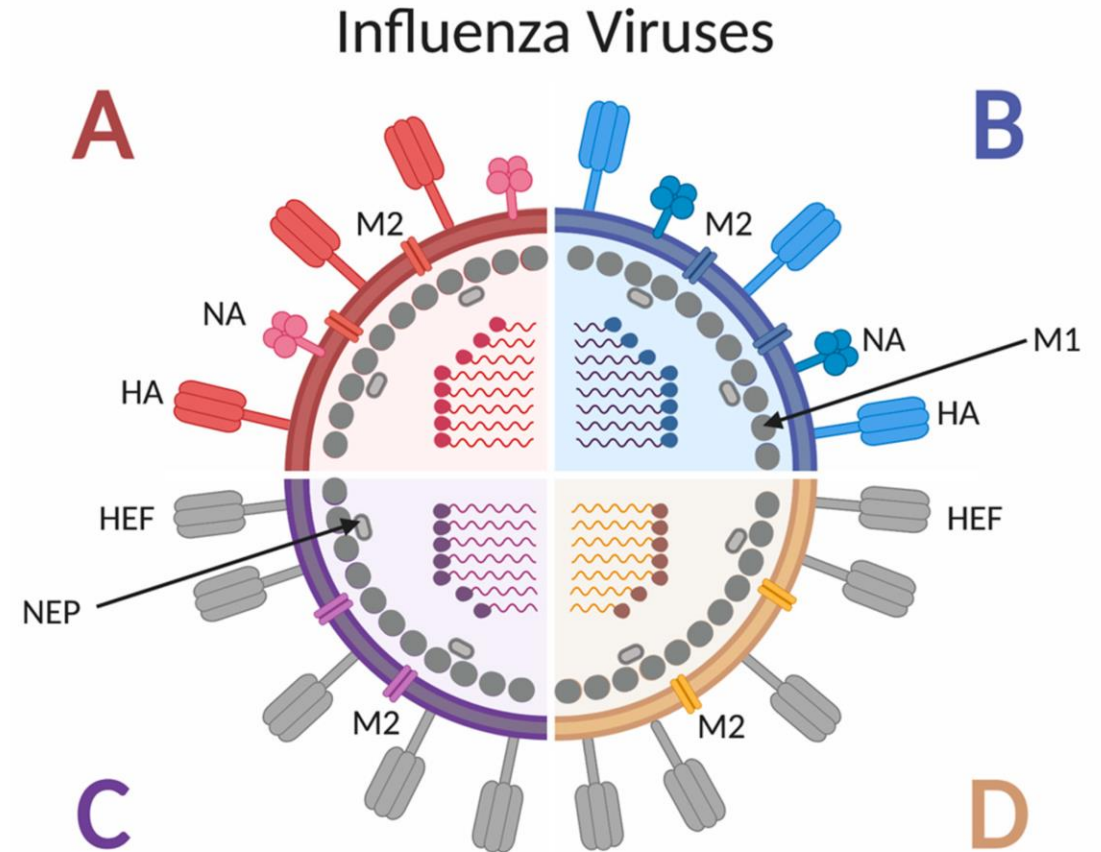


Intro to Project 1: Phylogenetics of Influenzavirus A

301520 VO+UE Virus Evolution and Ecology (2025W)

Influenza

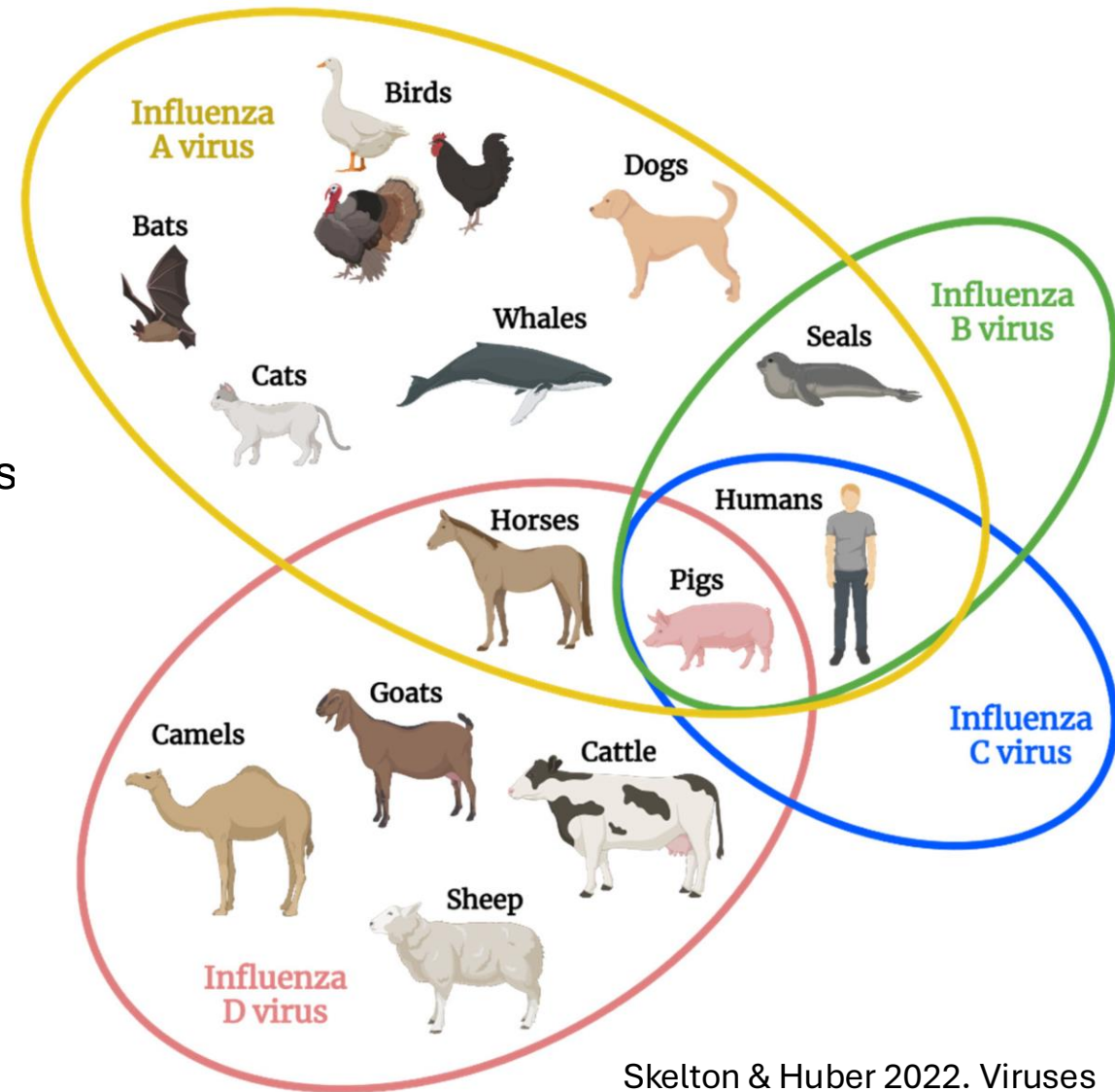
- Family: Orthomyxoviridae
 - Enveloped, spherical (~100 nm) or filamentous (>300 nm)
 - segmented -ss vRNA genome
- 4 types of Influenza: A, B, C and D
 - Only A and B are circulating and causing **seasonal epidemics** aka "the flu"
 - Only A caused **pandemics** so far
- Encodes full replication machinery



