Surveillance for detection and assessment of virus evolution to inform vaccination programs including vaccine selection and updates

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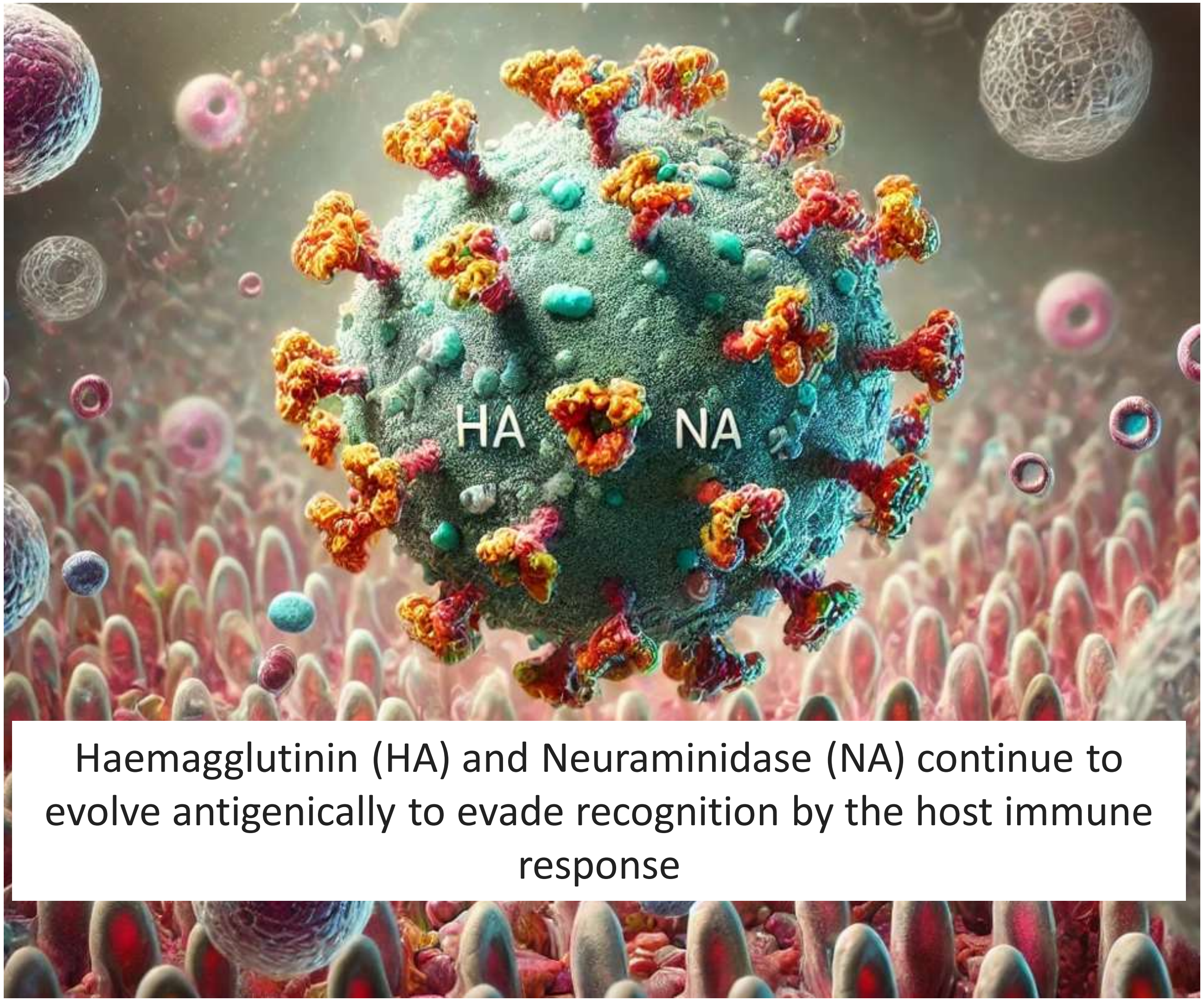
Vaccination and Surveillance for HPAI in poultry:
Current Situation and Perspectives
October 22-23, 2024
WOAH, Paris

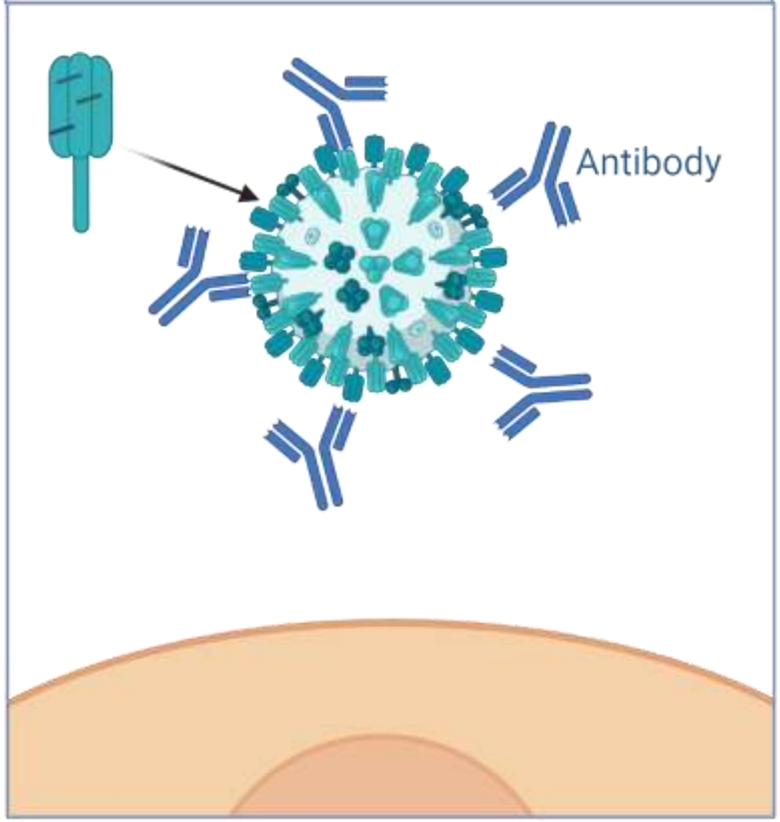

VIRUS
IMMUNE SYSTEM



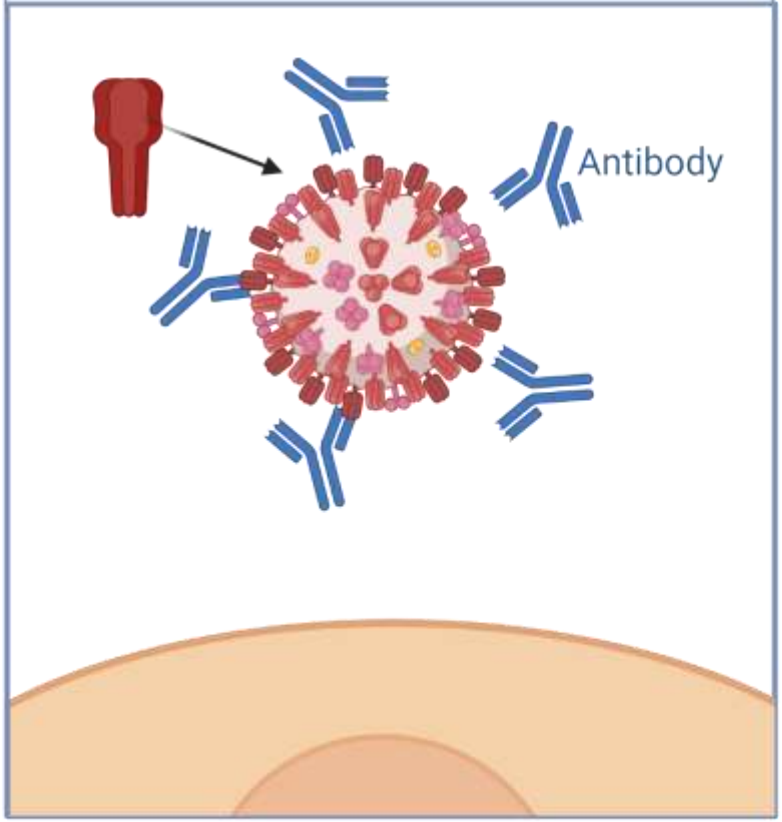
Haemagglutinin (HA) and Neuraminidase (NA) continue to evolve antigenically to evade recognition by the host immune response

Two major types of antigenic evolution of IAV

Antigenic drift
(accumulation of mutations)



Antigenic shift
(HA gene of a circulating virus is
replaced by a novel HA gene)



Created with BioRender.com

What is behind the antigenic drift?

High evolutionary rate:
No proofreading capability
Replication speed
(~ 46 substitutions per genome, per year)*

