

FLUZOVA PROJECT

Swine influenza surveillance with
emphasis on vaccine strain selection
and zoonotic risk

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OFFLU SWINE INFLUENZA EXPERTS TECHNICAL MEETING

28 – 29 April 2026

WOAH Headquarters, Paris



GHENT
UNIVERSITY



Health
Food Chain Safety
Environment

Summary of previous swlAV studies in Belgium (2014-2021)

- Subtype diversity:

H1N1, H1N2, and H3N2 were detected, with H1N1 consistently dominant across sampling periods

- Lineage distribution:

H1 lineages: avian-like 1C (predominant), human-like 1B, and pandemic-derived 1A

H3 lineages: human-like H3

- Clade representation:

H1: 1C.2.1, 1C.2.2, 1B.1.2.1, 1A.3.3.2

**SCIENTIFIC
REPORTS**
nature research

Genetic and antigenic evolution of H1 swine influenza A viruses isolated in Belgium and the Netherlands from 2014 through 2019

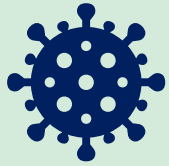
[Sharon Chepkwony](#)¹, [Anna Parys](#)¹, [Elien Vandoorn](#)¹, [Wojciech Stadejek](#)¹, [Jiexiong Xie](#)¹, [Jacqueline King](#)², [Annika Graaf](#)², [Anne Pohlmann](#)², [Martin Beer](#)², [Timm Harder](#)², [Kristien Van Reeth](#)^{1,✉}

EMERGING INFECTIOUS DISEASES[®]

Surveillance and Genomic Characterization of Influenza A and D Viruses in Swine, Belgium and the Netherlands, 2019–2021

[Anna Parys](#)^{1,2}, [Nick Vereecke](#)^{1,2}, [Elien Vandoorn](#)^{1,2}, [Sebastiaan Theuns](#)^{1,2}, [Kristien Van Reeth](#)^{1,2,✉}

Objectives



Surveillance and swIAV isolation (2024-2025)