Rioux 2020. Vaccines

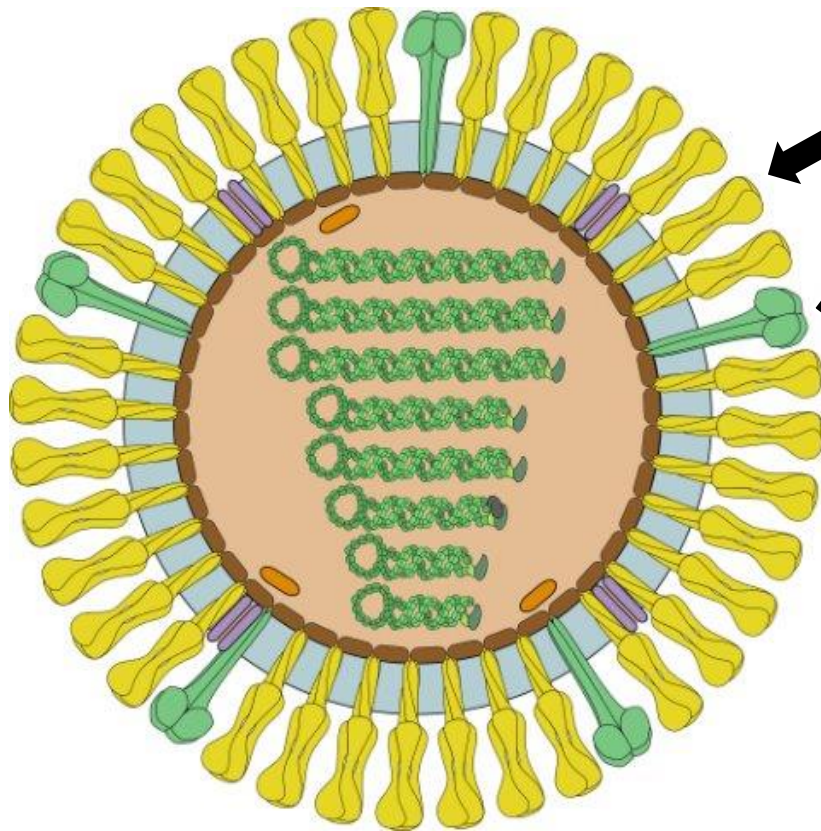
Natural host ranges

- Zoonotic viruses
- IAV: largest host range, natural reservoir: aquatic birds
- IBV: mostly restricted to human host
 - B/Yamagata and B/Victoria
- ICV: mild infections, no risk for public health
- IDV: no clinical cases, full host range not known



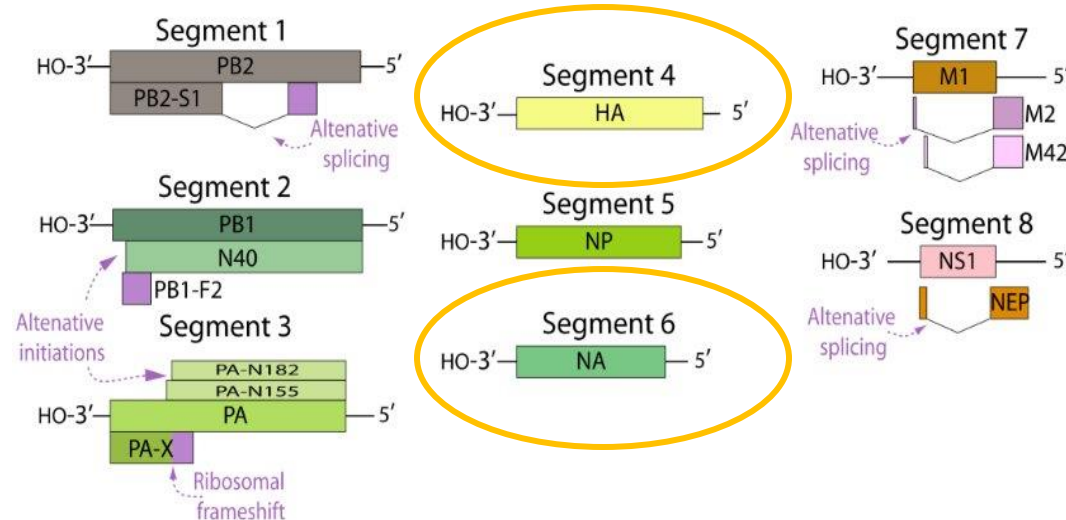
Skelton & Huber 2022. Viruses

Influenza A virus subtypes



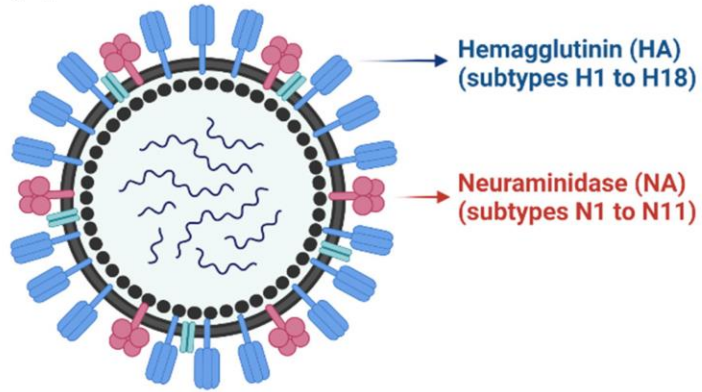
haemagglutinin (HA) determines host tropism

neuraminidase (NA) promotes efficient release of viral progeny from infected cells



Influenza A virus subtypes

(A)