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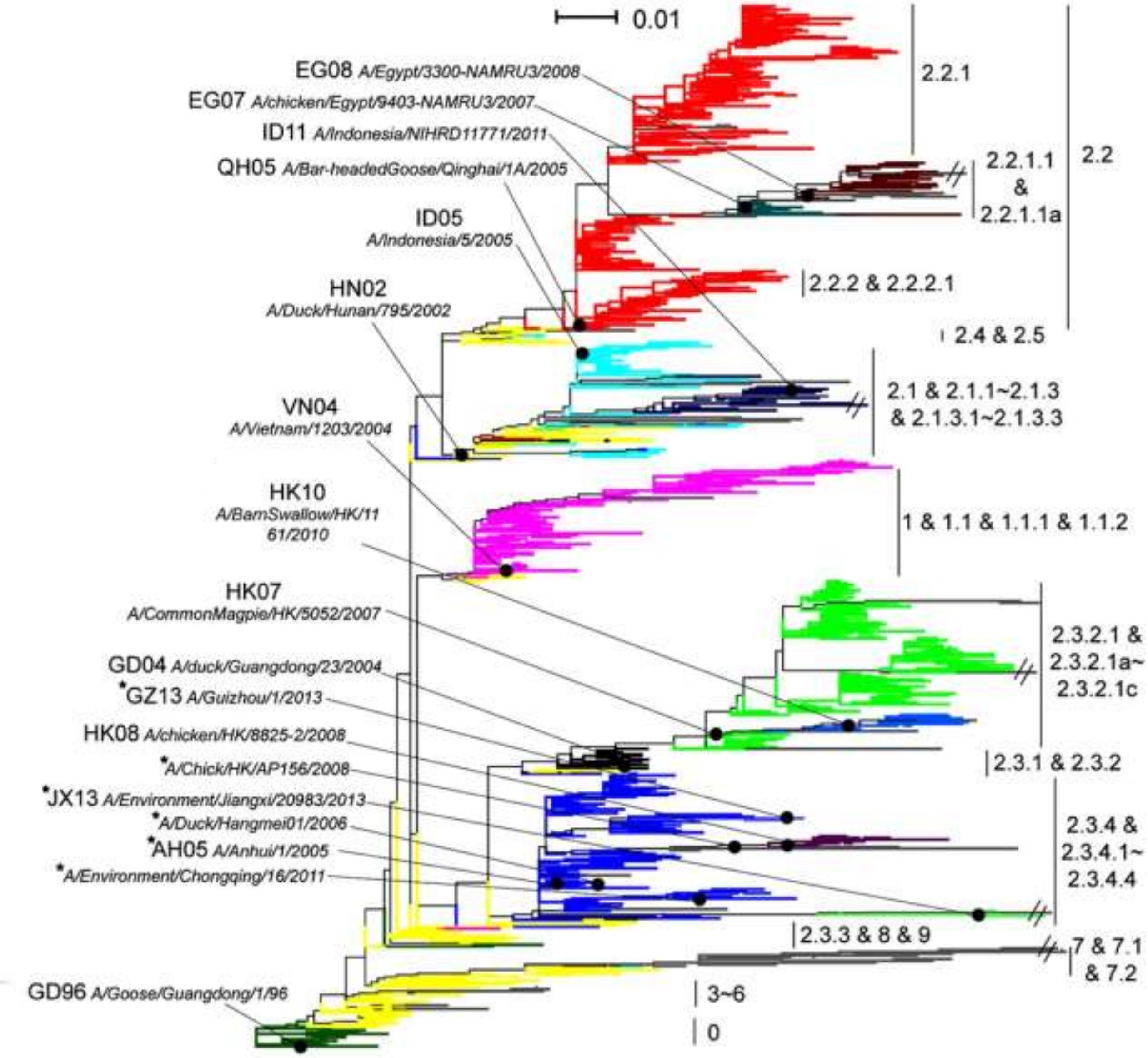
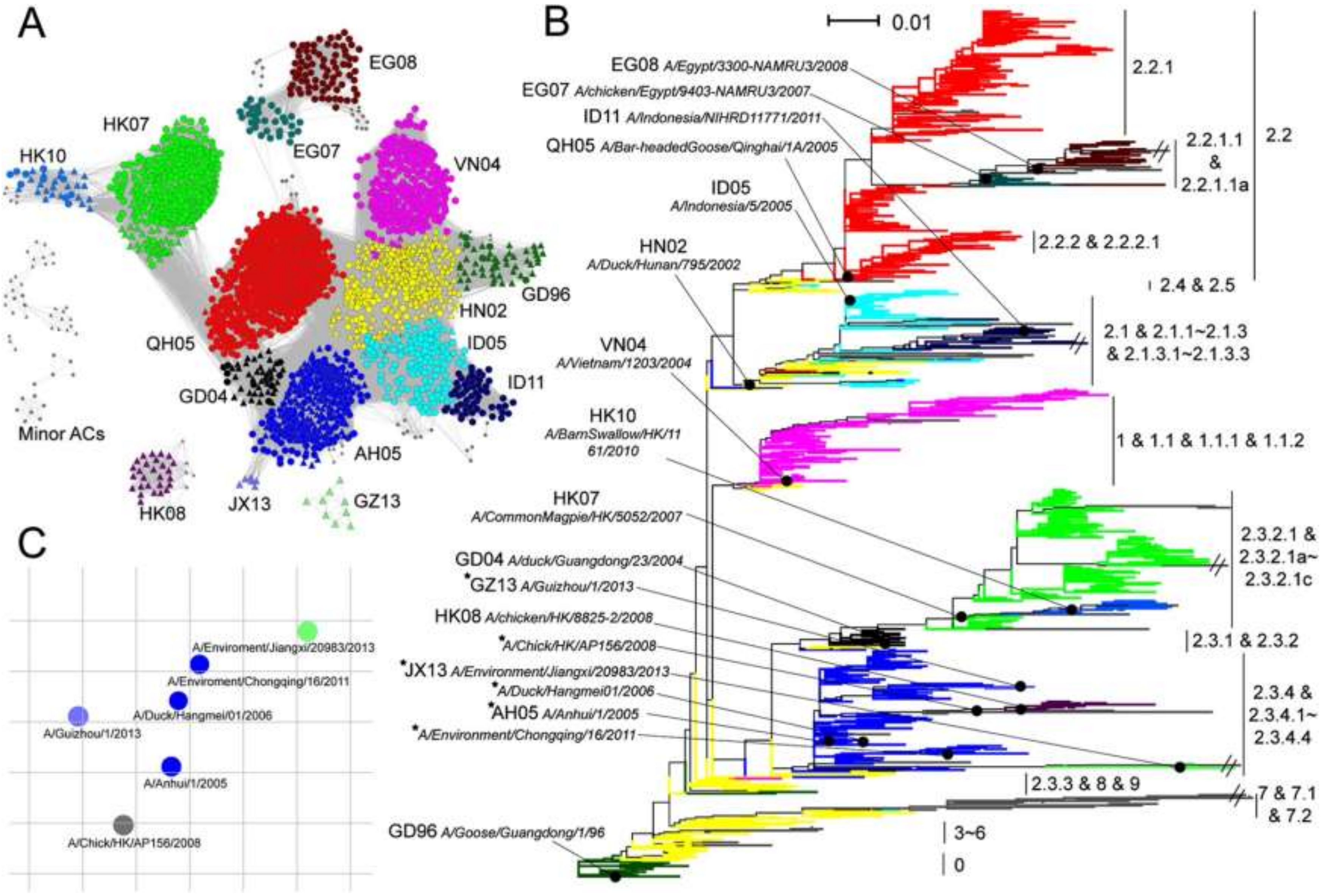
*Chen and Holmes, 2006 Mol Biol Evol 23(12):2336-2341;

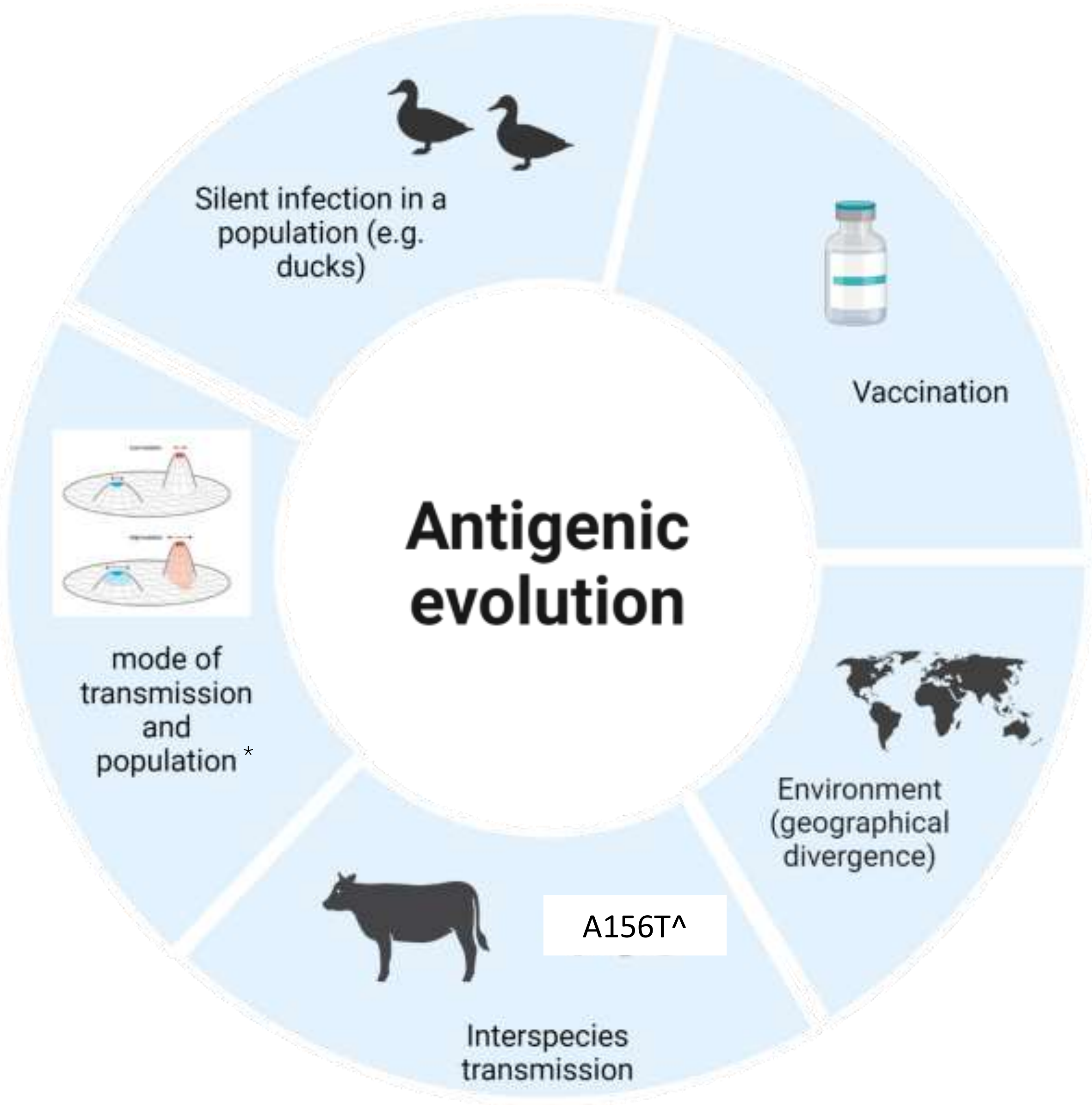


https://www.nature.com/articles/srep43566



https://www.nature.com/articles/srep43566

Selection forces driving the antigenic evolution of HPAI



Antigenic evolution

Silent infection in a population (e.g. ducks)

Vaccination

Environment (geographical divergence)

A156T^

Interspecies transmission

mode of transmission and population *

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^Dadonaite et al 2004 : https://doi.org/10.1101/2024.05.23.595634

*Fourment M et al. BMC Evol Biol. 2015

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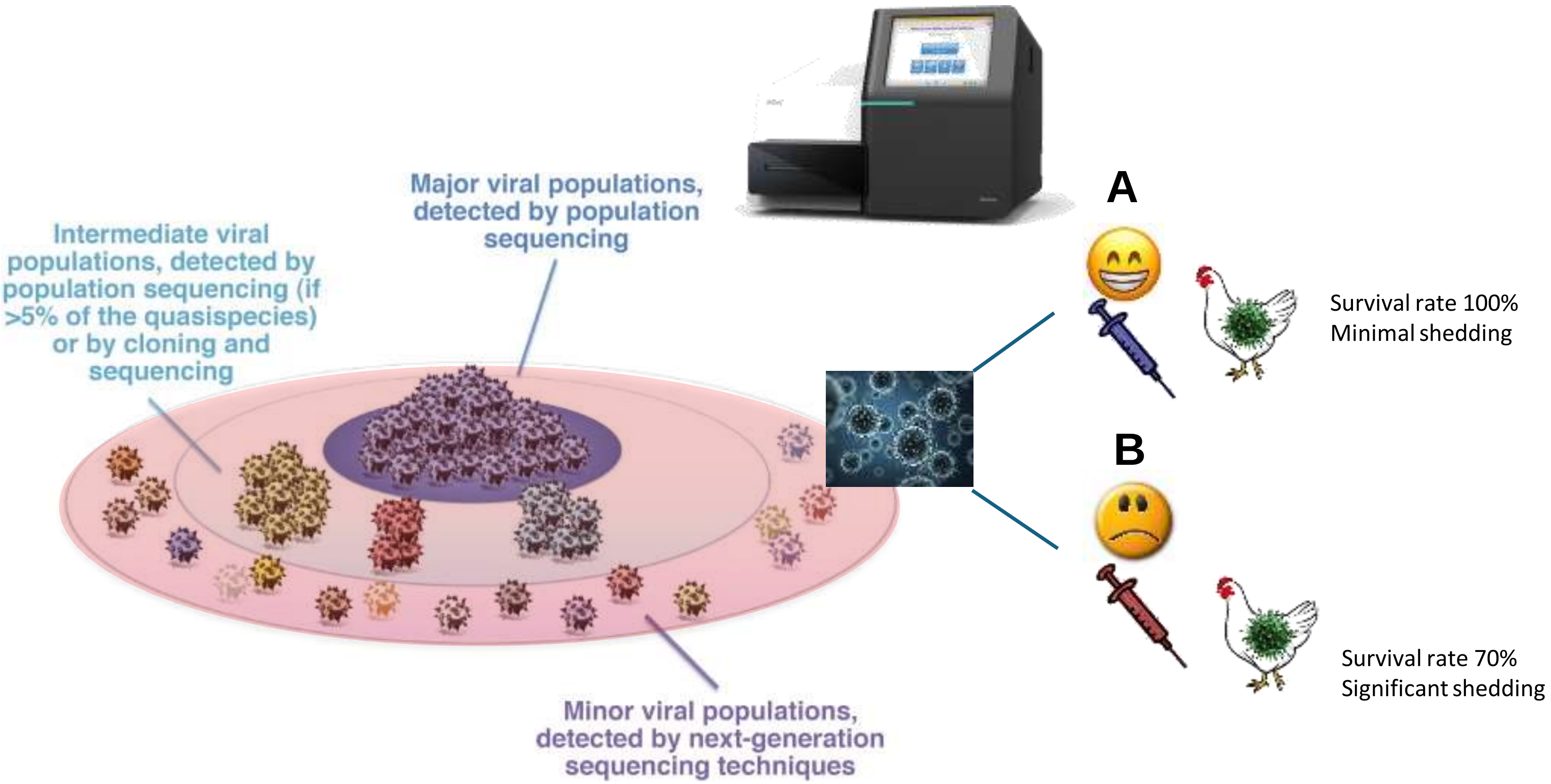
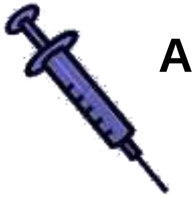
Characterization of the complexity of the viral population



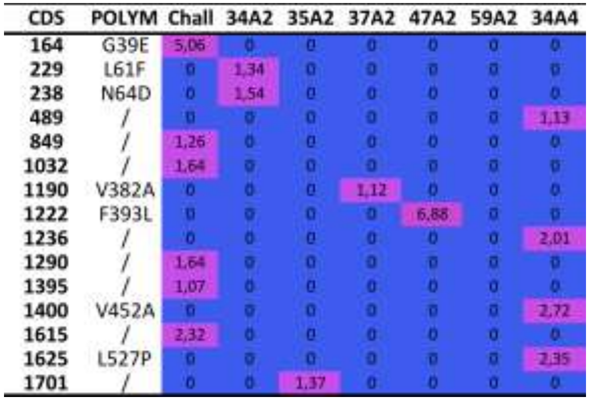
Survival rate 100%
Minimal shedding

Survival rate 70%
Significant shedding

Milani et al. 2017 Vet Mic.