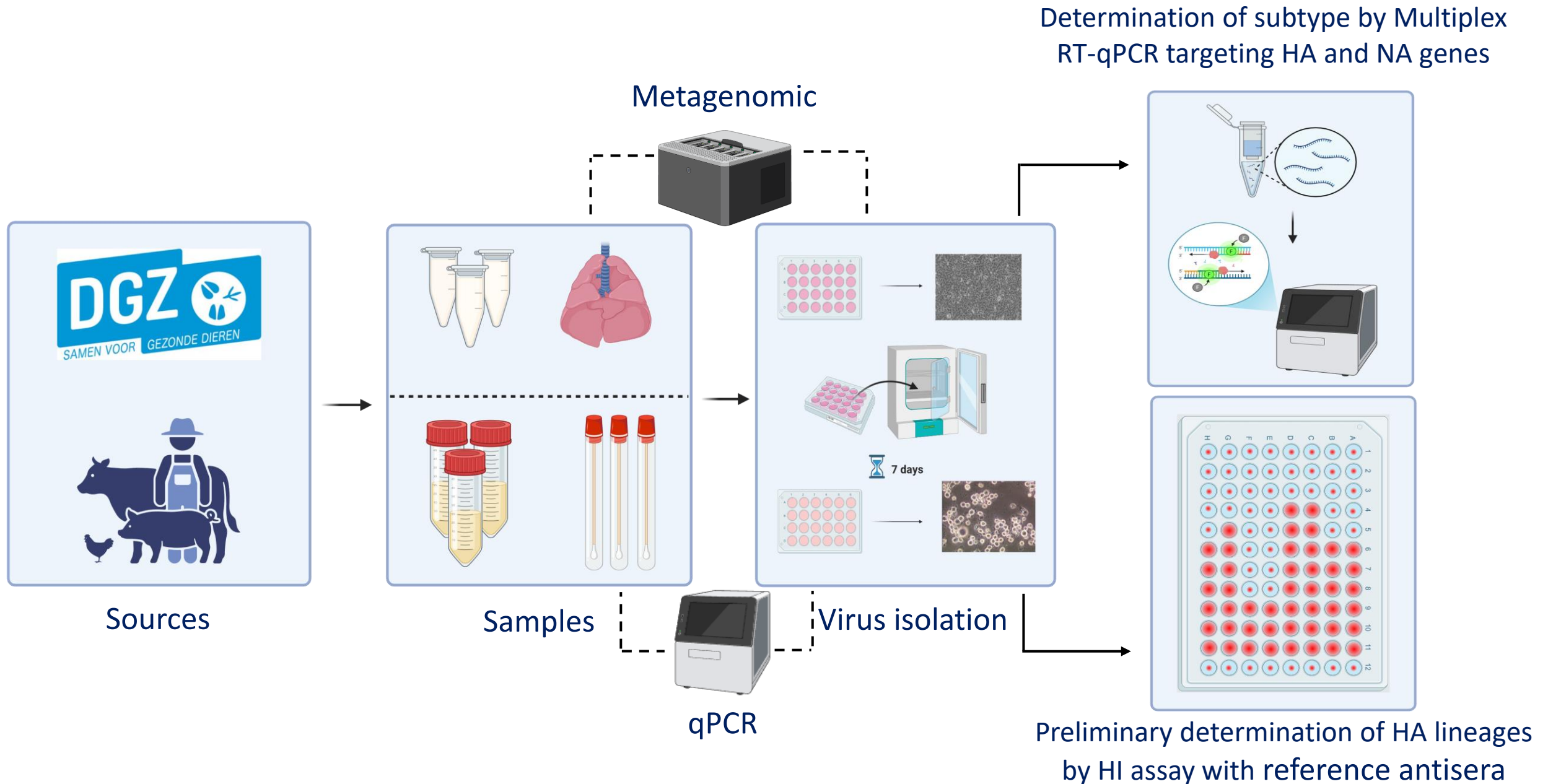


Genetic characterization of isolates

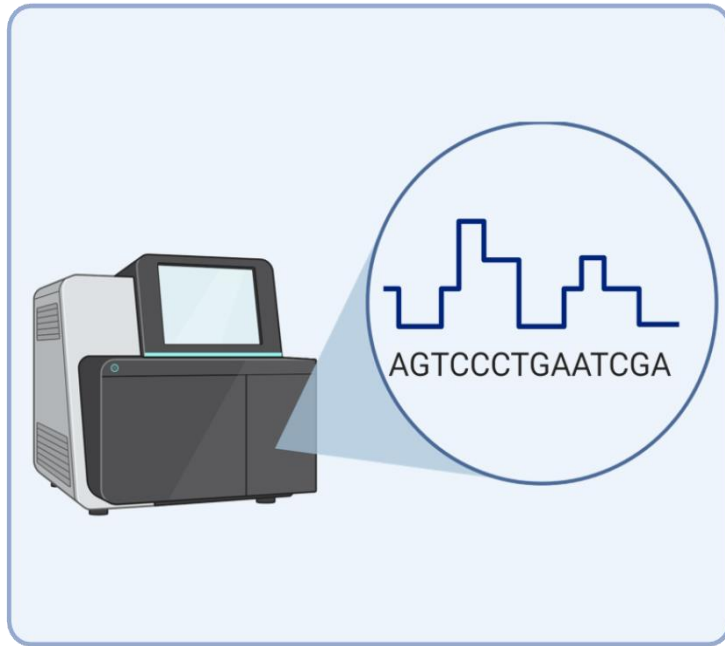


Antigenic characterization of the HA protein

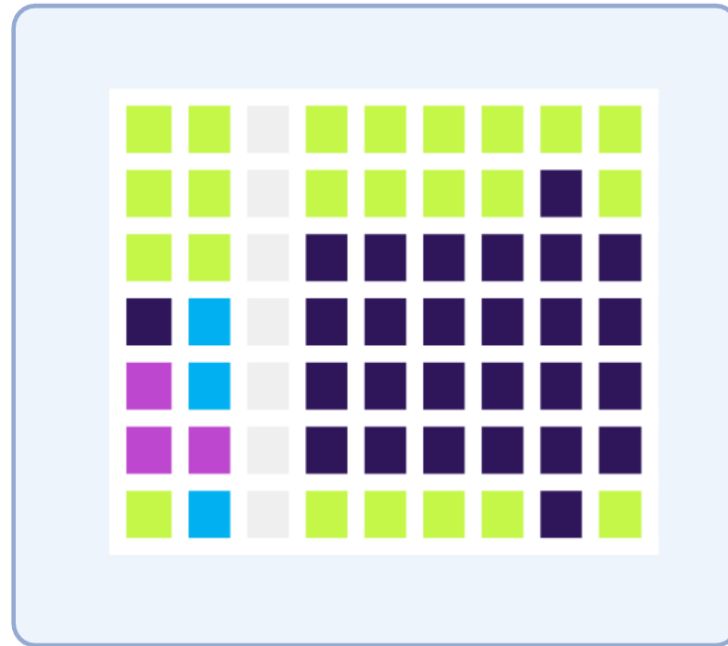
Methods for surveillance



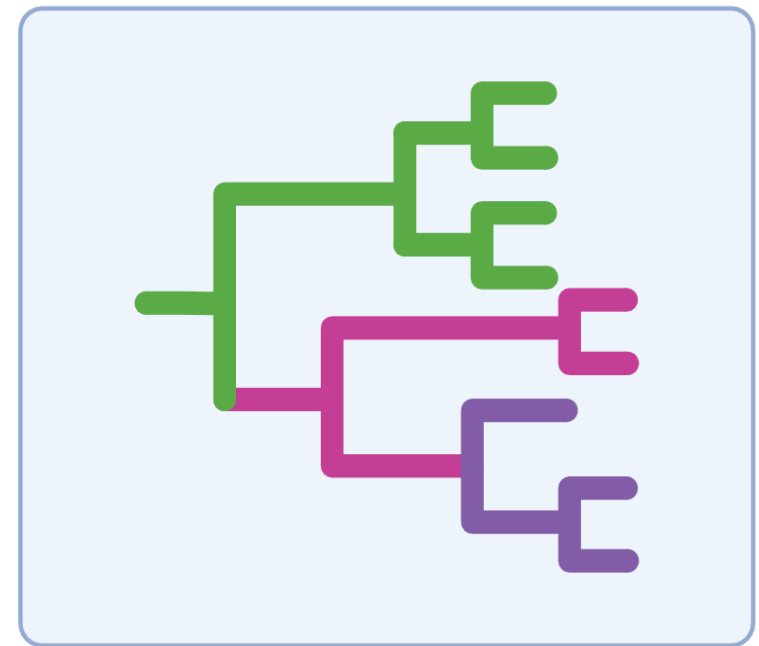
