

Swine Influenza Surveillance in Hong Kong and Vietnam

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OFFLU SWINE INFLUENZA EXPERTS TECHNICAL MEETING

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Influenza human-animal interfaces in Hong Kong & Vietnam Surveillance

- Longitudinal surveillance at the Van Phuc slaughterhouse in Hanoi, which sources pigs from 23 provinces across the country.
- Monthly visits to slaughterhouses and collect swabs and sera from 300 animals as they enter the supply chain in Hong Kong and Vietnam.
- Isolate and characterize viruses.

Hong Kong, China

- 2021-2025
- Geographic source (Mainland provinces):
 - ✓ Guangxi
 - ✓ Guizhou
 - ✓ Guangdong
 - ✓ Hunan
 - ✓ Jiangxi

Viet Nam

- 2013-2025
- Geographical source (provinces):
 - ✓ Ha Noi
 - ✓ Bac Ninh
 - ✓ Hung Yen
 - ✓ Nghe An
 - ✓ Yen Bai
 - ✓ Ha Nam
 - ✓ Vinh Phuc
 - ✓ Thanh Hoa

Influenza human-animal interfaces in Hong Kong & Vietnam in 2025

Sampling carried out at swine abattoirs in Hanoi and Hong Kong

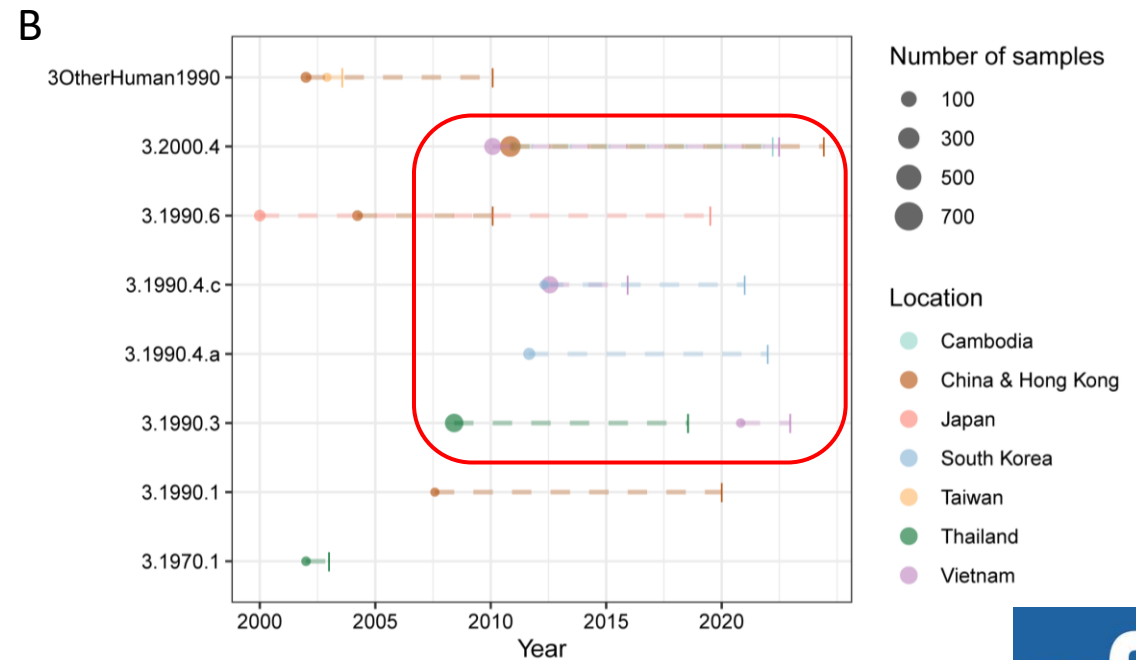
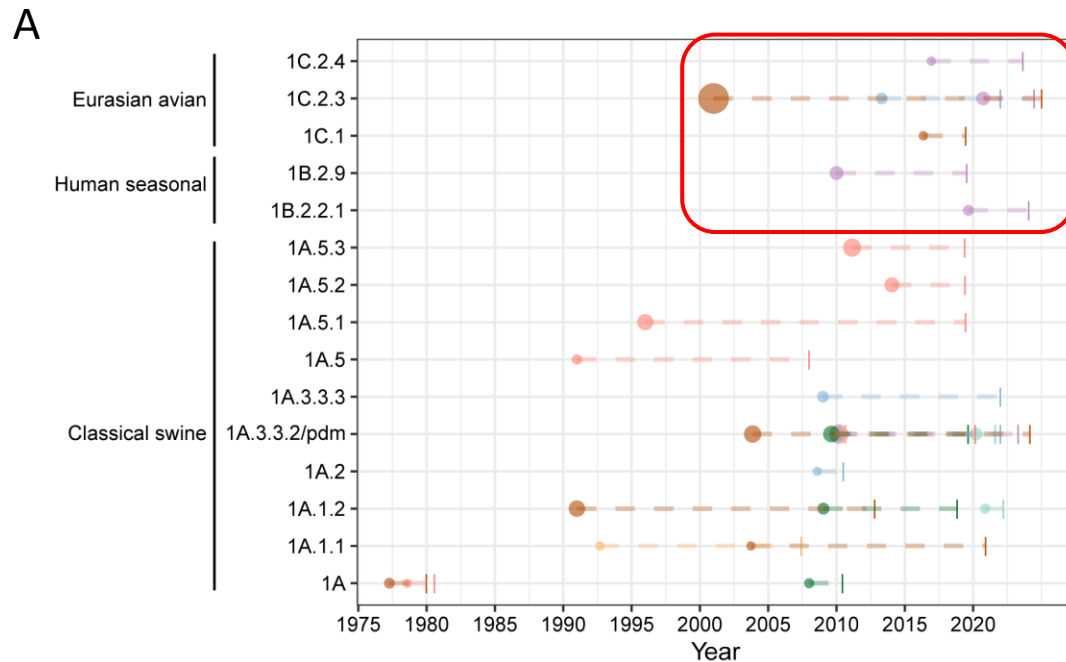
Hanoi