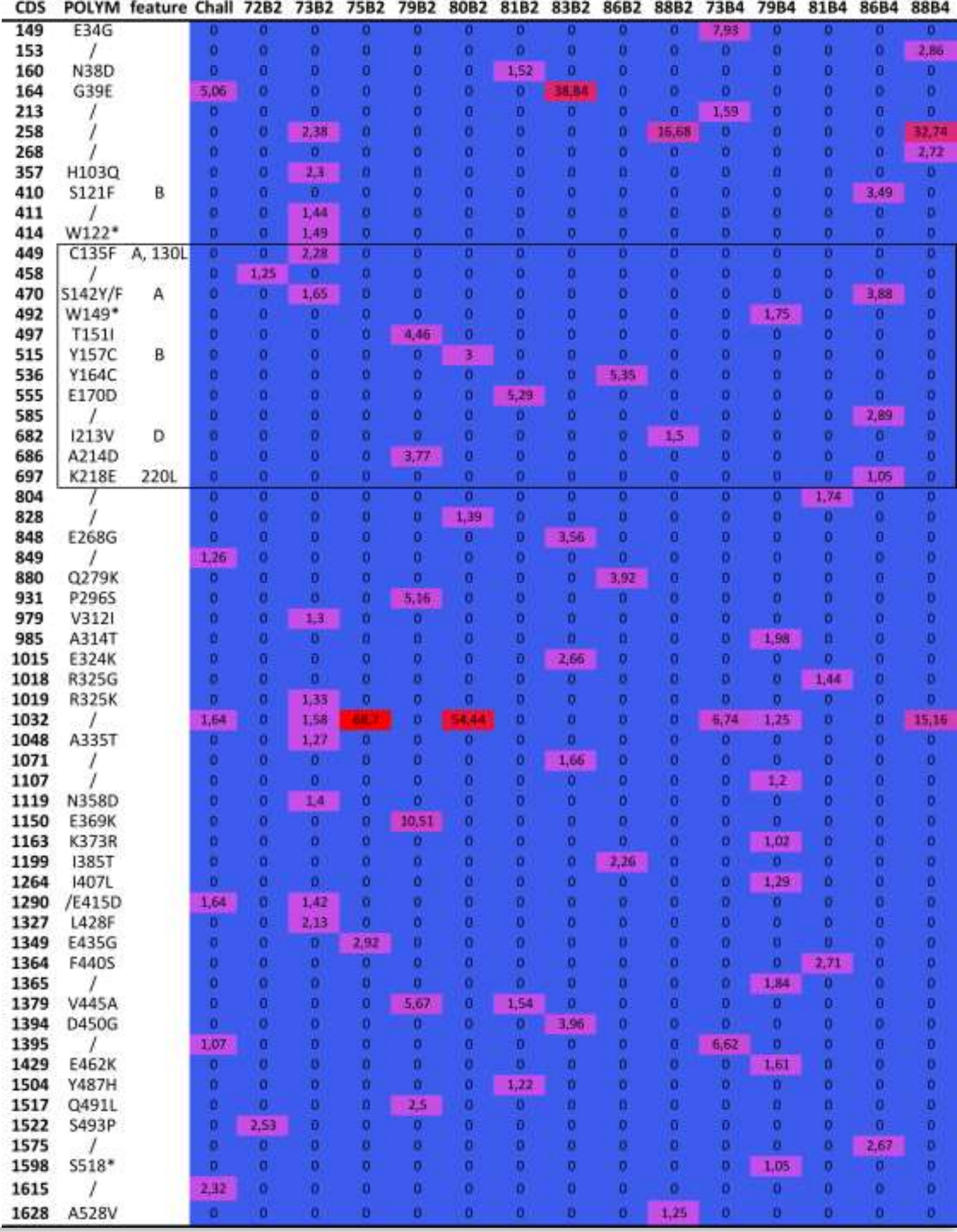
A 😁



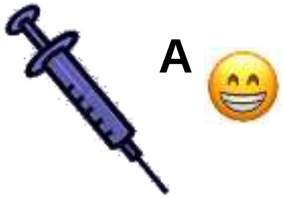
CDS	POLYM	Chall	34A2	35A2	37A2	47A2	59A2	34A4
164	G39E	5,06	0	0	0	0	0	0
229	L61F	0	1,34	0	0	0	0	0
238	N64D	0	1,54	0	0	0	0	0
489	/	0	0	0	0	0	0	1,13
849	/	1,26	0	0	0	0	0	0
1032	/	1,64	0	0	0	0	0	0
1190	V382A	0	0	0	1,12	0	0	0
1222	F393L	0	0	0	0	6,88	0	0
1236	/	0	0	0	0	0	0	2,01
1290	/	1,64	0	0	0	0	0	0
1395	/	1,07	0	0	0	0	0	0
1400	V452A	0	0	0	0	0	0	2,72
1615	/	2,32	0	0	0	0	0	0
1625	L527P	0	0	0	0	0	0	2,35
1701	/	0	0	1,37	0	0	0	0

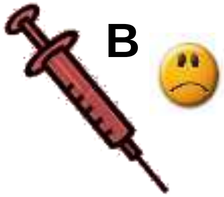
Analysis of genetic polymorphisms

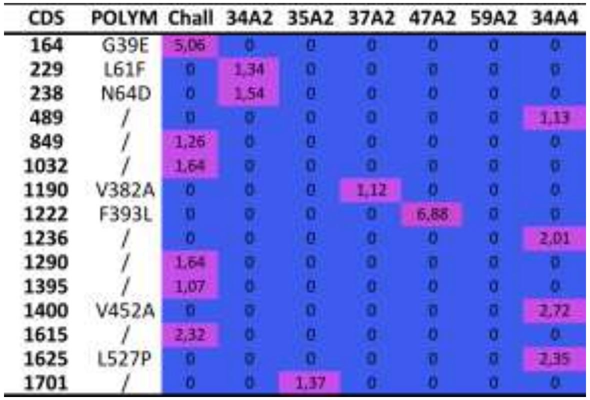
B 🙁



CDS	POLYM	feature	Chall	72B2	73B2	75B2	79B2	80B2	81B2	83B2	86B2	88B2	73B4	79B4	81B4	86B4	88B4
149	E34G		0	0	0	0	0	0	0	0	0	0	7,93	0	0	0	0
153	/		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2,86
160	N38D		0	0	0	0	0	0	1,52	0	0	0	0	0	0	0	0
164	G39E		5,06	0	0	0	0	0	0	38,84	0	0	0	0	0	0	0
213	/		0	0	0	0	0	0	0	0	0	0	1,59	0	0	0	0
258	/		0	0	2,38	0	0	0	0	0	0	16,68	0	0	0	0	32,74
268	/		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2,72
357	H103Q		0	0	2,3	0	0	0	0	0	0	0	0	0	0	0	0
410	S121F	B	0	0	0	0	0	0	0	0	0	0	0	0	0	3,49	0
411	/		0	0	1,44	0	0	0	0	0	0	0	0	0	0	0	0
414	W122*		0	0	1,49	0	0	0	0	0	0	0	0	0	0	0	0
449	C135F	A, 130L	0	0	2,28	0	0	0	0	0	0	0	0	0	0	0	0
458	/		0	1,25	0	0	0	0	0	0	0	0	0	0	0	0	0
470	S142Y/F	A	0	0	1,65	0	0	0	0	0	0	0	0	0	0	3,88	0
492	W149*		0	0	0	0	0	0	0	0	0	0	0	1,75	0	0	0
497	T151I		0	0	0	0	4,46	0	0	0	0	0	0	0	0	0	0
515	Y157C	B	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
536	Y164C		0	0	0	0	0	0	0	0	5,35	0	0	0	0	0	0
555	E170D		0	0	0	0	0	0	5,29	0	0	0	0	0	0	0	0
585	/		0	0	0	0	0	0	0	0	0	0	0	0	0	2,89	0
682	I213V	D	0	0	0	0	0	0	0	0	0	1,5	0	0	0	0	0
686	A214D		0	0	0	0	3,77	0	0	0	0	0	0	0	0	0	0
697	K218E	220L	0	0	0	0	0	0	0	0	0	0	0	0	0	1,05	0
804	/		0	0	0	0	0	0	0	0	0	0	0	0	1,74	0	0
828	/		0	0	0	0	0	1,39	0	0	0	0	0	0	0	0	0
848	E268G		0	0	0	0	0	0	0	3,56	0	0	0	0	0	0	0
849	/		1,26	0	0	0	0	0	0	0	0	0	0	0	0	0	0
880	Q279K		0	0	0	0	0	0	0	0	3,92	0	0	0	0	0	0
931	P296S		0	0	0	0	5,16	0	0	0	0	0	0	0	0	0	0
979	V312I		0	0	1,3	0	0	0	0	0	0	0	0	0	0	0	0
985	A314T		0	0	0	0	0	0	0	0	0	0	0	1,98	0	0	0
1015	E324K		0	0	0	0	0	0	0	2,66	0	0	0	0	0	0	0
1018	R325G		0	0	0	0	0	0	0	0	0	0	0	0	1,44	0	0
1019	R325K		0	0	1,33	0	0	0	0	0	0	0	0	0	0	0	0
1032	/		1,64	0	1,58	68,7	0	54,44	0	0	0	0	6,74	1,25	0	0	15,16
1048	A335T		0	0	1,27	0	0	0	0	0	0	0	0	0	0	0	0
1071	/		0	0	0	0	0	0	0	1,66	0	0	0	0	0	0	0
1107	/		0	0	0	0	0	0	0	0	0	0	0	1,2	0	0	0
1119	N358D		0	0	1,4	0	0	0	0	0	0	0	0	0	0	0	0
1150	E369K		0	0	0	0	10,51	0	0	0	0	0	0	0	0	0	0
1163	K373R		0	0	0	0	0	0	0	0	0	0	0	1,02	0	0	0
1199	I385T		0	0	0	0	0	0	0	0	2,26	0	0	0	0	0	0
1264	I407L		0	0	0	0	0	0	0	0	0	0	0	1,29	0	0	0
1290	/E415D		1,64	0	1,42	0	0	0	0	0	0	0	0	0	0	0	0
1327	L428F		0	0	2,13	0	0	0	0	0	0	0	0	0	0	0	0
1349	E435G		0	0	0	2,92	0	0	0	0	0	0	0	0	0	0	0
1364	F440S		0	0	0	0	0	0	0	0	0	0	0	0	2,71	0	0
1365	/		0	0	0	0	0	0	0	0	0	0	0	1,84	0	0	0
1379	V445A		0	0	0	0	5,67	0	1,54	0	0	0	0	0	0	0	0
1394	D450G		0	0	0	0	0	0	0	3,96	0	0	0	0	0	0	0
1395	/		1,07	0	0	0	0	0	0	0	0	0	6,62	0	0	0	0
1429	E462K		0	0	0	0	0	0	0	0	0	0	0	1,61	0	0	0
1504	Y487H		0	0	0	0	0	0	1,22	0	0	0	0	0	0	0	0
1517	Q491L		0	0	0	0	2,5	0	0	0	0	0	0	0	0	0	0
1522	S493P		0	2,53	0	0	0	0	0	0	0	0	0	0	0	0	0
1575	/		0	0	0	0	0	0	0	0	0	0	0	0	0	2,67	0
1598	S518*		0	0	0	0	0	0	0	0	0	0	0	1,05	0	0	0
1615	/		2,32	0	0	0	0	0	0	0	0	0	0	0	0	0	0
1628	A528V		0	0	0	0	0	0	0	0	0	1,25	0	0	0	0	0







