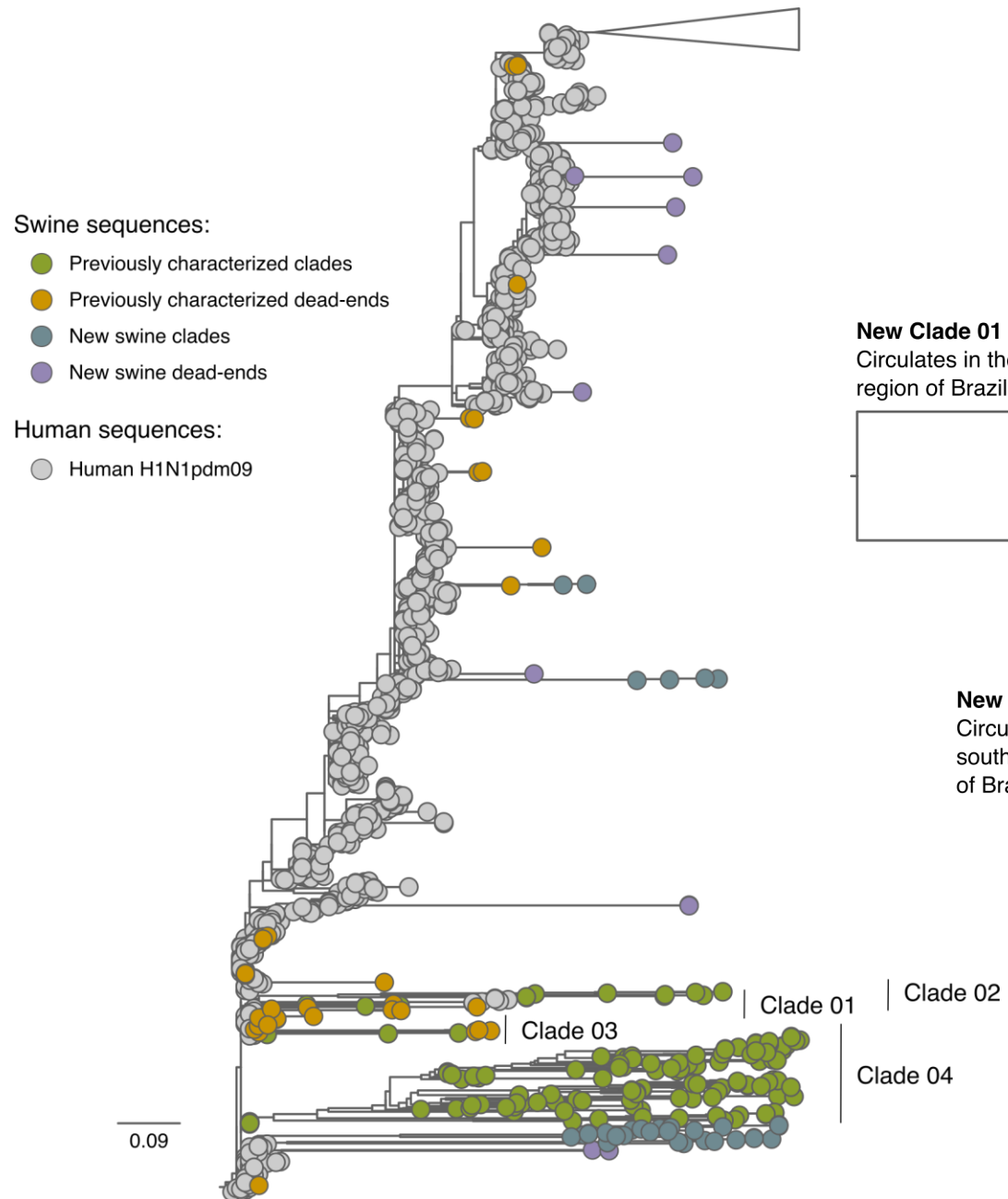
- Previously characterized clades
- Previously characterized dead-ends
- New swine clades
- New swine dead-ends

Human sequences:

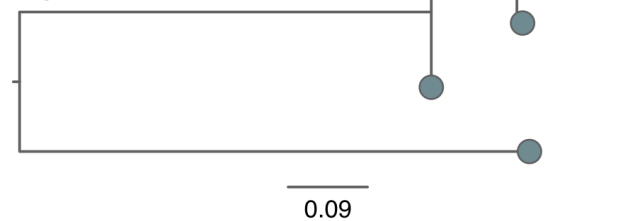
- Human H1N1pdm09



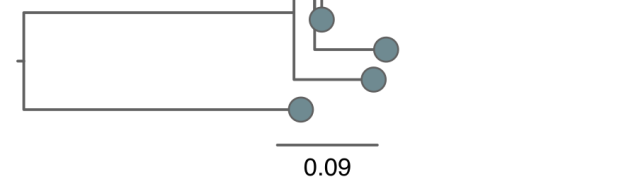
HA – H1 Clade 1A.3.3.2 (pdm09-lineage)



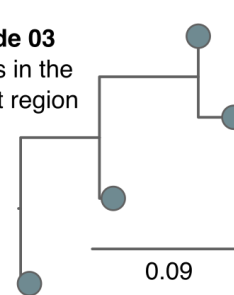
New Clade 01
Circulates in the midwest
region of Brazil



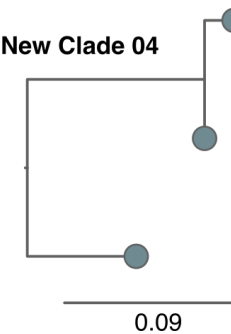
New Clade 02
Circulates in
southern Brazil



New Clade 03
Circulates in the
southeast region
of Brazil



New Clade 04



HA – H1 Clade 1A.3.3.2 (pdm09-lineage)

SIV - Brazil

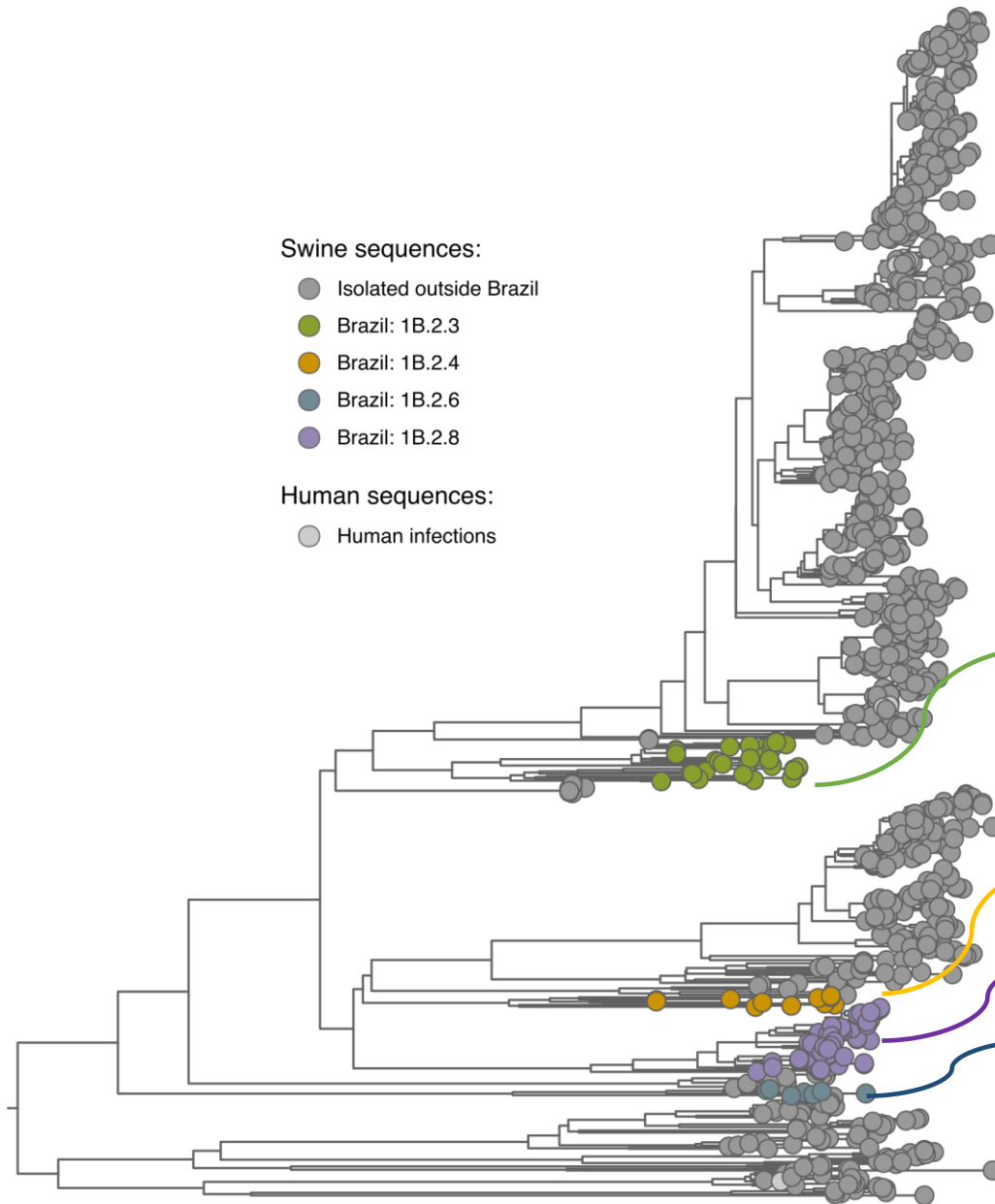
HA - H1- 1B (pre-2009 human seasonal origin)