Hong Kong

	Samples	Viruses	Subtype		Samples	Viruses	Subtypes
Jan	150	0			150	1	H1N1
Feb	150	2	H1N2		150	1	H1N1
Mar	150	0			150	0	
Apr	147	1	H1N1		150	2	H3N2
May	153	0			150	0	
Jun	150	7	H1N1, H1N2		150	0	
Jul	150	9	H1N1,H1N2		150	5	H1N2
Aug	150	2	H3N2		150	0	
Sep	150	4	H1N1		150	0	
Oct	150	4	H1N2		150	0	
Nov	150	8	Pending		150	0	
Dec	150	3	Pending		150	0	
Total	1800	40			1800	9	

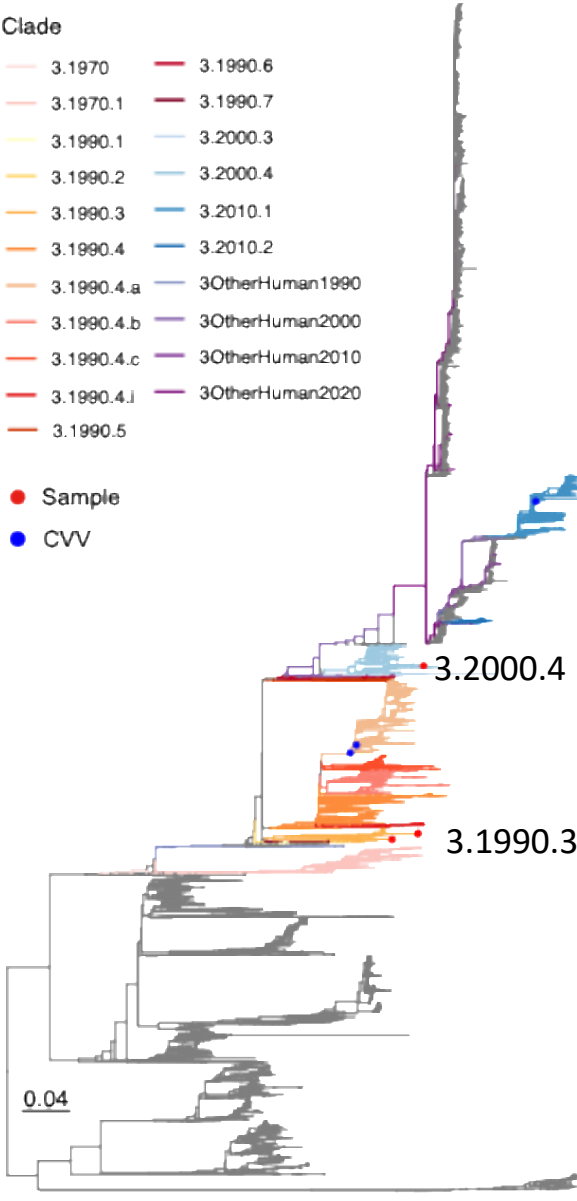