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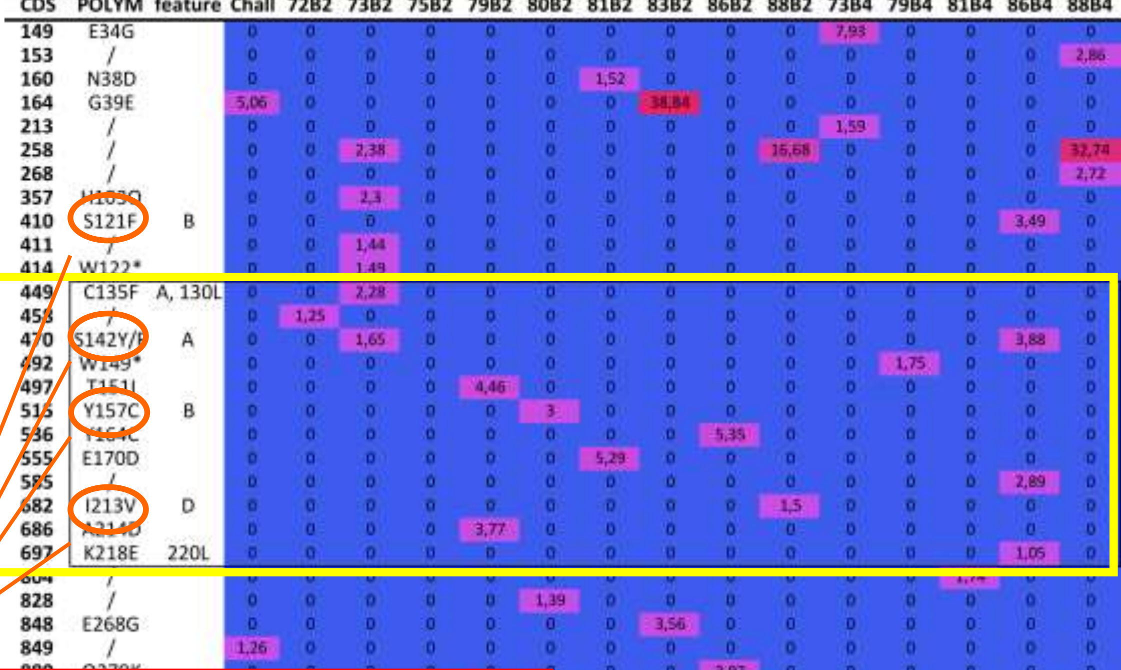
229	L61F	0	1,34	0	0	0	0	0
238	N64D	0	1,54	0	0	0	0	0
489	/	0	0	0	0	0	0	1,13
849	/	1,26	0	0	0	0	0	0
1032	/	1,64	0	0	0	0	0	0
1190	V382A	0	0	0	1,12	0	0	0
1222	F393L	0	0	0	0	6,88	0	0
1236	/	0	0	0	0	0	0	2,01
1290	/	1,64	0	0	0	0	0	0
1395	/	1,07	0	0	0	0	0	0
1400	V452A	0	0	0	0	0	0	2,72
1615	/	2,32	0	0	0	0	0	0
1625	L527P	0	0	0	0	0	0	2,35
1701	/	0	0	1,37	0	0	0	0

RBD

Ag site



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149	E34G		0	0	0	0	0	0	0	0	0	0	7,93	0	0	0	0
153	/		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2,86
160	N38D		0	0	0	0	0	0	1,52	0	0	0	0	0	0	0	0
164	G39E		5,06	0	0	0	0	0	0	38,84	0	0	0	0	0	0	0
213	/		0	0	0	0	0	0	0	0	0	0	1,59	0	0	0	0
258	/		0	0	2,38	0	0	0	0	0	0	16,68	0	0	0	0	32,74
268	/		0	0	0	0	0	0	0	0	0	0	0	0	0	0	2,72
357	H103Q		0	0	2,3	0	0	0	0	0	0	0	0	0	0	0	0
410	S121F	B	0	0	0	0	0	0	0	0	0	0	0	0	0	3,49	0
411	/		0	0	1,44	0	0	0	0	0	0	0	0	0	0	0	0
414	W122*		0	0	1,49	0	0	0	0	0	0	0	0	0	0	0	0
449	C135F	A, 130L	0	0	2,28	0	0	0	0	0	0	0	0	0	0	0	0
453	/		0	1,25	0	0	0	0	0	0	0	0	0	0	0	0	0
470	S142Y/F	A	0	0	1,65	0	0	0	0	0	0	0	0	0	0	3,88	0
492	W149*		0	0	0	0	0	0	0	0	0	0	0	1,75	0	0	0
497	T151I		0	0	0	0	4,46	0	0	0	0	0	0	0	0	0	0
515	Y157C	B	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
536	Y164C		0	0	0	0	0	0	0	0	5,35	0	0	0	0	0	0
555	E170D		0	0	0	0	0	0	5,29	0	0	0	0	0	0	0	0
585	/		0	0	0	0	0	0	0	0	0	0	0	0	0	2,89	0
682	I213V	D	0	0	0	0	0	0	0	0	0	1,5	0	0	0	0	0
686	A214D		0	0	0	0	3,77	0	0	0	0	0	0	0	0	0	0
697	K218E	220L	0	0	0	0	0	0	0	0	0	0	0	0	0	1,05	0
828	/		0	0	0	0	0	1,39	0	0	0	0	0	0	0	0	0
848	E268G		0	0	0	0	0	0	0	3,56	0	0	0	0	0	0	0
849	/		1,26	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Suboptimal immune protection may induce an increase of the complexity in the viral population from the early stages of infection and may promote the selection of minority variants some of which may be **involved in antigenic drift**.

9 minority variants
9 HA positions showing mutations
1 to 4 variants per sample

0 minority variants in the RBD
0 minority variants in the Ag sites

0 variants shared between samples

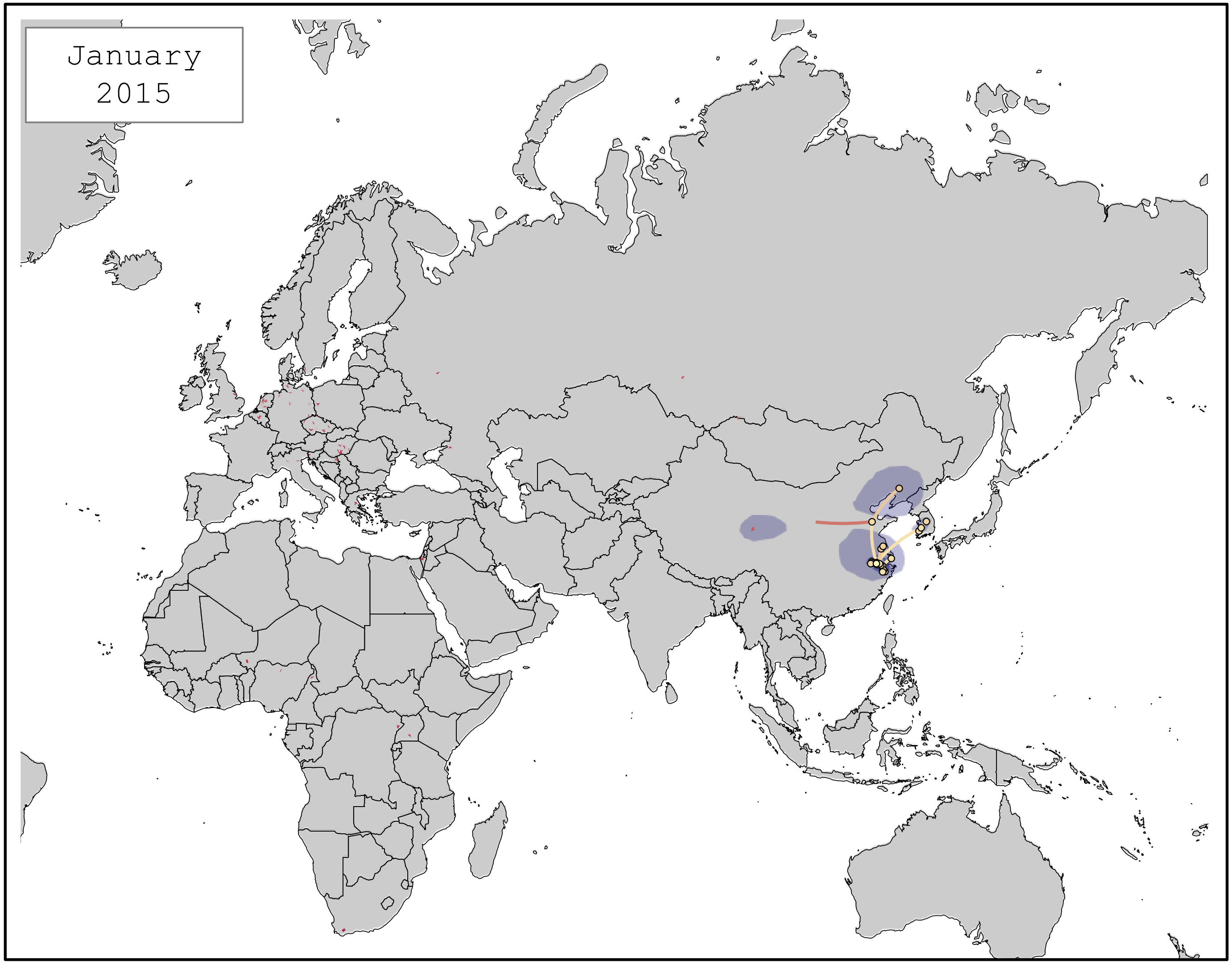
64 minority variants + 2 fixed mutation
57 HA positions showing mutations
2 to 13 variants per sample