Swine sequences:

- Isolated outside Brazil
- Brazil: 1B.2.3
- Brazil: 1B.2.4
- Brazil: 1B.2.6
- Brazil: 1B.2.8

Human sequences:

- Human infections



1B2.3 (sequences from viruses collected in 2011-2023). Estimated human-to-swine transmission: middle 2000s

1B2.4 (2011-2024). Estimated human-to-swine transmission: early 2000s

1B2.8 (2022-2024). Estimated human-to-swine transmission: not dated

1B2.6 (2019-2022). Estimated human-to-swine transmission: late 1980s

0.03

SIV - Brazil

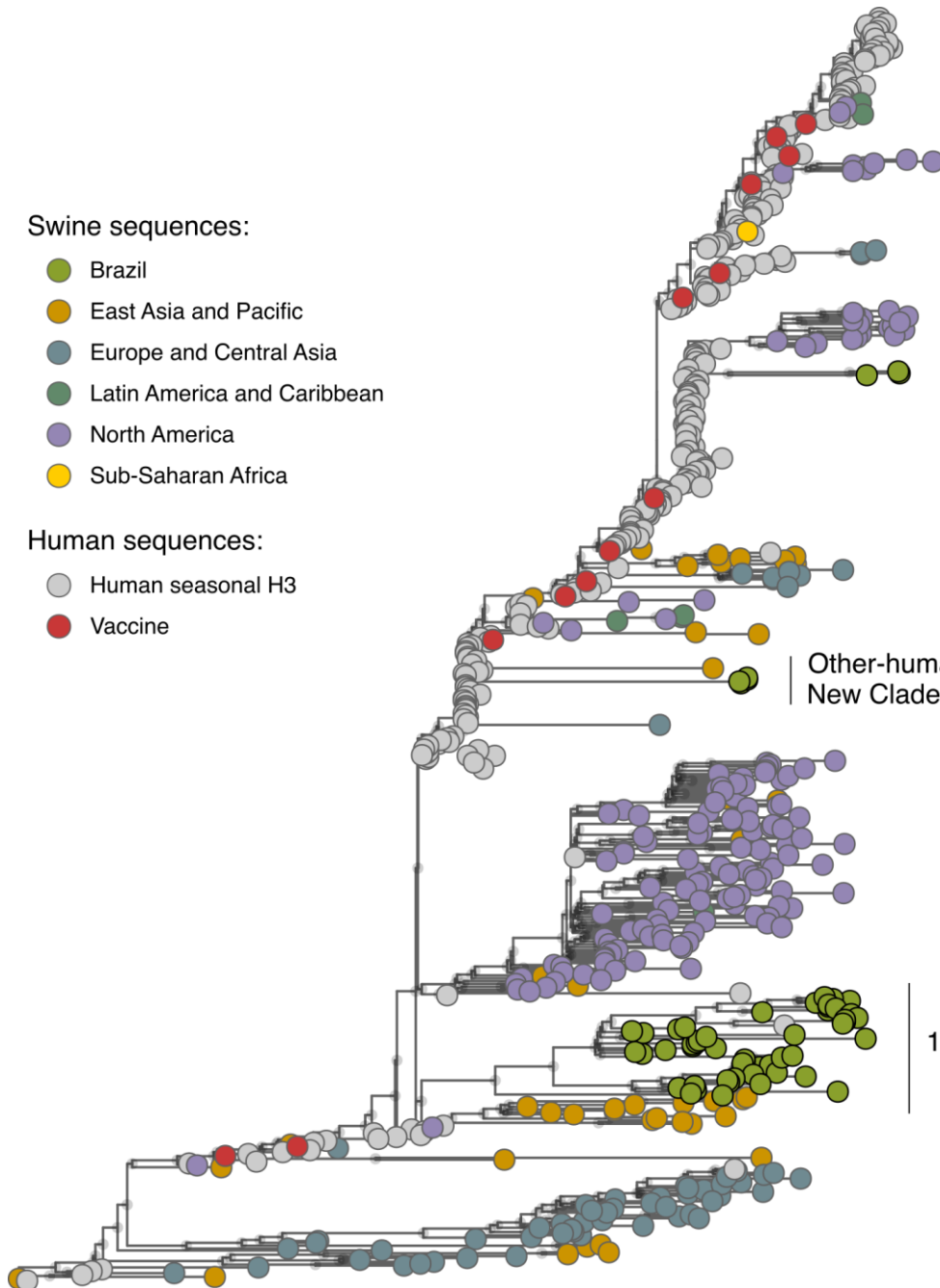
HA – H3N2

Swine sequences:

- Brazil
- East Asia and Pacific
- Europe and Central Asia
- Latin America and Caribbean
- North America
- Sub-Saharan Africa

Human sequences:

- Human seasonal H3
- Vaccine



Three sequences (2023-2024)
Human-to-swine transmission:
Dec2011-Nov2013
H3N2v (MS; Sep/2025)

Four sequences (2023)
Human-to-swine transmission: February-
October/2022

52 sequences (2011-2025), 4 subclusters
Human-to-swine transmission: late 1990s

Detection of variant viruses: 2020-2023

Article

<https://doi.org/10.1038/s41467-024-53815-z>

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Accepted: 22 October 2024

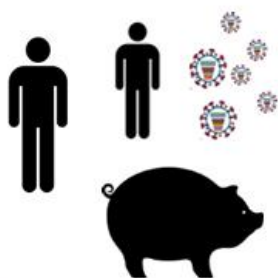
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 Check for updates

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Rejane Schaefer^{3,8} & Marilda M. Siqueira^{1,8}

Casos de detecção de Influenza A variante

Exemplo de sucesso da rede de vigilância de vírus respiratórios