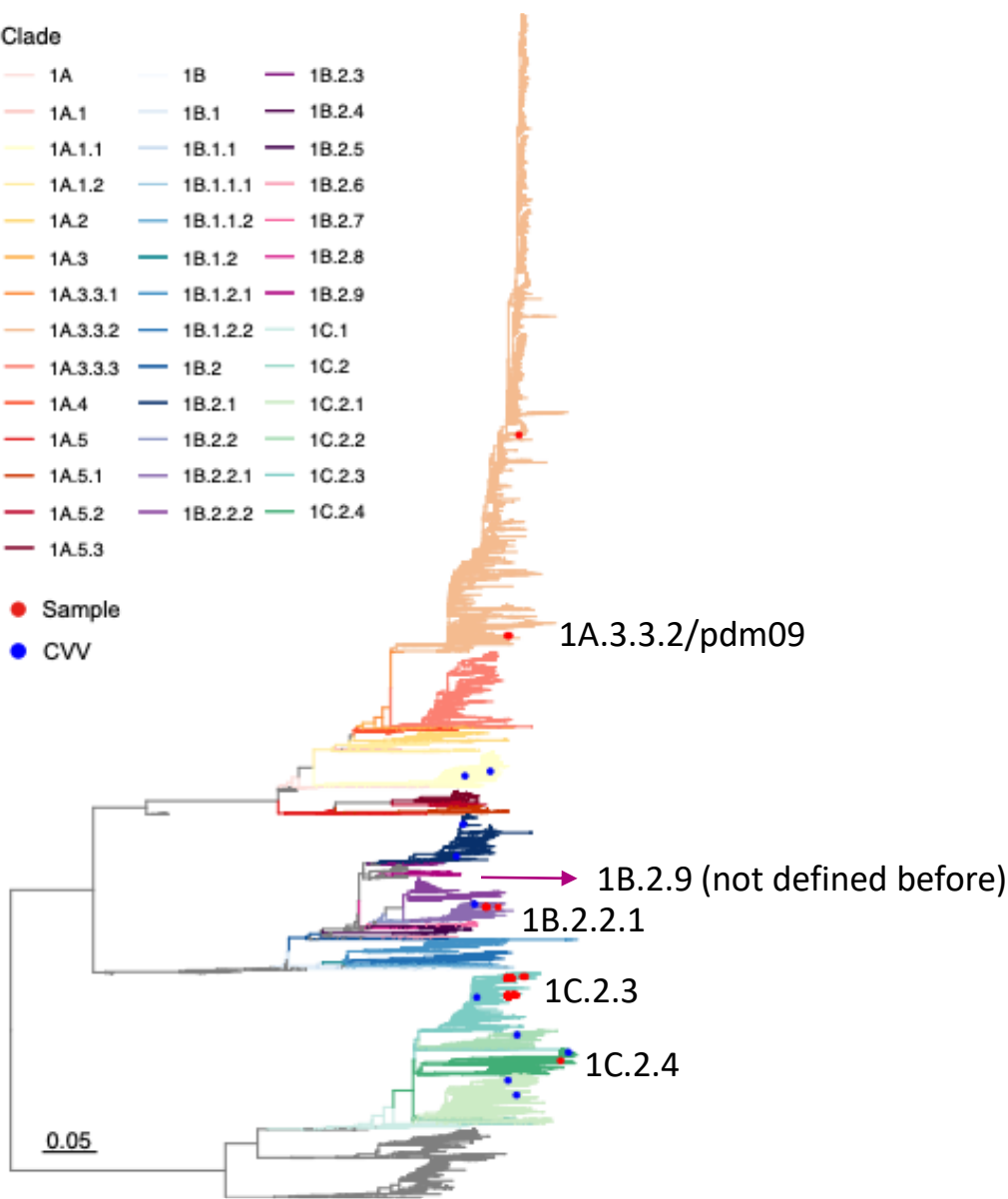
Persistence of clades in Asian countries

- 1B.2.2.1, 1B.2.9, and 1C.2.4 were only detected persistently in Vietnam among Asian countries.
- 1C.2.3 was first introduced to China, and then spread to South Korea and Vietnam.
- 3.2000.4 and 3.1990.4.c in Vietnam occurred around the same time as China and South Korea.
- 3.1990.3 in Vietnam occurred after the introduction to Thailand.