Methods for genetic characterization



Whole genome sequencing



Genetic constellation
determination



Phylogenetic analysis

Method for antigenic characterization of the HA protein

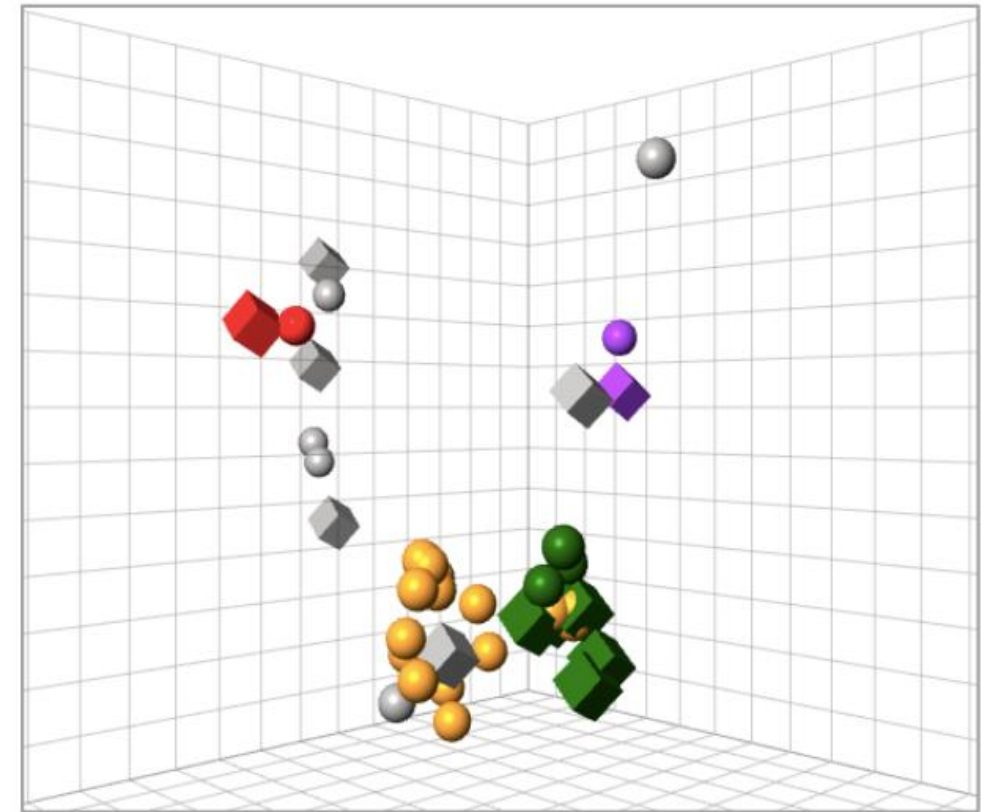
Cross-HI assay with
reference strains for HA characterization