13 minority variants in the RBD
6 minority variants in the Ag sites

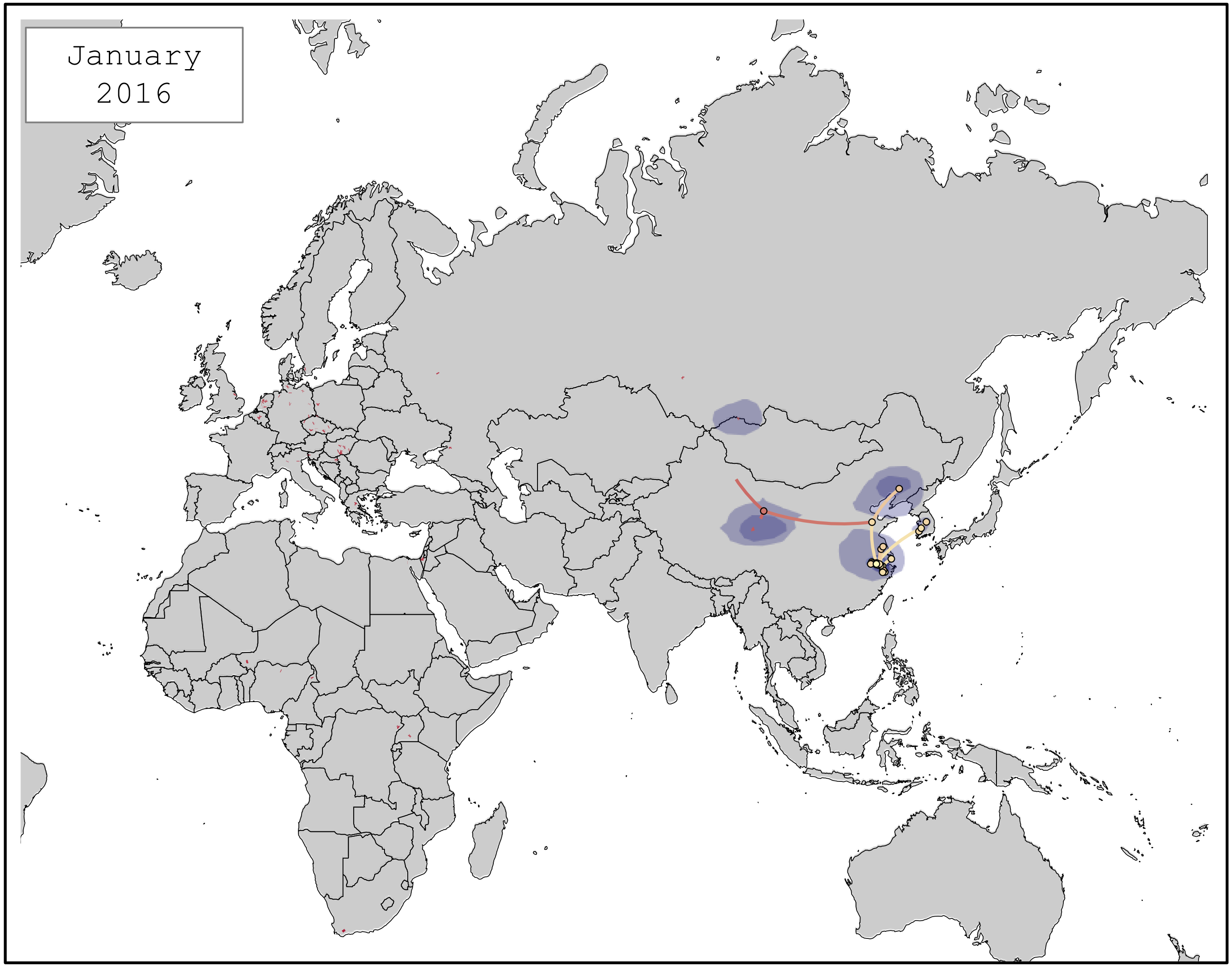
4 variants shared between samples

HPAI gs/GD:
Fast to Evolve, Faster to Spread

The initial steps across continents of the 2.3.4.4b clade



Fusaro, A., et al (2019). https://doi.org/10.1038/s41467-019-13287-y



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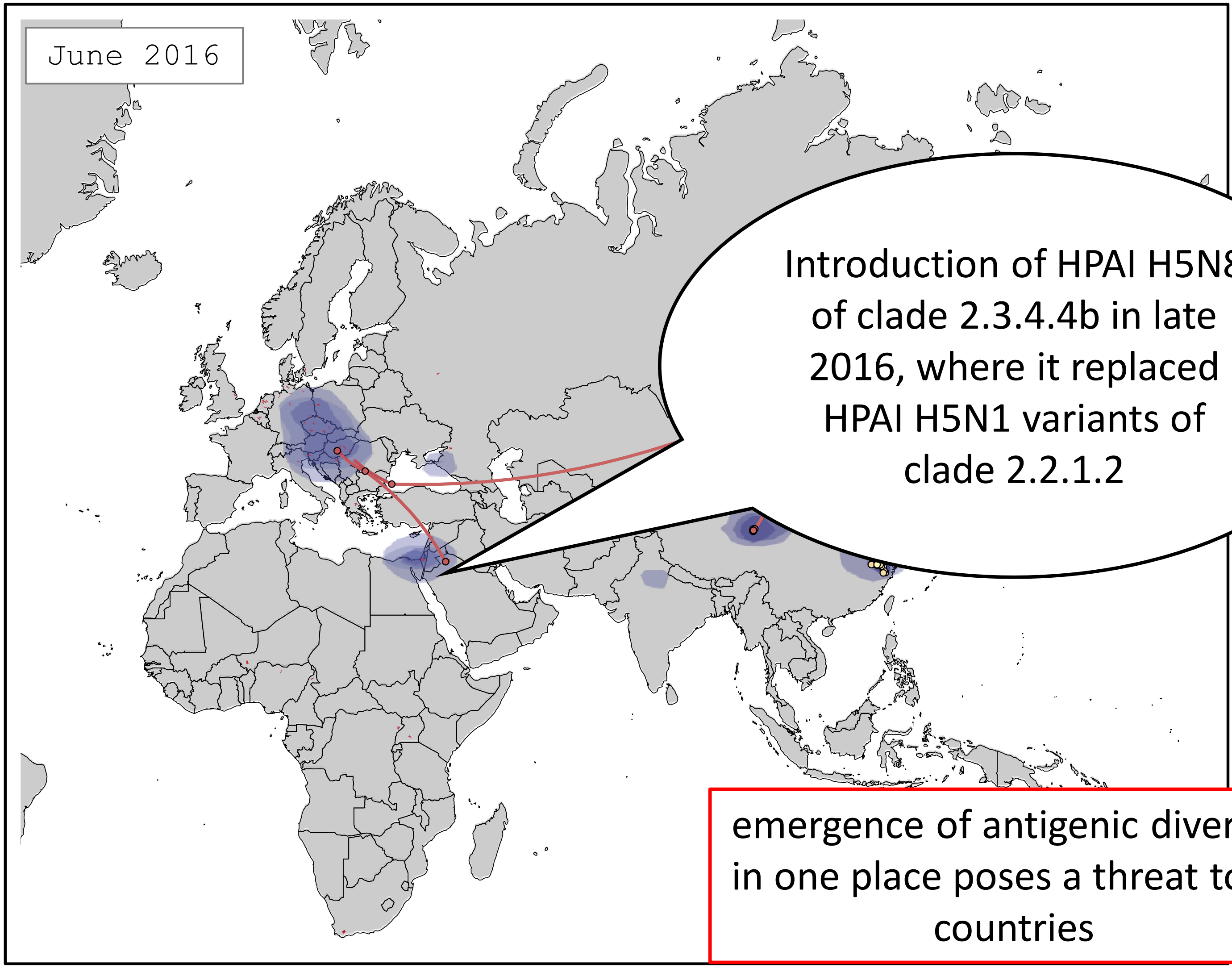
The initial steps across continents of the 2.3.4.4b clade

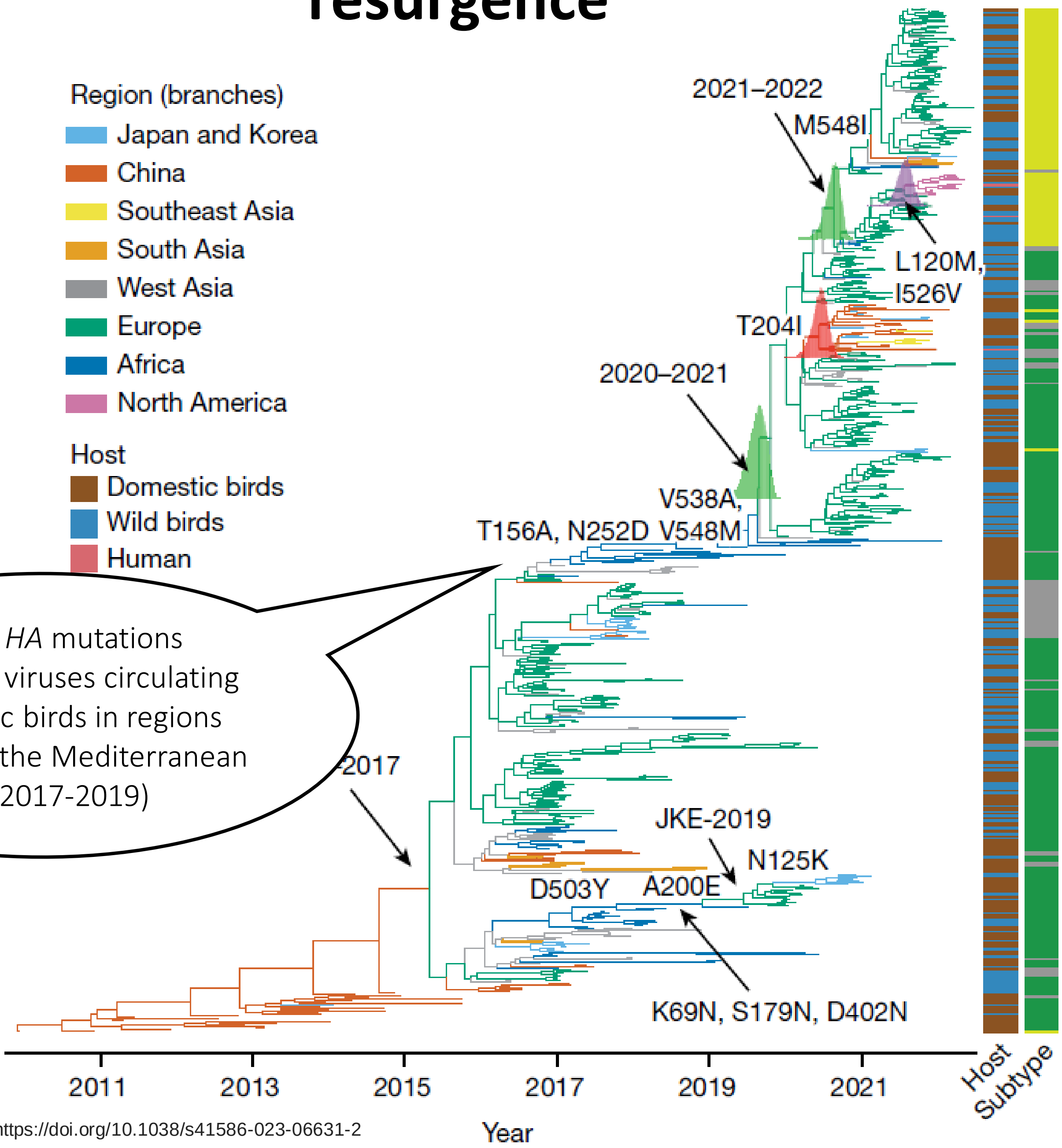


Introduction of HPAI H5N8 of clade 2.3.4.4b in late 2016, where it replaced HPAI H5N1 variants of clade 2.2.1.2