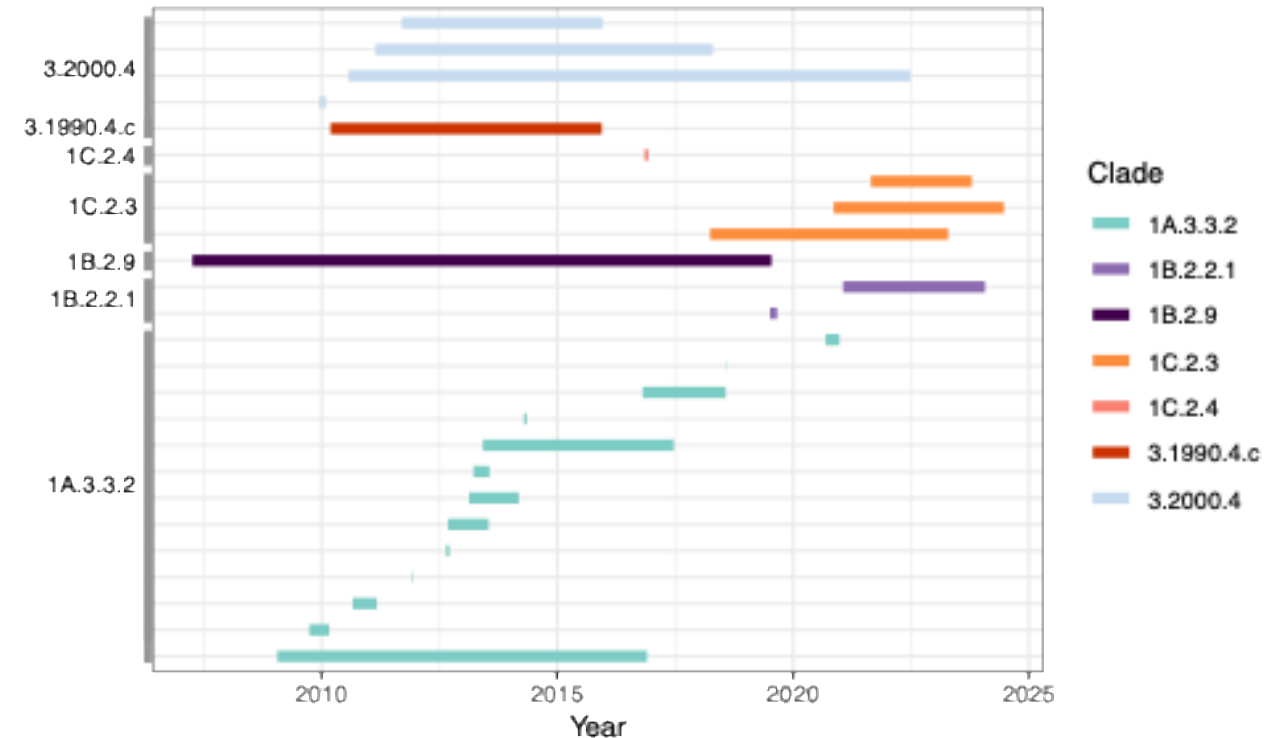
(A) Persistent duration of swine H1 clades in Asia. (B) Persistent duration of swine H3 clades in Asia. The dots are the times of the first samples. The vertical bars are the times of the latest samples. The size of the dots represents the total number of samples of the clade in that location.