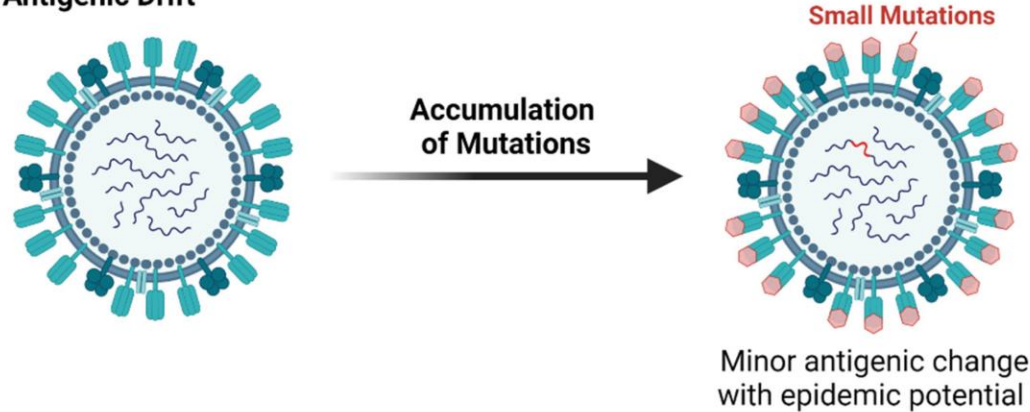


(B)

Human	Swine	Domestic Poultry	Waterfowl Shorebirds	Equine	Sea Mammals	Bat
H1/N1	H1/N1	H1/N1	H1/N1		H1	
H2/N2	H2/N2	H2/N2	H2/N2		N2	
H3/N3	H3	H3/N3	H3/N3	H3	H3/N3	
N4	H4	H4/N4	H4/N4		H4	
H5	H5	H5/N5	H5/N5		N5	
H6/N6	H6/N6	H6/N6	H6/N6			
H7/N7		H7/N7	H7/N7	H7/N7	H7/N7	
N8		H8/N8	H8/N8	N8		
H9/N9	H9	H9/N9	H9/N9		N9	
H10		H10	H10		H10	N10
		H11	H11			N11
		H12	H12			
		H13	H13		H13	
		H14	H14			
		H15	H15			
		H16	H16			
						H17
						H18

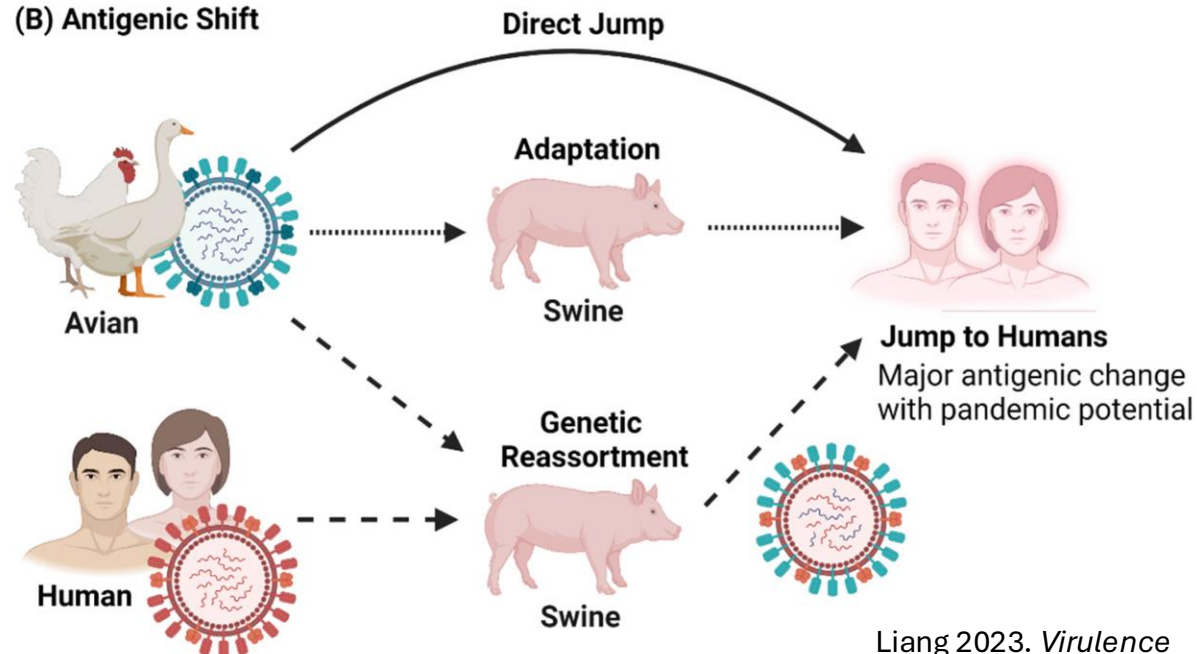
Antigenic drift and shift in Influenza A viruses