emergence of antigenic diversity in one place poses a threat to all countries

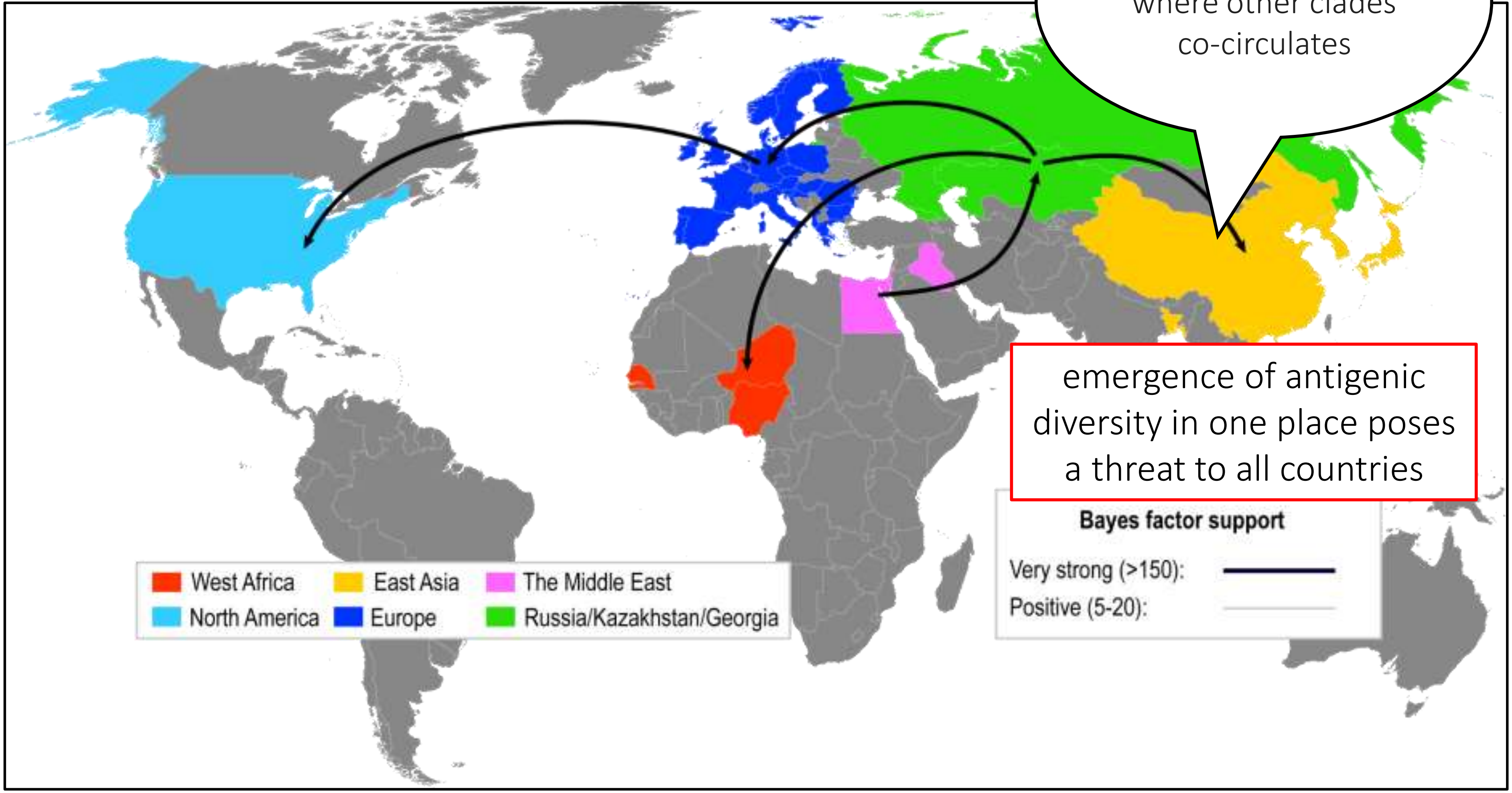
Fusaro, A., et al (2019). https://doi.org/10.1038/s41467-019-13287-y

The evolution of 2.3.4.4b clade before the 2020-2021 resurgence



Several *HA* mutations occurred in viruses circulating in domestic birds in regions southern to the Mediterranean Sea (2017-2019)

Xie, R. *et al.* *Nature* **622**, 810–817 (2023). https://doi.org/10.1038/s41586-023-06631-2



2.3.4.4b landed
where other clades
co-circulates

emergence of antigenic diversity in one place poses a threat to all countries

Fusaro A., Zecchin B., et al. Virus Evolution, 2024; https://doi.org/10.1093/ve/veae027

Clade 2.3.4.4

Clade 2.3.2.1a

Clade 2.3.2.1e

Clade 2.3.2.1c

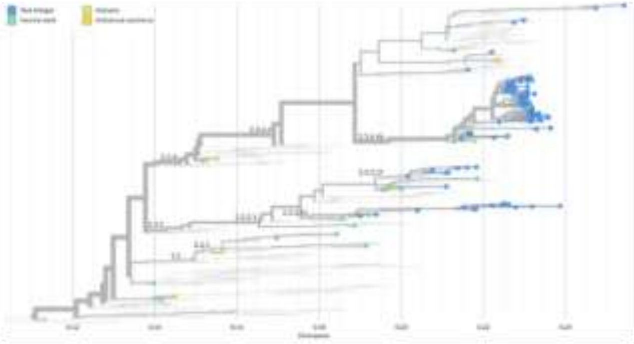
Clade 2.3.2.1a viruses are geographically restricted to South Asia
Clade 2.3.2.1c viruses are geographically restricted to the Mekong delta
Clade 2.3.2.1e viruses are restricted to the Indonesian archipelago

Cocirculation with 2.3.4.4b viruses

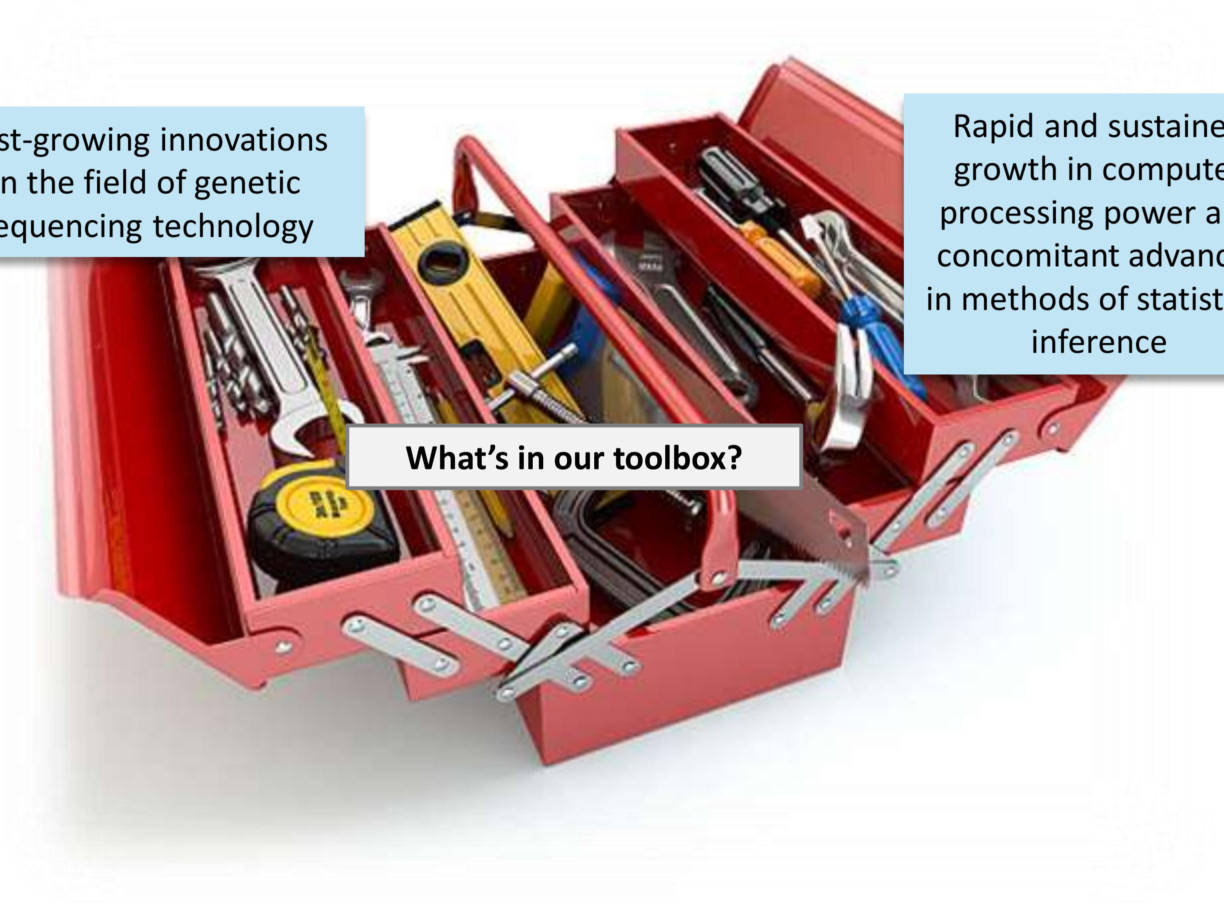
What to do to assess virus evolution to inform vaccination programs?

1.

Gene Sequences for assessing possible antigenic changes



An age of genomic plenty:
Next-generation evolutionary epidemiology

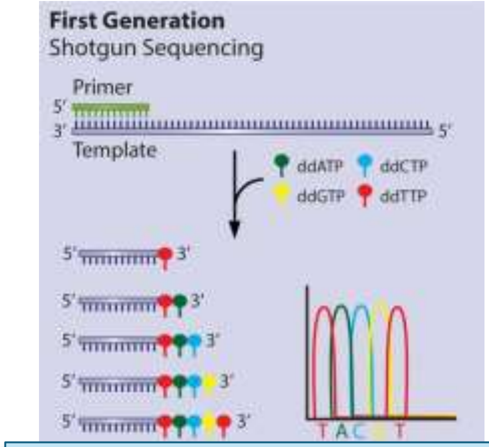


Fast-growing innovations in the field of genetic sequencing technology

Rapid and sustained growth in computer processing power and concomitant advances in methods of statistical inference

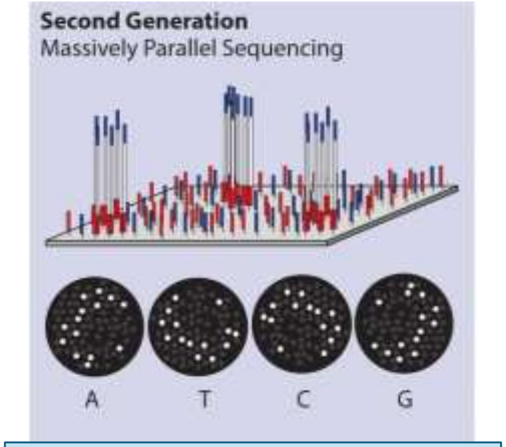
What’s in our toolbox?

Sequencing an Influenza A virus full genome (13.5Kb)



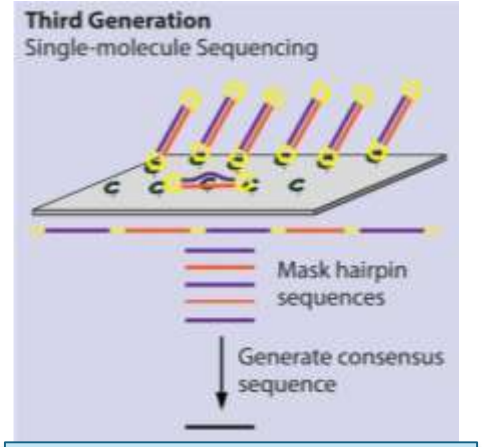
1st Generation Sequencing
(*Sanger*)

Time: @ 2 weeks
Cost: @340 €



2nd Generation
Sequencing
(*Sequencing by Synthesis*)

Time: 3 days
Cost: @70 €



3rd Generation
Sequencing
(*Nanopore sequencing*)