			
1A.3.3.2	2019	1A.1.1	2015
1A.3.3.2	2023	1A.3.3.3	2014
1B.1.2.1	1999	1B.2.1	2016
1B.2.2.2	2009	1B.2.2.2	2010
1B.1.2.1	2012		
1B.1.2.1	2022		
1B.1.2.1	2024		
1C.1	1983	1B.2	1986
1C.2	1998	1B.2	1999
1C.2.1	2005	1B.2	2007
1C.2.1	2010	1A.3.3.2	2009
1C.2.2	2021	1A.3.3.2	2018
1C.2.2	2024	1A.3.3.2	2022



Swine and human vaccine strains

Antigenic Cartography



Results: Overview of swlAV subtypes and lineages isolated 2024-2025

Subtype	HA/NA Lineage	Number of isolates per year		Total
		2024	2025	
H1N1	EU H1avN1av	12	19	31
H1N2	EU H1huN2hu	10	4	14
	EU H1avN2hu	1	2	3
	H1pdm09N2hu	4	3	7
Total number of isolates		27	28	55
Total number of samples received		175	133	308

Results: Genetic constellation of swlAV isolated 2024-2025

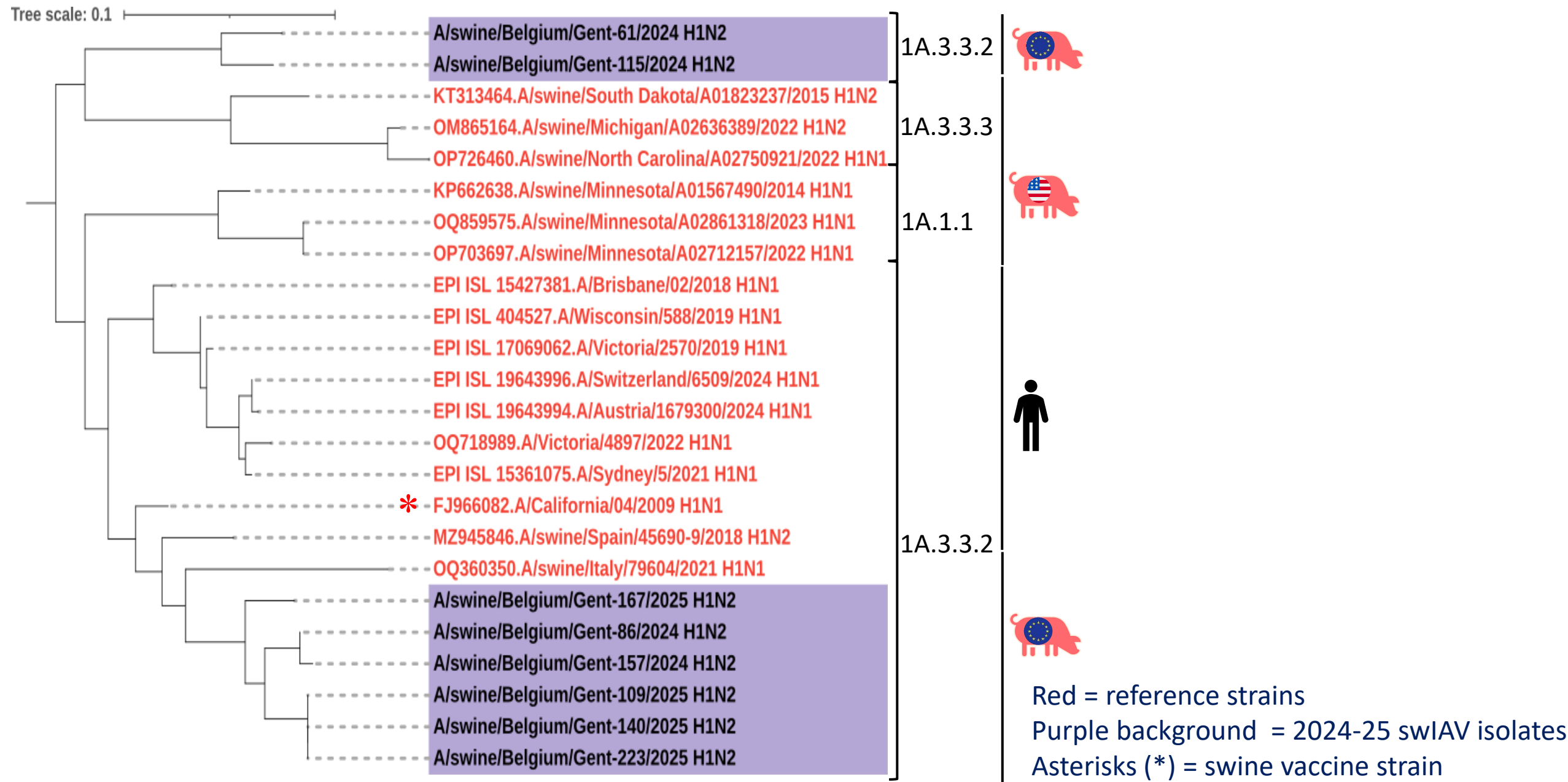
Subtype	Surface genes		Internal genes						Number of isolates	
	HA	NA	PB2	PB1	PA	NP	M	NS	2024	2025
H1N1									7	2
									1	18
									2*	0
H1N2									2	0
									5	3
									2*	2
									1*	1
									3	4
									1*	0
									1*	0
									0	2