(A) Antigenic Drift



--> seasonal selection of **new strains** with amino acid changes in HA and NA genes--> relevant for vaccine strain selection
--> causes seasonal influenza **epidemics**

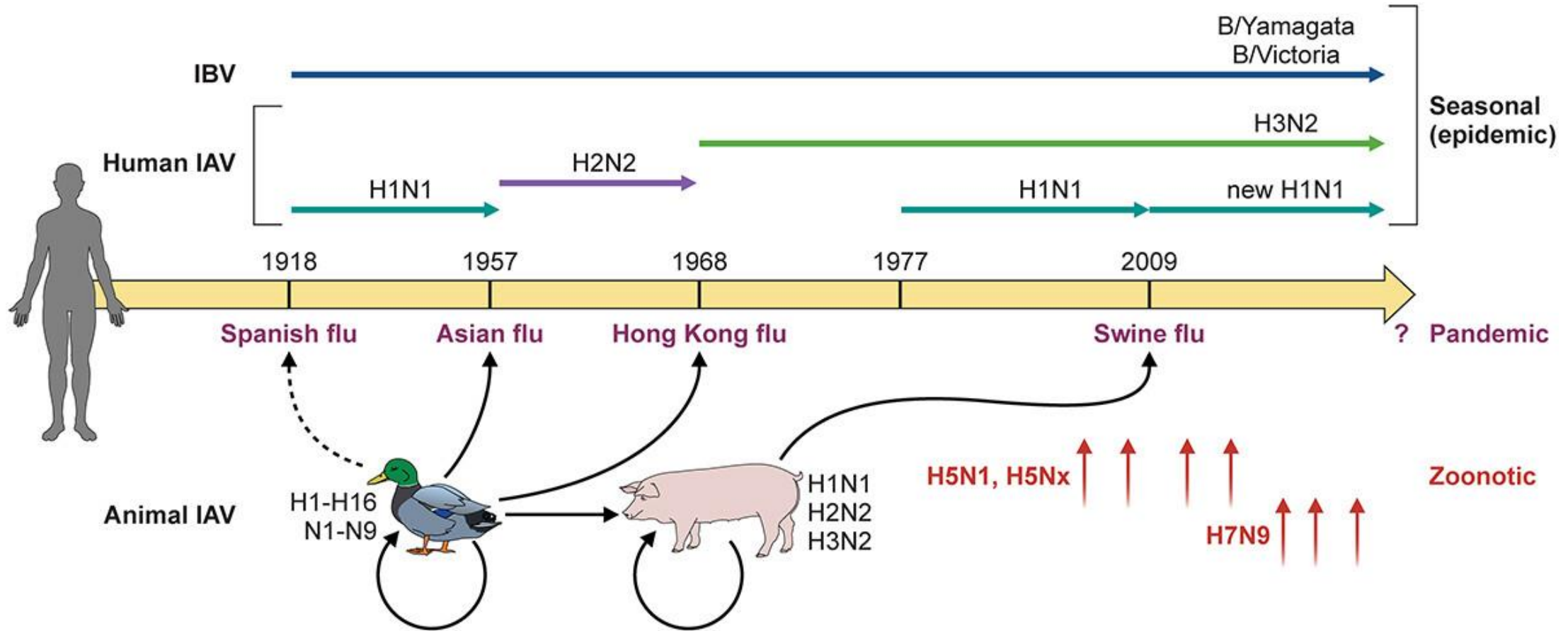
(B) Antigenic Shift



--> results in **new subtype**
--> potential emergence of **pandemic** virus

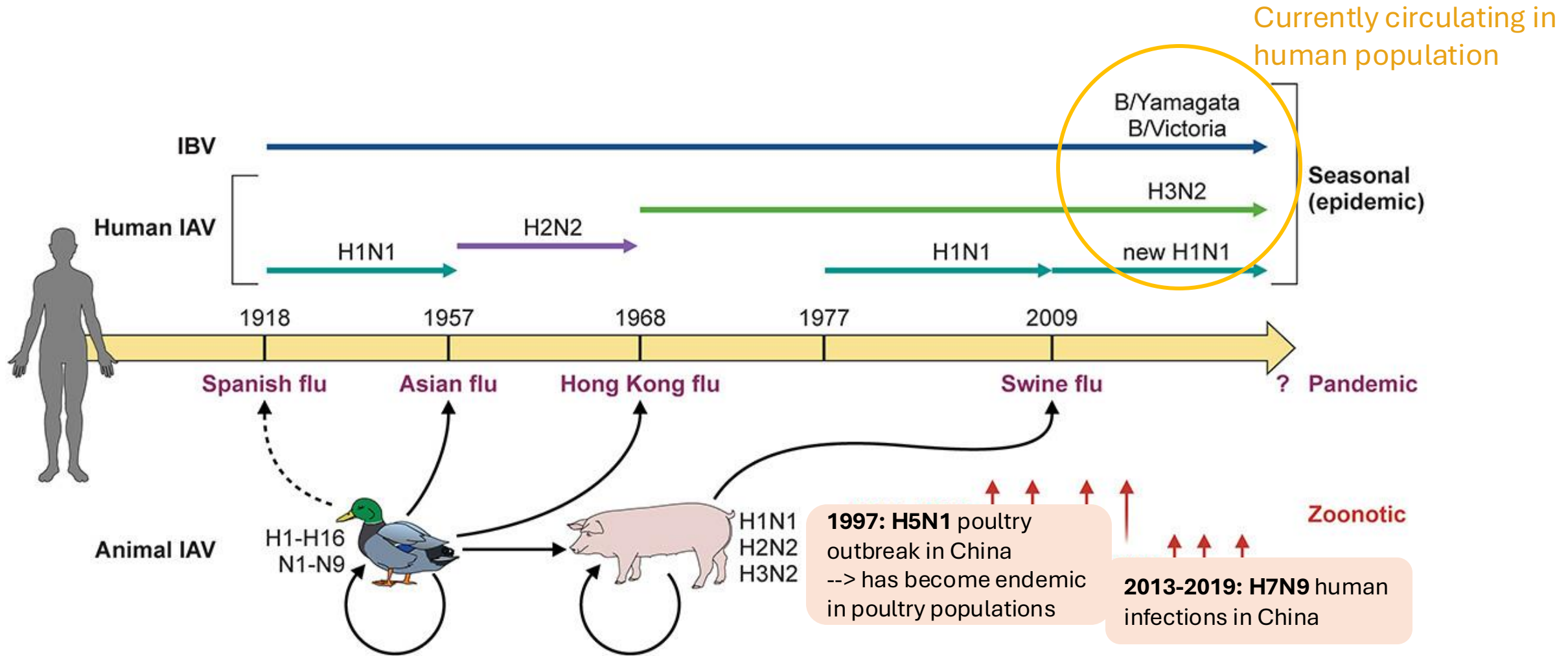
Liang 2023. *Virulence*