5.7. Além destas amostras dos vírus influenza, citadas acima, TODOS os Lacens também deverão enviar aos laboratórios de referência:

- Todas as amostras não subtipáveis
- Todas as amostras inconclusivas
- Todas as amostras de trabalhadores/colaboradores de granjas de avicultura, suinocultura e de frigoríficos
- Todas as amostras de pessoas em contato com aves, suínos ou aves migratórias
- Todas as mostras de óbitos: indivíduos com idade entre 5 anos e < 60 anos, vacinados recentemente ou em uso de oseltamivir até dois dias depois do início dos sintomas

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Table 2 | Phylogenetic clades defined to the influenza A virus variants described in this study

Case	Viral strain	HA	NA	PB2	PB1	PA	NP	MP	NS
1	A/Parana/3625/2020 (H1N2)v	H1 1B.2.3 ^a	N2 #4 ^a	pdm #2	pdm #2	pdm #2	pdm #1	pdm #3	pdm #3
2	A/Parana/28600/2020 (H1N2)v	H1 pdm #1	N2 #4 ^a	pdm #3	pdm #3	pdm #1	pdm #3	pdm #2	pdm #2
3	A/Parana/10835/2021 (H1N1)v	H1 pdm #3	N1 pdm #1	pdm #1	pdm #1	pdm #3	pdm #2	pdm #4	pdm #1
4	A/Parana/44706/2021 (H3N2)v	H3 1990.5.1 ^{a,b}	n/o	pdm #1 ^b	pdm #1 ^b	pdm #3 ^b	pdm #2 ^b	pdm #1 ^b	pdm #1 ^b
5	A/Parana/51528/2021 (H3N2)v	H3 1990.5.1 ^{a,b}	N2 #2 ^a	pdm #1 ^b	pdm #1 ^b	pdm #3 ^b	pdm #2 ^b	pdm #1 ^b	pdm #1 ^b
6	A/Parana/20675/2022 (H1N1)v	H1 pdm #2	N1 pdm #1	pdm #1	pdm #1	pdm #3	pdm #2	pdm #4	pdm #1
7	A/Parana/5210/2023 (H1)v	H1 pdm #2	n/o	n/o	n/o	n/o	n/o	pdm #4	n/o
8	A/Parana/13897/2023 (H1N1)v	H1 pdm #2	N1 pdm #1	pdm #1	pdm #1	pdm #3	pdm #2	pdm #4	pdm #1

n/o = not obtained.