HA and NA origin:

- European avian-like H1N1
- 2009 pandemic H1N1
- Human-like H3N2
- European human-like H1N2

* New genotype in Belgium

Results: Phylogenetic tree of HA1/1A lineage

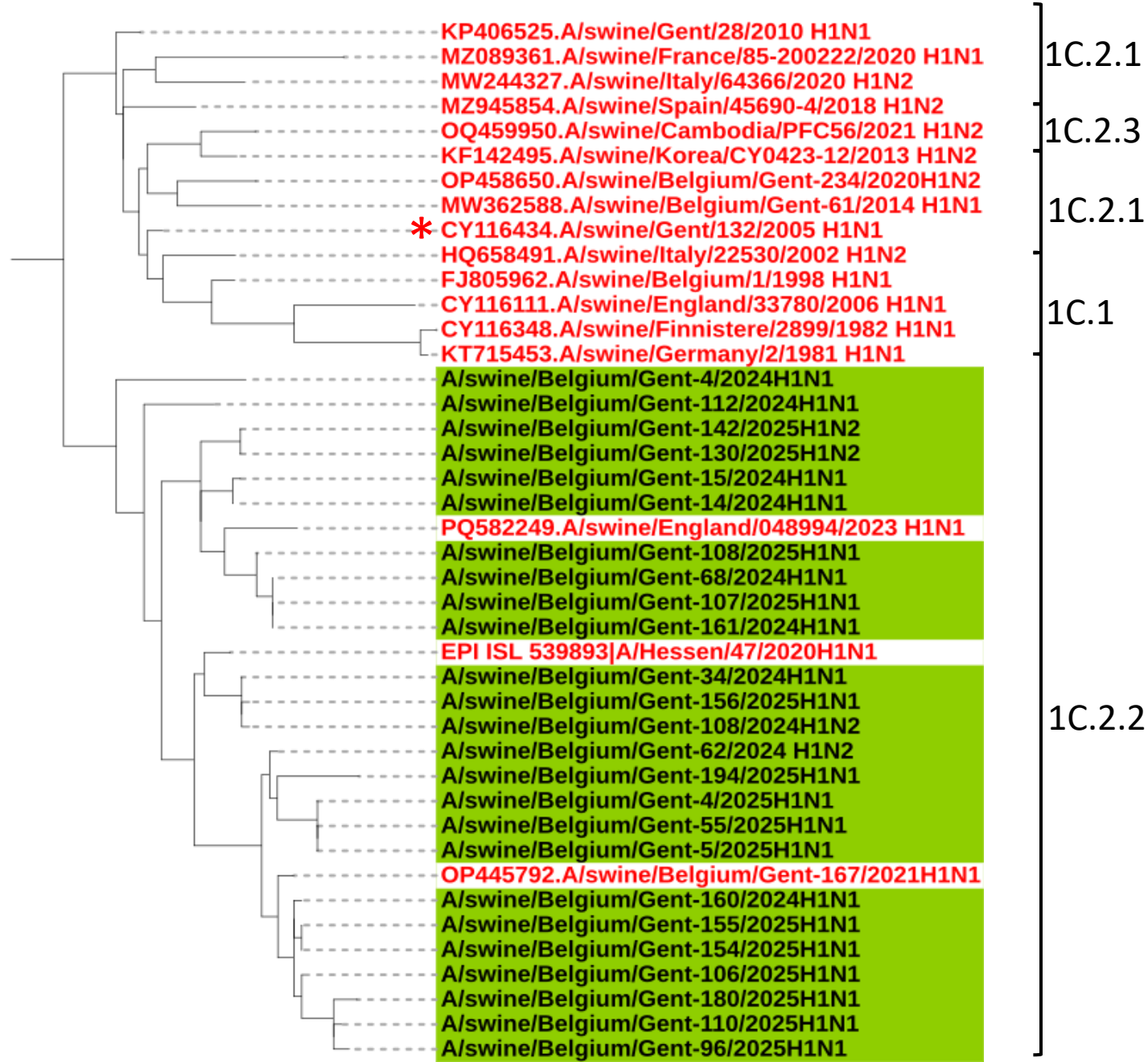