Influenza virus evolution



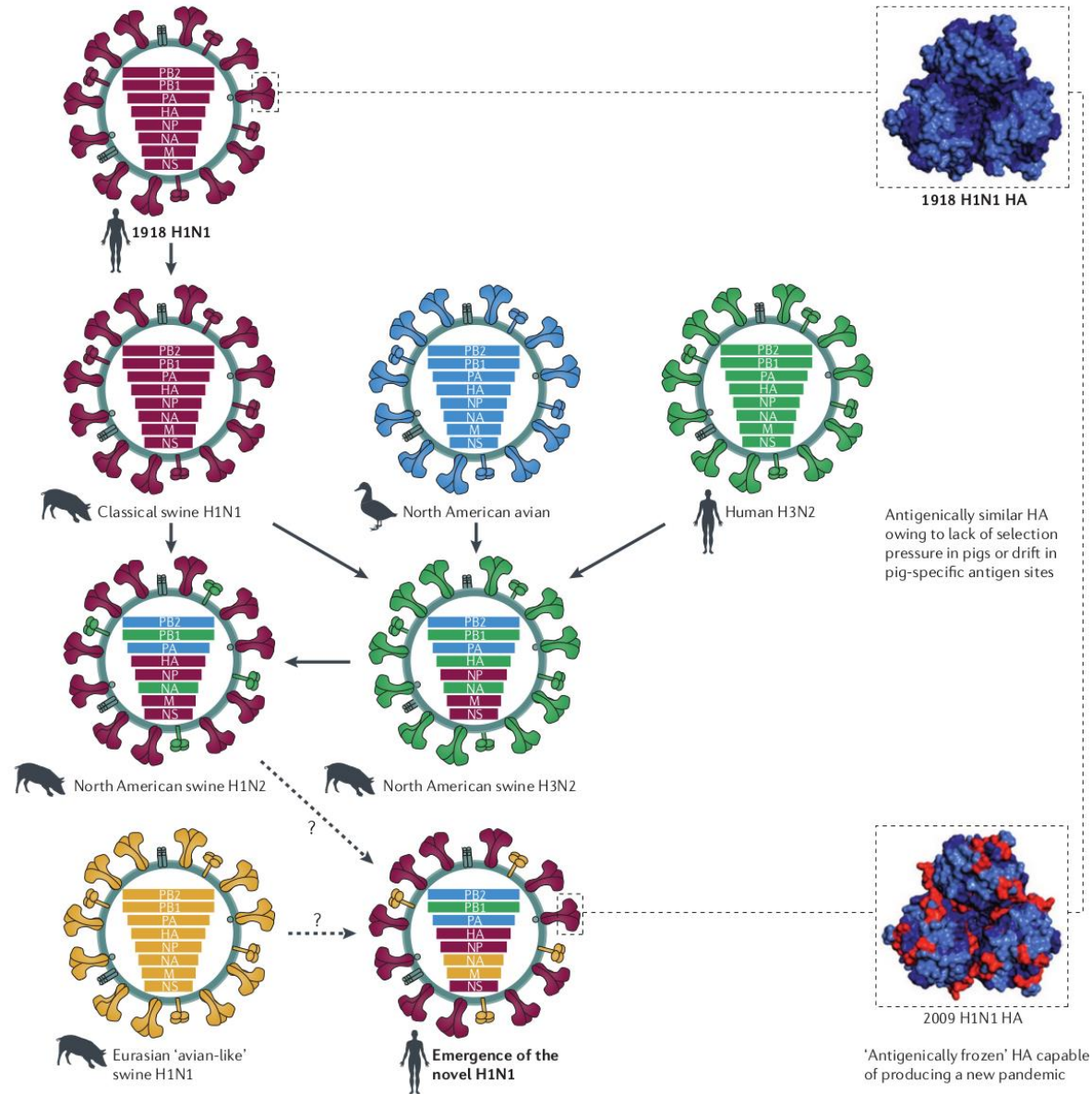
Liang 2023. *Virulence*

Influenza virus evolution

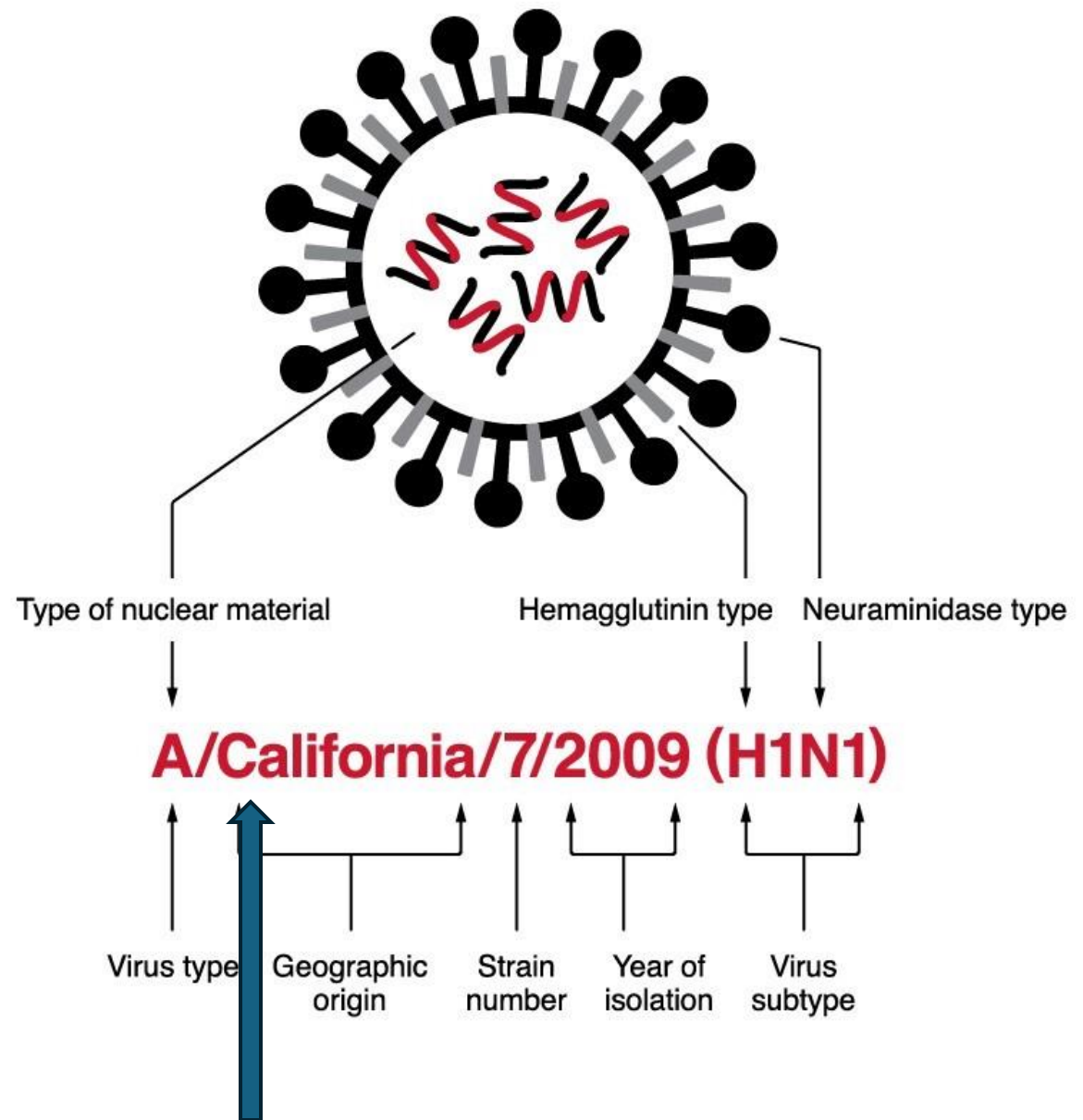


Liang 2023. *Virulence*

Emergence of novel viruses



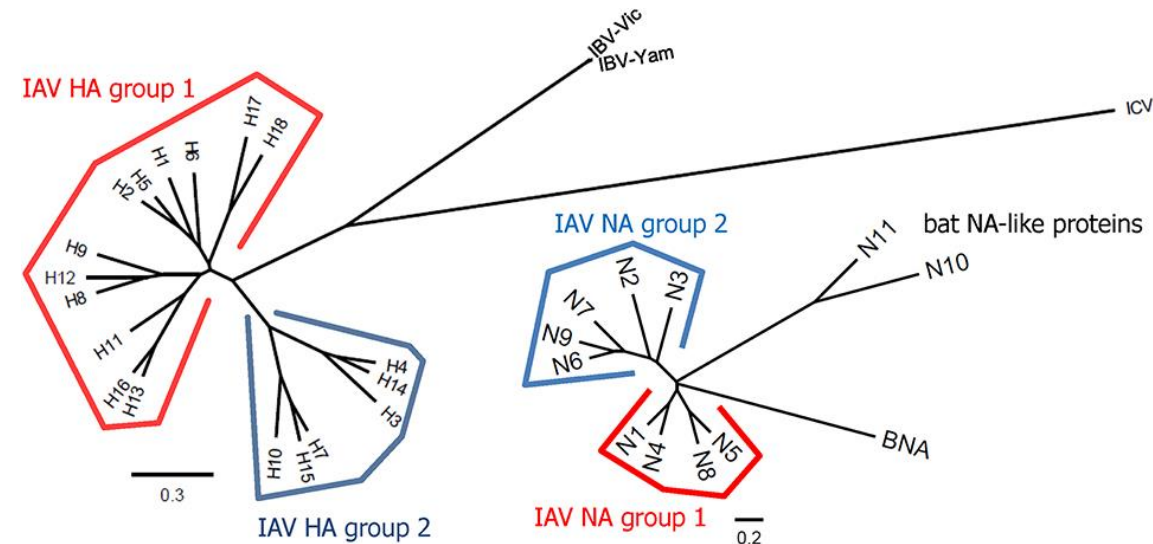
Say my name...



Non-human hosts: host origin added here

Outline of Project I

- Download genome sequences of HA and NA
- Process genome sequences
- Translate genes and align sequences
- Backtranslate to nucleotide sequence and generate both phylogenetic trees
- Visualise and annotate your trees in iTol
- Discussion



<https://doi.org/10.3389/fcimb.2019.00344>

References

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https://moodle.univie.ac.at/pluginfile.php/31872918/mod_folder/content/0/L2_Virus_growth_potential_and_adaptability.pdf?forcedownload=1

Rioux M, McNeil M, Francis ME, Dawe N, Foley M, Langley JM, Kelvin AA. The Power of First Impressions: Can Influenza Imprinting during Infancy Inform Vaccine Design? *Vaccines*. 2020; 8(3):546. <https://doi.org/10.3390/vaccines8030546>

Skelton RM, Huber VC. Comparing Influenza Virus Biology for Understanding Influenza D Virus. *Viruses*. 2022; 14(5):1036. <https://doi.org/10.3390/v14051036>