Time: 1 day
Cost: @80 €

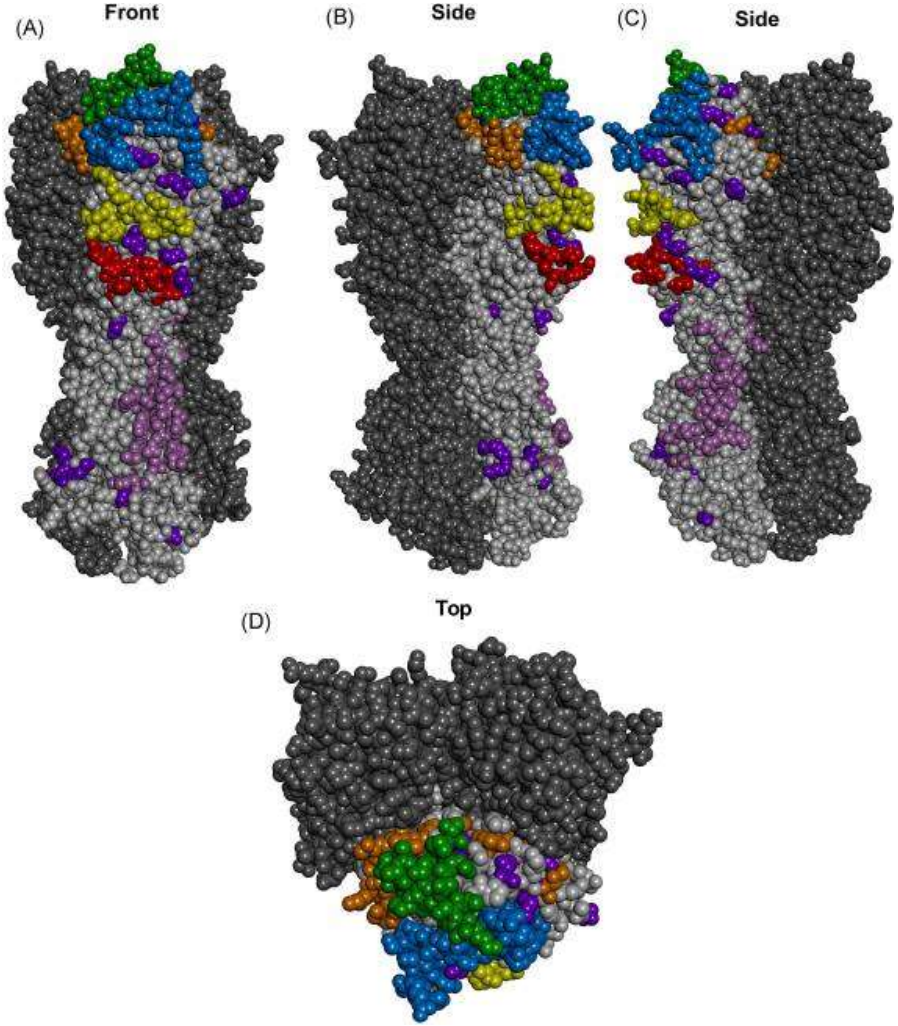
Guidance for genomic monitoring of AIV can be found here: https://www.izsvenezie.com/documents/reference-laboratories/avian-influenza/useful-resources/guidance-representative-genomic-avian-influenza-virus.pdf

PICTURE modified from J. Ronholm et al. Clin. Microbiol. Rev. 2016;29:837-857

Screening of antigenic sites (antibody mediated antigenic site)

Although genetic variation
results in antigenic variation, genetic and
antigenic distance do not always correlate.

Antigenic distances could better be predicted
screening for changes in putative antigenic sites
instead of checking the variation in the entire
HA1 target

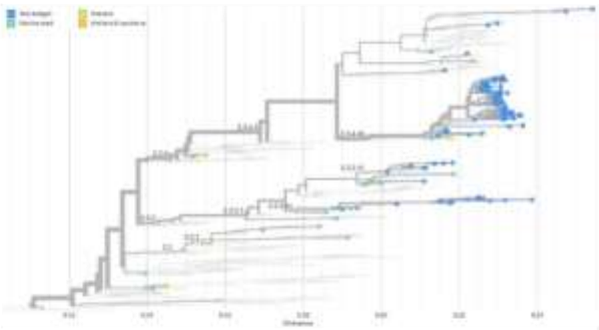


Luczo, et al, *FEMS Microbiology Reviews*, Volume 48, Issue 3, May 2024, fuae014, https://doi.org/10.1093/femsre/fuae014

What to do to assess virus evolution to inform vaccination programs?

1.

Gene Sequences for assessing possible antigenic changes



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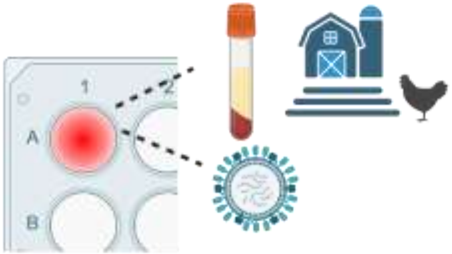
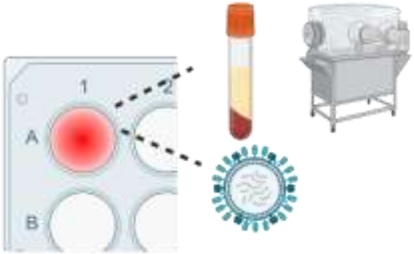


OR



Antigenic matching
Cross-HI testing using **sera** from vaccinated birds versus an antigen/virus obtained from a **field isolate** of interest.

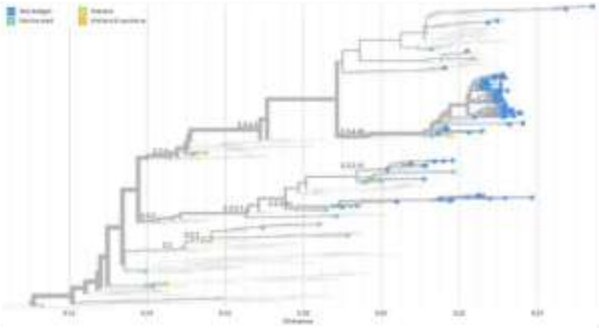
Antigenic matching
Cross-HI testing using **sera** raised against the vaccine antigen (or a closely related proxy) versus an antigen/virus obtained from a **field isolate** of interest.

Created with BioRender.com

What to do to assess virus evolution to inform vaccination programs?

1.

Gene Sequences for assessing possible antigenic changes



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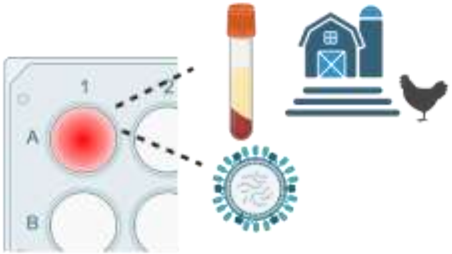
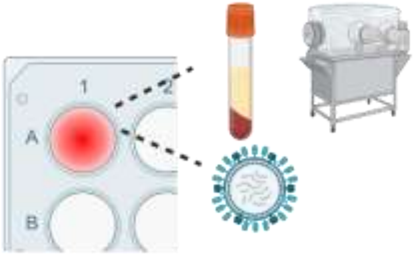


Antigenic matching
Cross-HI testing using **sera** from vaccinated birds versus an antigen/virus obtained from a **field isolate** of interest.

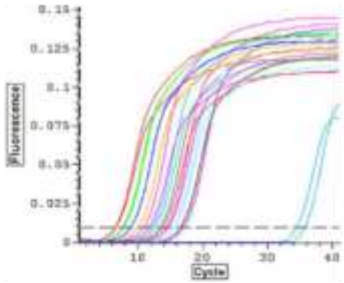
OR



Antigenic matching
Cross-HI testing using **sera** raised against the vaccine antigen (or a closely related proxy) versus an antigen/virus obtained from a **field isolate** of interest.

3.

Challenge of immunized animals



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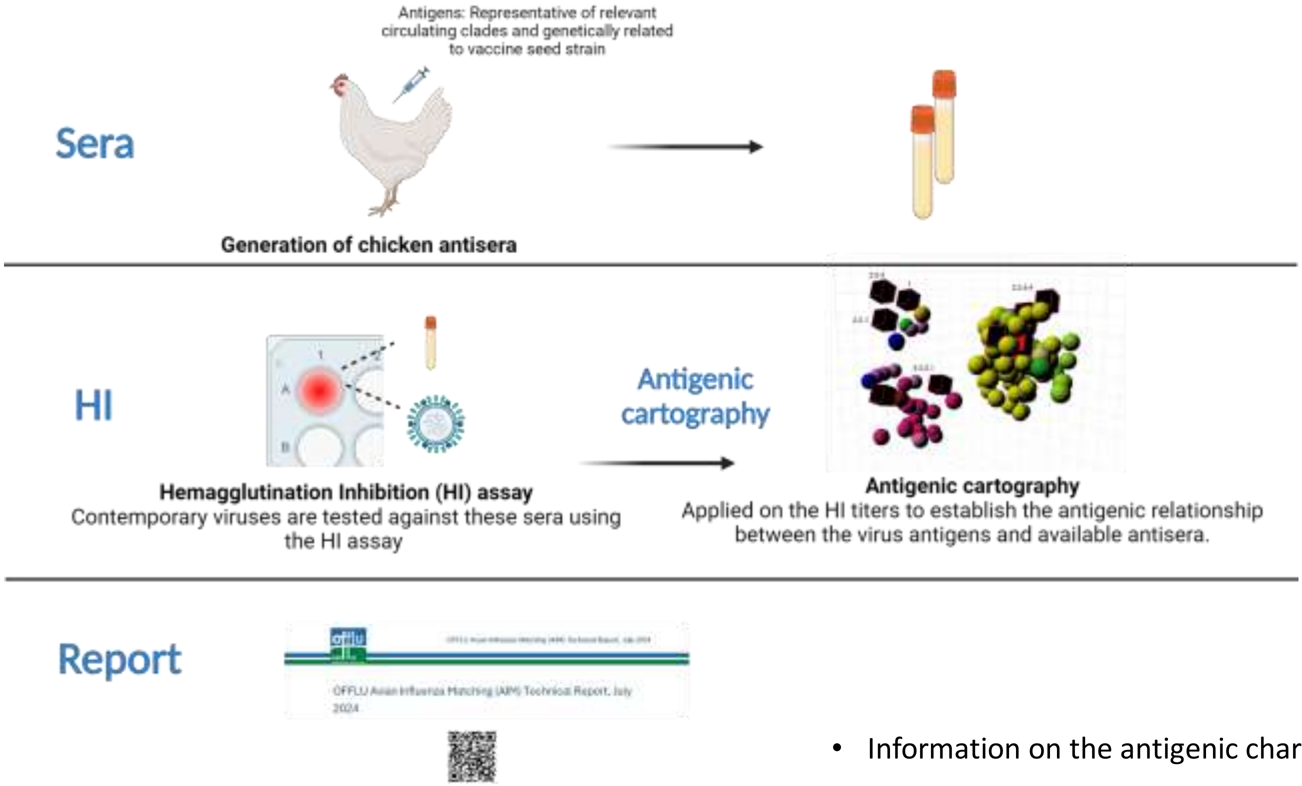
Think Globally to Protect Locally

Avian Influenza Matching (AIM) for poultry vaccines

Avian Influenza Matching (AIM) for poultry vaccines

A system for providing information to countries on the antigenic characteristics of circulating HPAI

Avian Influenza Matching (AIM) for poultry vaccines



Sera

Antigens: Representative of relevant circulating clades and genetically related to vaccine seed strain

Generation of chicken antisera

HI

Hemagglutination Inhibition (HI) assay

Contemporary viruses are tested against these sera using the HI assay

Antigenic cartography

Antigenic cartography

Applied on the HI titers to establish the antigenic relationship between the virus antigens and available antisera.