Results: Phylogenetic tree of HA1/1B lineage



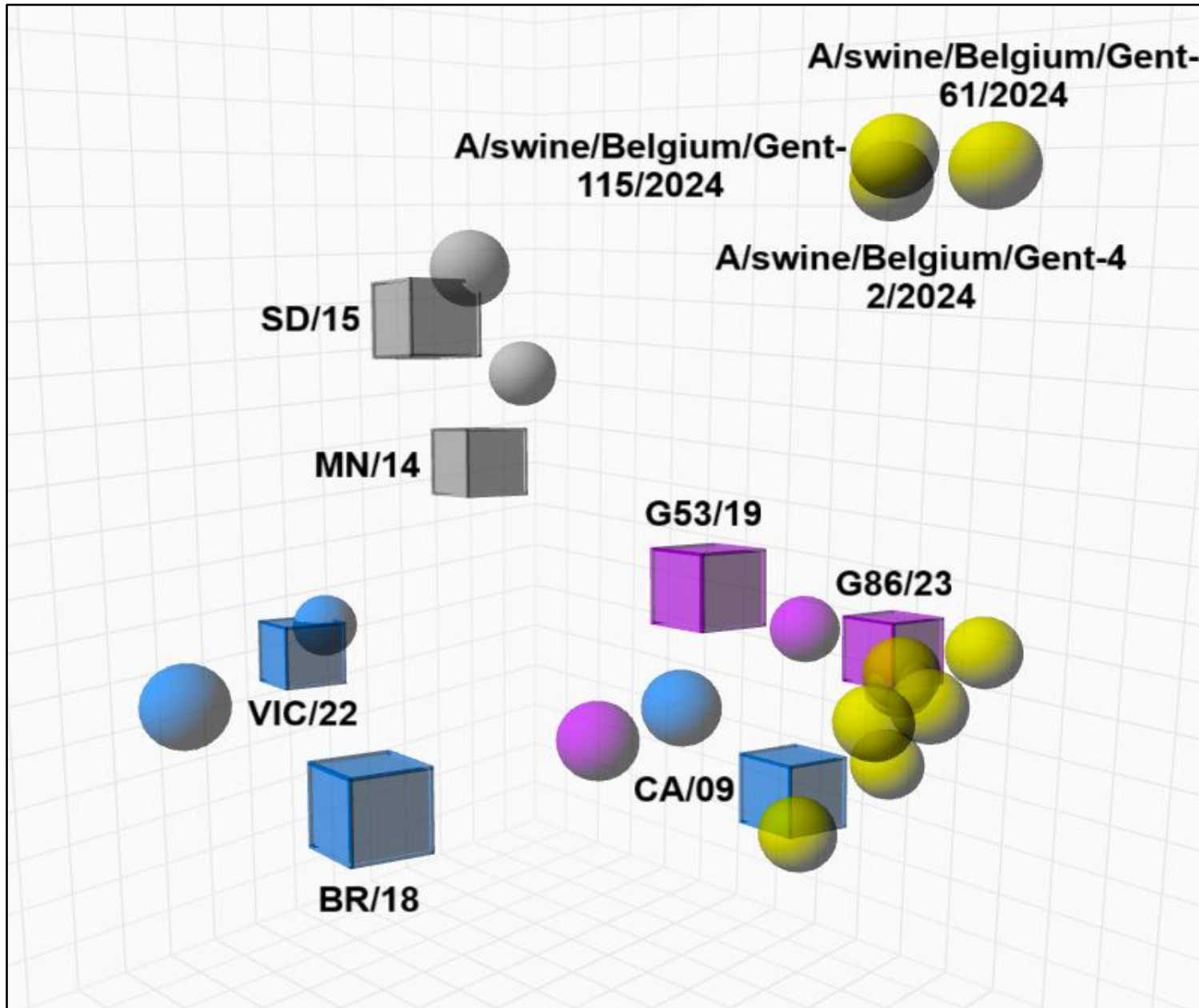
Results: Phylogenetic tree of HA1/1C lineage

Tree scale: 0.1



Red = reference strains
Green background = 2024-25 swIAV isolates
Asterisks (*) = swine vaccine strain