H1 and H3 phylogeny with swine influenza surveillance samples from Vietnam



Introductions of swine influenza to Vietnam

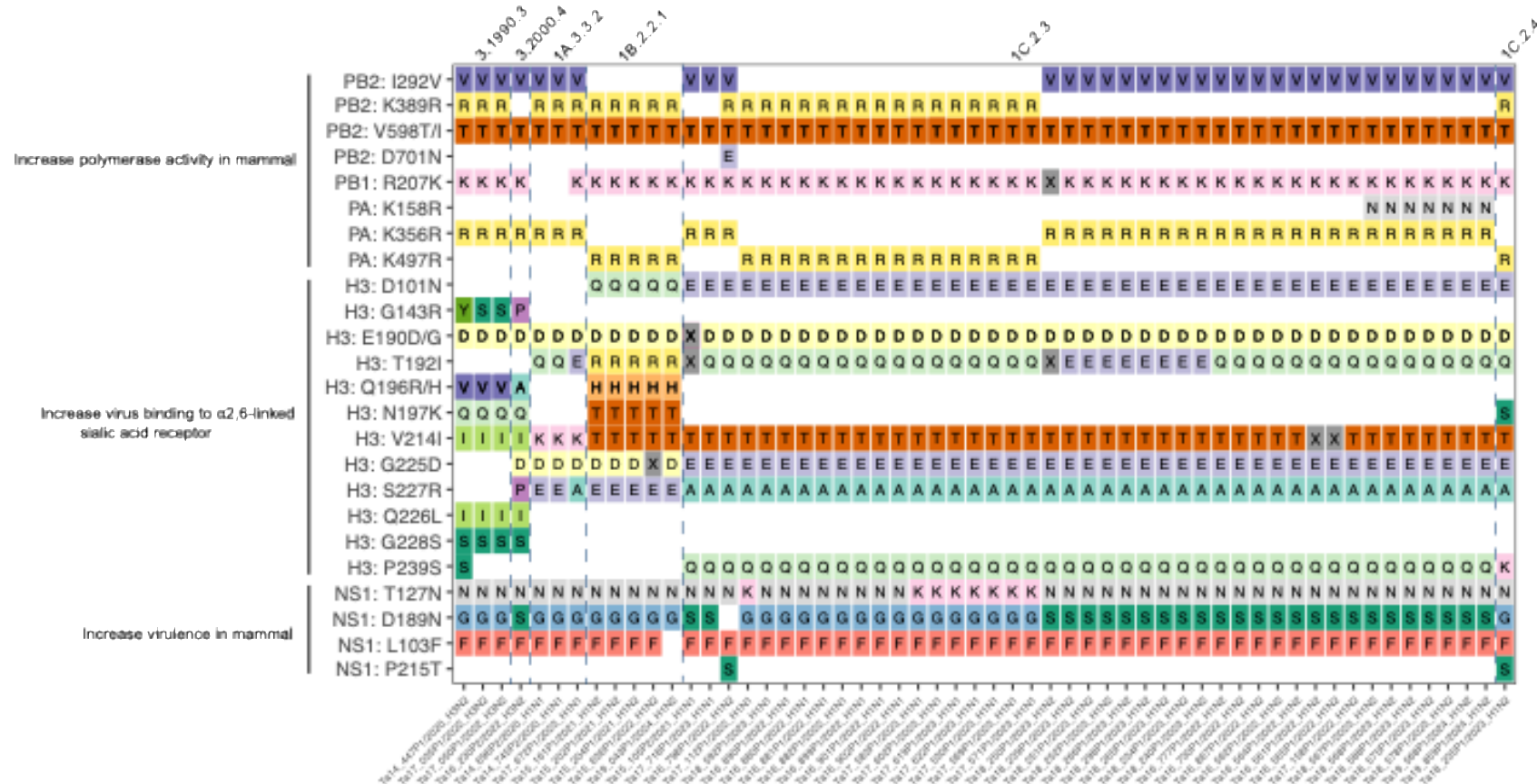
- 1C.2.3 and 3.2000.4
Multiple introductions from Asian countries
- 1B.2.9
Persisting for up to 12 years exclusively in Vietnam
- 1B.2.2.1
Sustained local transmission 2021–2024



Persistent duration of monophyletic clusters of swine influenza in Vietnam

Mutations of swine influenza in Vietnam

- PB2 K389R and D701E in clade 1C.2.3 (Eurasian avian-like).
- PA K158N in clade 1C.2.3 sustained in 2023–2024.
- H1 Q189E (H3 Q192E) within Sb antigenic site was found in a monophyletic 1C.2.3 cluster in 2023.
- NS1 N127K and S189G in 1C.2.3 resembling the 189G in other human-related swine samples.



Swine influenza in Vietnam during 2020–2024 surveillance

Sample collection

56 influenza isolates

- a. 21 H1N1
- b. 31 H3N2
- c. 4 H3N2

Clades identification

H1 clades identified

- 1A.3.3.2 (pdm09)
- 1B.2.2.1*
- 1B.2.9*
- 1C.2.3 (Eurasian avian like)#
- 1C.2.4 (European)*