^a genetic clade nomenclature defined for swine influenza A viruses.

^b identical sequences.

H1 pdm, 1A.3.3.2 lineage of H1 swine viruses.

H1 1B, human seasonal lineage of H1 swine influenza viruses.

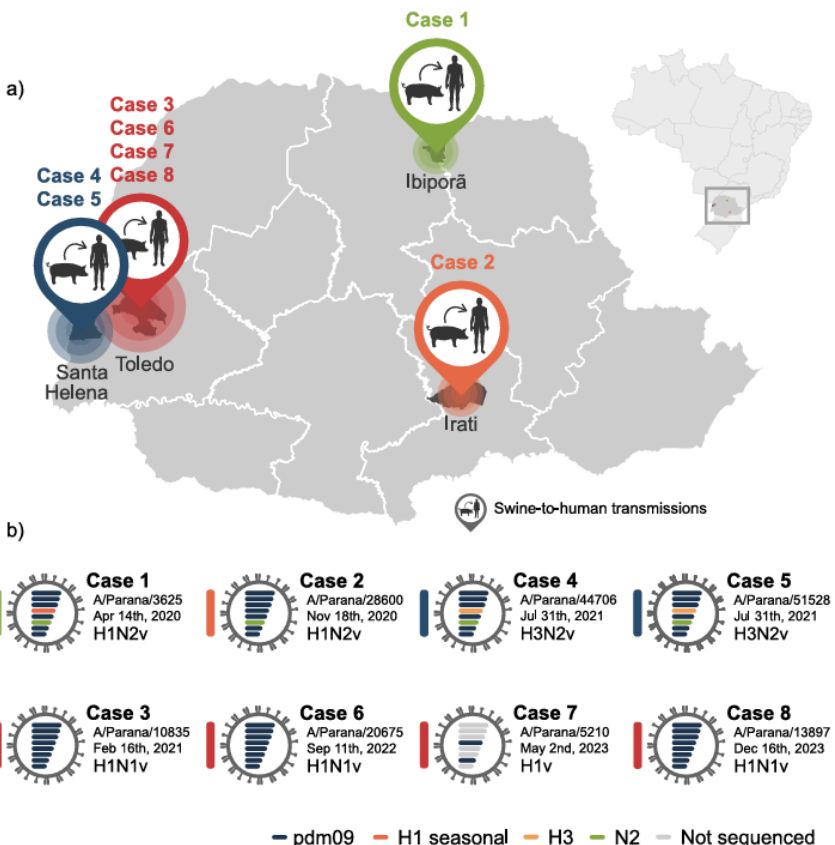


Fig. 1 | Geographic and sample information of eight influenza A variant viruses collected from human infections in Brazil. **a** Locations in the State of Paraná, Brazil, where cases were detected. Concentric circles depict the proportion of cases identified in each location. **b** Genetic composition of viruses identified in the swine-to-human transmissions. The vertical bars correspond to the colors of the locations in (a). Horizontal bars identify the eight genomic segments of IAVs: (i) PB2, (ii) PB1, (iii) PA, (iv) HA, (v) NP, (vi) NA, (vii) MP, and (viii) NS. The figure key shows the subtype of each segment.

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Final notes

- The extensive genetic diversity observed in swIAV in Brazil was mainly influenced by successful incursions of human seasonal viruses into pigs.
- Related to IAVs that circulated in humans decades ago.
- IAVs derived from these earlier incursions have reassorted with H1N1pdm09 and continue to circulate in swine.
- 4 genetic clades of H1 viruses of the 1B lineage (1B.2.3, 1B.2.4, 1B.2.6, 1B2.8).
- 3 genetic clades of H3 viruses (1990.5, 2010.4, Other-human 2020).
- Not detected in any other country.
- Continued IAV surveillance is critical to detect novel strains and select representative vaccine strains to better control IAV in swine and to evaluate the risk that swine viruses pose to humans.

Acknowledgements



Thank you