Results: Antigenic characterization of 1A.3.3.2 clade



1A.3.3.2 2024-25 swlAV

1A.3.3.2 European swlAV

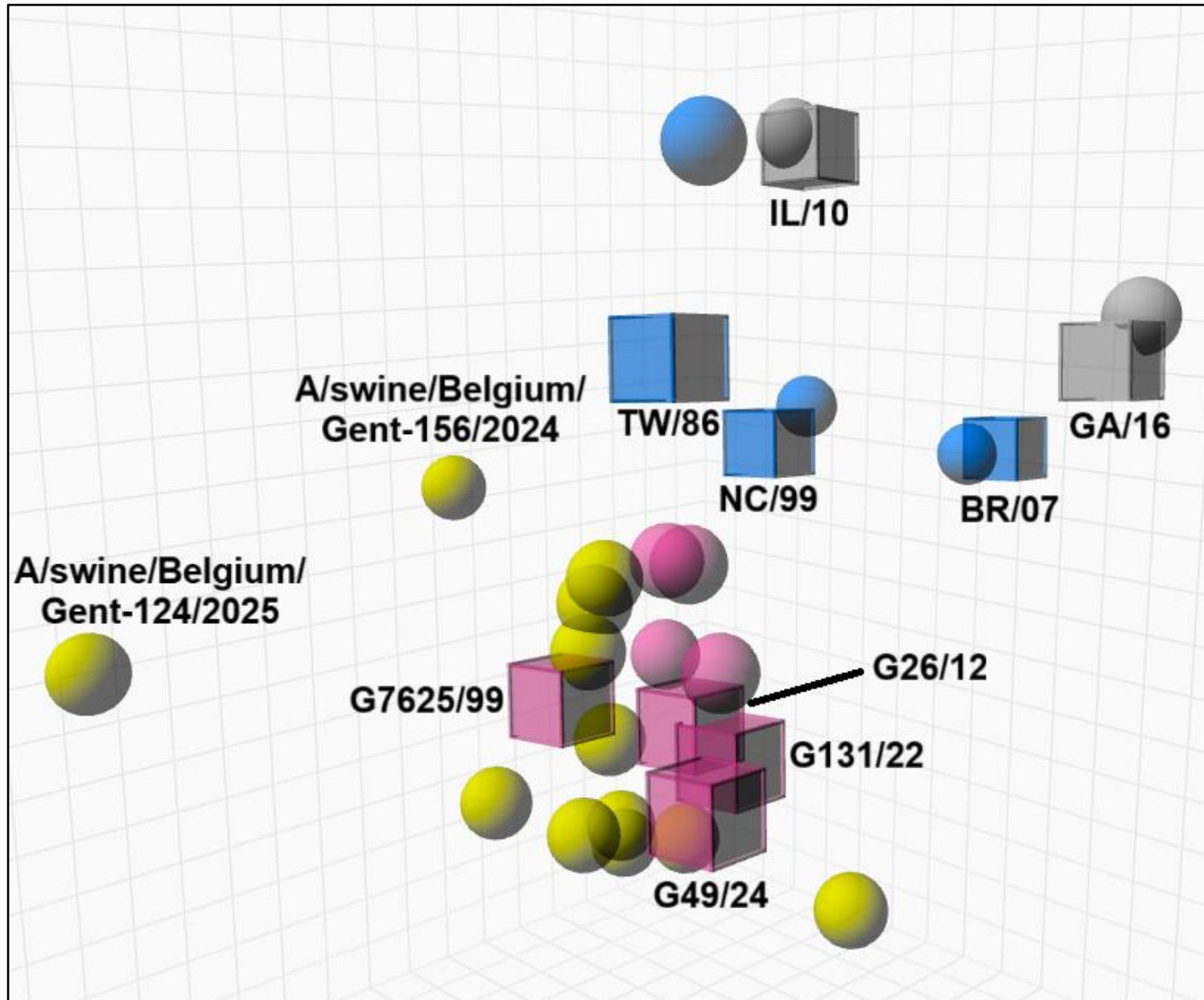
1A.3.3.2 human swlAV

1A.1.1 and 1A.3.3.3 US swlAV

○ Virus

□ Antisera

Results: Antigenic characterization of 1B.1.2.1 clade



1B.1.2.1 2024-25 swIAV

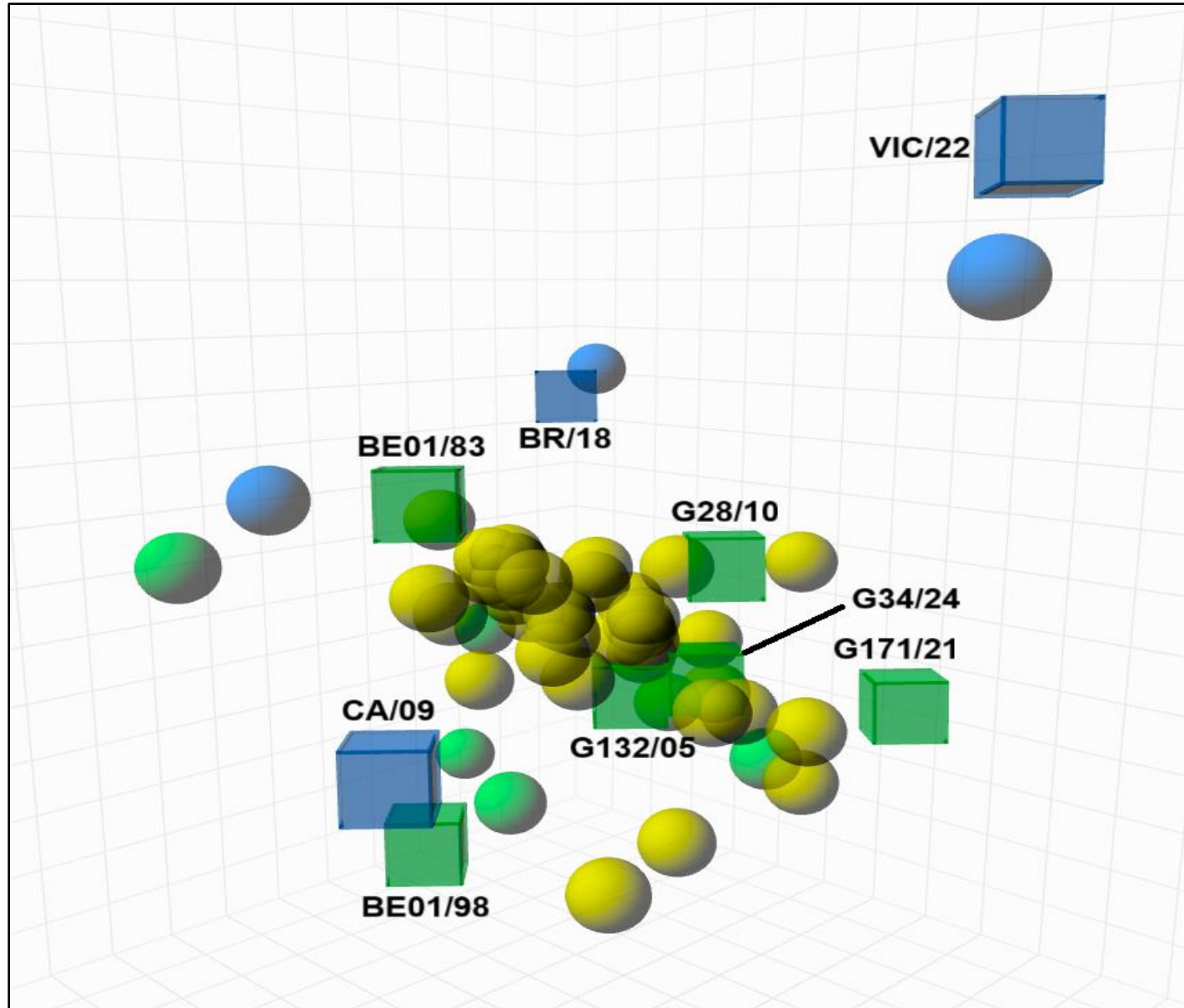
1B.1.2.1 EU swIAV

1B.2 human strains

1B.2.1 and 1B.2.2.2 US swIAV

○ Virus □ Antisera

Results: Antigenic characterization of 1C.2.2 clade



1C.2.2 2024-25 swIAV

1C.1, 1C.2 , 1C.2.1 and 1C.2.2
EU swIAV

1A.3.3.2 human strains



Virus



Antisera

Conclusion

- EU H1avN1av was the predominant subtype (56%), followed by H1huN2 (25%) and H1pdm09N2 (12%), consistent with earlier Belgian surveillance.
- H3N2 was not detected in 2024–25, continuing its long-term decline.
- Three H1 clades (1A.3.3.2, 1B.1.2.1, 1C.2.2) co-circulate in Belgium, with the dominant genotype carrying an M gene from the 1A lineage.
- Belgian swIAV strains are antigenically distinct from recent human vaccine strains; 1A.3.3.2 and 1C.2.2 viruses show no cross-reactivity.

Thank you



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Environment