Dominant, inter-regional Tx

* Sustained circulation (up to 12 years),
exclusively in Vietnam within Asia

H3 clades identified

- 3.2000.4.3#
- 3.1990.3
- 3.1990.4.c

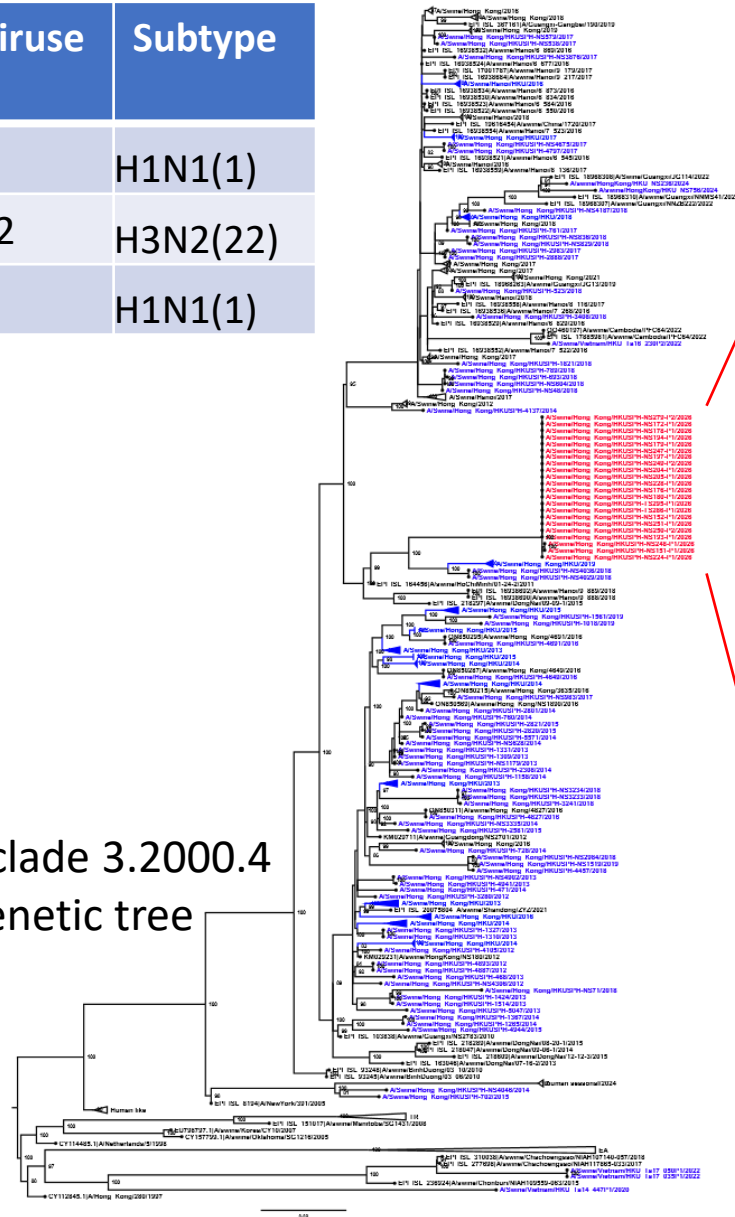
Conclusion

- Multiple independent introductions of SIV from North America, Europe, China, Thailand, Cambodia
- Suggests Vietnam as a recipient as well as possible source
- Extensive reassortment between co-circulating lineages; frequently involving H1N1pdm09 derived internal genes in H1N2 and H3N2 SIV
- Lineage specific mammalian adaptive & virulence mutations
- PB2: K389R D701E; PA K158N
- Receptor binding: H1 Q189E
- NS1: N127K S189G

Sample collection: Hong Kong

Month	Samples	Viruses	Subtypes
Jan 2026	150	1	H1N1(1)
Feb 2026	150	22	H3N2(22)
Mar 2026	150	1	H1N1(1)

H3 HA clade 3.2000.4
phylogenetic tree



Month	Virus name	Origin
Feb 2026	A/swine/HongKong/HKU_NS197/2026(H3N2)	Guangdong
Feb 2026	A/swine/HongKong/HKU_NS205/2026(H3N2)	Guangdong
Feb 2026	A/swine/HongKong/HKU_NS250/2026(H3N2)	Guangdong
Feb 2026	A/swine/HongKong/HKU_NS279/2026(H3N2)	Guangdong
Feb 2026	A/swine/HongKong/HKU_NS194/2026(H3N2)	Guangxi
Feb 2026	A/swine/HongKong/HKU_NS151/2026(H3N2)	Hunan
Feb 2026	A/swine/HongKong/HKU_NS179/2026(H3N2)	Hunan
Feb 2026	A/swine/HongKong/HKU_NS249/2026(H3N2)	Hunan
Feb 2026	A/swine/HongKong/HKU_NS152/2026(H3N2)	Jiangxi
Feb 2026	A/swine/HongKong/HKU_NS172/2026(H3N2)	Jiangxi
Feb 2026	A/swine/HongKong/HKU_NS176/2026(H3N2)	Jiangxi
Feb 2026	A/swine/HongKong/HKU_NS178/2026(H3N2)	Jiangxi
Feb 2026	A/swine/HongKong/HKU_NS180/2026(H3N2)	Jiangxi
Feb 2026	A/swine/HongKong/HKU_NS193/2026(H3N2)	Jiangxi
Feb 2026	A/swine/HongKong/HKU_NS204/2026(H3N2)	Jiangxi
Feb 2026	A/swine/HongKong/HKU_NS224/2026(H3N2)	Jiangxi
Feb 2026	A/swine/HongKong/HKU_NS228/2026(H3N2)	Jiangxi
Feb 2026	A/swine/HongKong/HKU_NS247/2026(H3N2)	Jiangxi
Feb 2026	A/swine/HongKong/HKU_NS248/2026(H3N2)	Jiangxi
Feb 2026	A/swine/HongKong/HKU_NS251/2026(H3N2)	Jiangxi
Feb 2026	A/swine/HongKong/HKU_TS286/2026(H3N2)	Jiangxi
Feb 2026	A/swine/HongKong/HKU_TS295/2026(H3N2)	Jiangxi

Conclusions



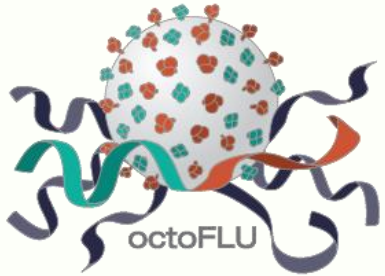
Hong Kong 2021-2026

- H1 – 1C.2.3
- H3 – 3.2000.4

Vietnam 2013-2026

- H1 – 1A.3.3.2, 1B.2, 1B.2.2.1, 1C.2.3, 1C.2.4
- H3 – 3.1990.3, 3.2000.4

Current Swine Influenza Genotyping Tools



flu-crew.org / octoFLU

USDA-maintained platform for automated clade classification

- Real-time surveillance dashboard
- Phylogenetic classification
- Public USDA surveillance data
- Regional trend analysis



FluGenome Influenza Virus Genotype Tool

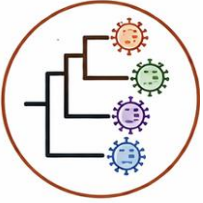
flugenome.org / FluGenome

Web tool for comprehensive genotype analysis

- 8-segment genotype nomenclature
- Reassortment detection
- Lineage assignment
- Historical genotype database

1. Arendsee ZW, Chang J, Hufnagel DE, Markin A, Janas-Martindale A, Vincent AL, Anderson TK. *octoFLUshow: an Interactive Tool Describing Spatial and Temporal Trends in the Genetic Diversity of Influenza A Virus in U.S. Swine*. Microbiol Resour Announc. 2021 Dec 16;10(50):e0108121. doi: 10.1128/MRA.01081-21.
2. Lu G, Rowley T, Garten R, Donis RO. *FluGenome: a web tool for genotyping influenza A virus*. Nucleic acids research. 2007 Jul 1;35(suppl_2):W275-9.

Key Challenges in Swine Influenza Genotyping



Evolutionary Complexity

- Continuous reassortment between lineages
- Eight-segment genome creates multiple genotypes
- Rapid adaptation to new hosts
- Bidirectional spillover events



Technical Limitations

- Mixed infections difficult to resolve
- Short-read assembly challenges
- Sample degradation in oral fluids
- Coverage bias in large segments



Nomenclature Issues

- Inconsistent global classification systems
- Regional discrepancies in taxonomy
- Internal segment nomenclature gaps
- Lack of standardized frameworks



Surveillance Gaps

- Ascertainment bias in clinical sampling
- Limited global data sharing
- Economic constraints on monitoring
- Delayed detection of novel genotypes

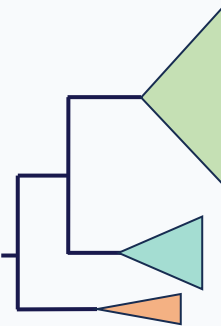
Global genotyping of H5 avian influenza virus (ggFlu): Methodology Overview

Foundation & Identification



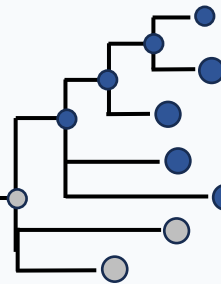
1. Foundation: Database & Tree Construction

Collects global influenza genomes and builds Maximum Likelihood (ML) phylogenetic trees for all 8 gene segments.



2. Identification: Major Clusters

Defines broad genetic sources based on genetic distance, host (e.g. avian, swine), and geography (e.g. Eurasia, America).



3. Identification: Minor Clusters

Identifies monophyletic groups within major clusters to capture specific reassortment events into a target virus population.

Nomenclature

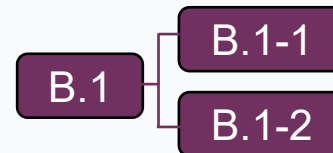
4. Nomenclature: Major genotypes (e.g., 1.2.4.1/B.1)



Assigns hierarchical numeric names based on the gene constellation, with letter aliases for sustained and significant genotypes.



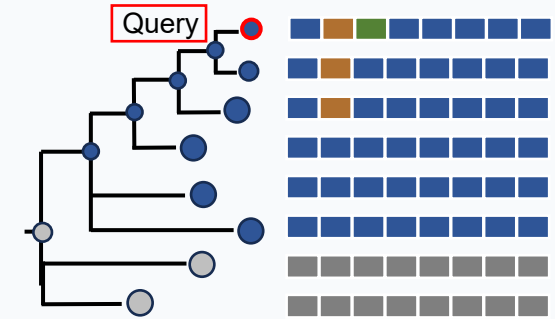
5. Nomenclature: Minor Genotypes (e.g. B.1-1, B.1-2)



Appends a hyphenated number and reference to the major genotype to designate distinct sub-lineages from specific reassortment events.

Analysis & Maintenance

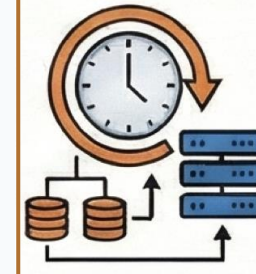
6. Analysis: Query New Genomes



Places new virus genomes onto the reference trees to assign them to existing or newly defined genotypes.



7. Maintenance: System Updates



Updates the entire system biannually with new sequence data to ensure the framework remains current and robust.

Highly pathogenic avian influenza H5 genotyping tool: ggFlu (www.ggflu.org)



Tools for Global Genotyping of Influenza Virus Beta

Powered by TIPars • Snakemake Pipeline • GISAID Data • 

Upload & Analysis

 **Input Format Requirements**

Your FASTA sequence headers must end with a gene segment identifier: |PB2, |PB1, |PA, |HA, |NP, |NA, |MP, |NS

Example header format: >A/Sample/Location/001/2024|PB2

▲ Maximum 200 sequences per submission. Larger files will be truncated.

 Browse

Choose FASTA file...

 Upload your influenza sequences in FASTA format

Or try with sample data:

 Load Example Input

 File loaded: input.fas (Example)

40 sequences • 65.8 KB

▶ Run Genotype Analysis

Results



Enter Job ID to retrieve results...

Lookup

 Genotype Classification Results

 Download Results (.tsv)

Search:

qid	HAclade	MajorGenotype_alias	MajorGenotype_lineage	MinorGenotype	MinorGenotype
A/Cambodia/J05273701/2025 EPL_ISL_19885766 H5N1 2025-05-26	2.3.2.1e	A.10.1	1.10.1	*	Not assigned
A/chicken/Ohio/25-003105-001-R2/2025 EPL_ISL_19786015 H5N1 2025-01-26	2.3.4.4b	P.5	1.2.4.23.2.6.5.5	P.5-1	D1.3
A/dairy_cow/California/25_004231-002/2024 EPL_ISL_19786013 H5N1 2024-11-25	2.3.4.4b	E.2	1.2.4.16.1.2	E.2-1	B3.13
A/dairy_cow/California/25_004231-003/2024 EPL_ISL_19786012 H5N1 2024-11-25	2.3.4.4b	E.2	1.2.4.16.1.2	E.2-1	B3.13
A/mink/Hong_Kong/RG-DeINS1-p1/2024 EPL_ISL_19733237 H5N1 2024-05-01	2.3.4.4b	*	*	*	Not assigned

Showing 1 to 5 of 5 entries

Previous

1

Next

15

Acknowledgement

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Thank you