Report

OFFLU Avian Influenza Matching (AIM) Technical Report, July 2024

- Information on the antigenic characteristics of currently circulating AI viruses
- Facilitate the selection of appropriate vaccines for poultry
- Requires **sharing** of viral isolates from countries

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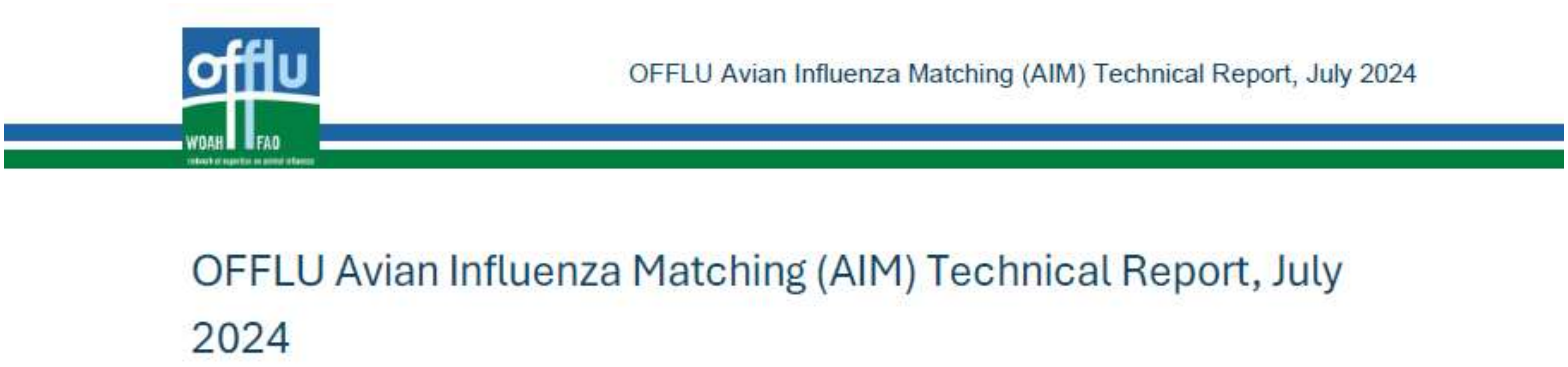


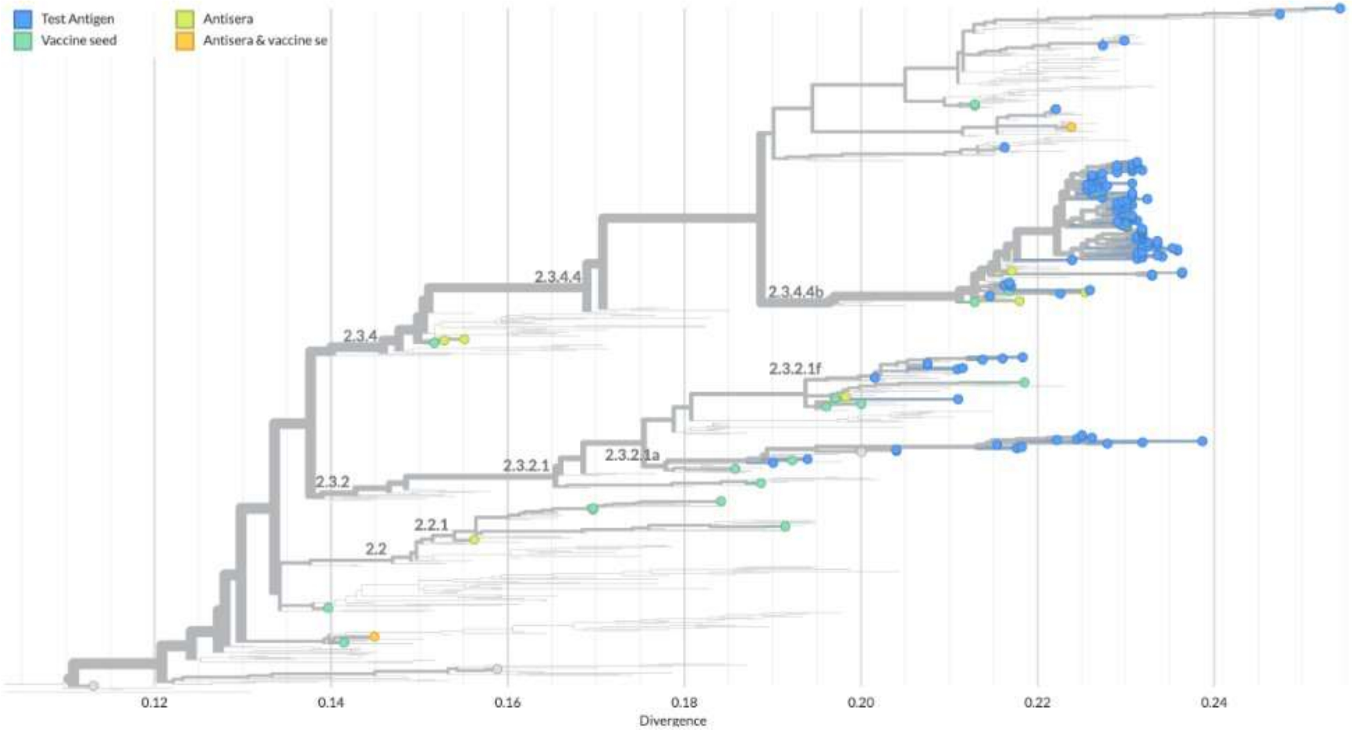
OFFLU Avian Influenza Matching (AIM) Technical Report, July 2024

OFFLU Avian Influenza Matching (AIM) Technical Report, July 2024

see technical report available online

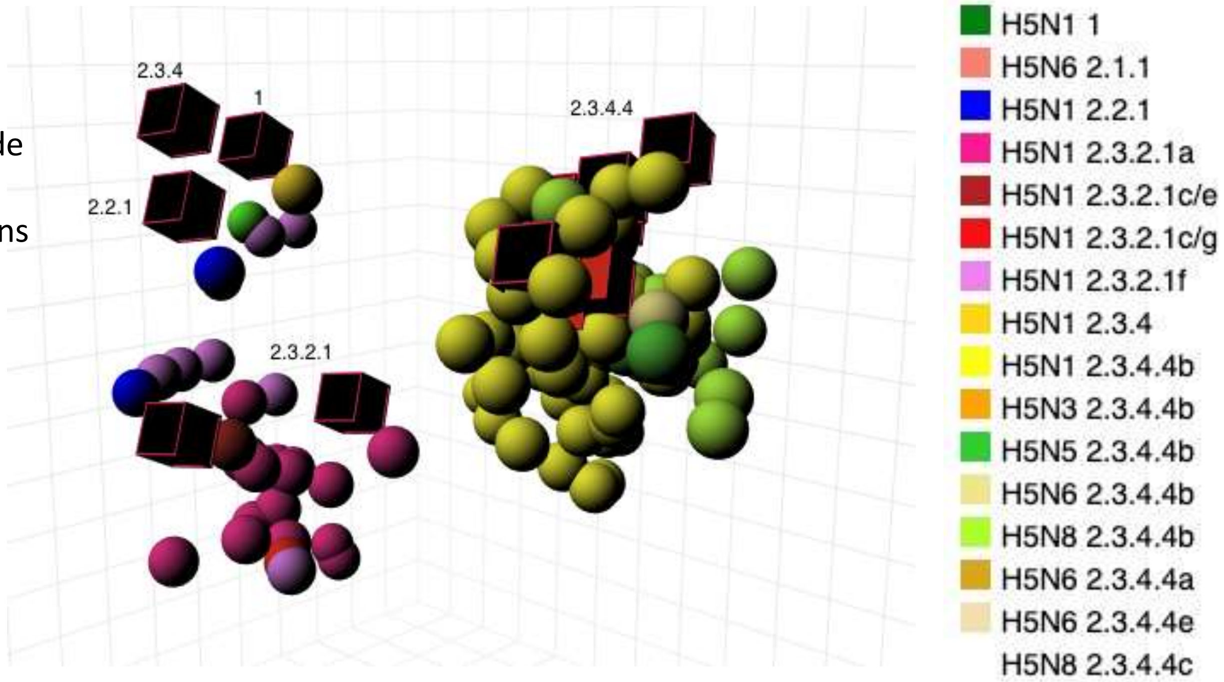
Access to sequence data is essential for initial genetic assessment

- Global dominance of H5Nx clade 2.3.4.4b has led to this clade being **over sampled** within the analyses



Antigenic assessment gives an indication of diversity

- Vaccine antigens not within the clade 2.3.4.4 are antigenically distant from clade 2.3.4.4b viruses and would not be expected to be suitable candidate antigens for inactivated whole virus vaccines against these strains



It is important to understand geographical features of viral evolution

- Antigenically clade 2.3.4.4b moderately stable

- To maintain sample anonymity within the data set samples are not named but are simply stated as representatives of geographical regions using continent level criteria

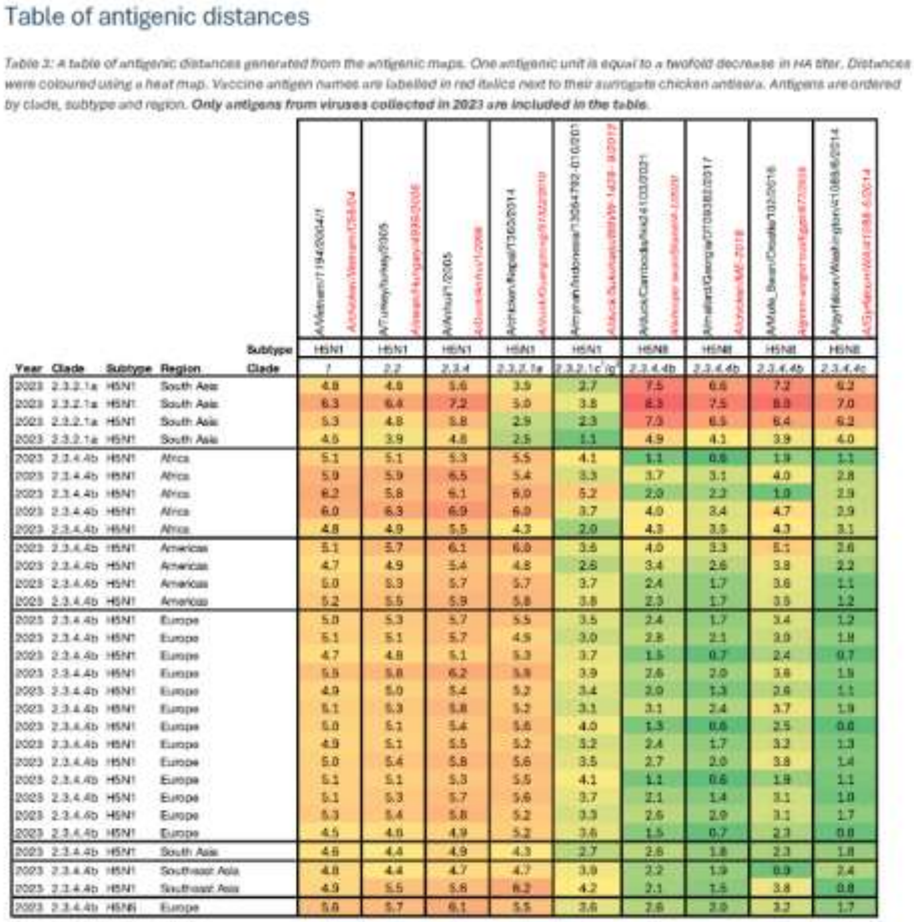


Table of antigenic distances

Table 3: A table of antigenic distances generated from the antigenic maps. One antigenic unit is equal to a twofold decrease in HA titer. Distances were coloured using a heat map. Vaccine antigen names are labelled in red italics next to their surrogate chicken antisera. Antigens are ordered by clade, subtype and region. ***Only antigens from viruses collected in 2023 are included in the table.***

					A/Vietnam/1194/2004/1 *A/chicken/Vietnam/C58/04*	A/Turkey/turkey/2005 *A/swan/Hungary/4999/2006*	A/Anhui/1/2005 *A/Duck/Anhui/1/2006*	A/chicken/Nepal/T360/2014 *A/duck/Guangdong/S1322/2010*	A/myna/Indonesia/13064792-010/201 *A/duck/Sukoharjo/BBVW-1428-9/2012*	A/duck/Cambodia/AAd24103/2021 *A/whooper swan/Shanxi/4-1/2020*	A/mallard/Georgia/OT09382/2017 *A/chicken/ME-2018*	A/Mute_Swan/Croatia/102/2016 *A/green-winged teal/Egypt/877/2016*	A/gyrfalcon/Washington/41088/6/2014 *A/Gyrfalcon/WA/41088-6/2014*
				Subtype	H5N1	H5N1	H5N1	H5N1	H5N1	H5N8	H5N8	H5N8	H5N8
Year	**Clade**	**Subtype**	**Region**	**Clade**	*1*	*2.2*	*2.3.4*	*2.3.2.1a*	*2.3.2.1c'/g'*	*2.3.4.4b*	*2.3.4.4b*	*2.3.4.4b*	*2.3.4.4c*
2023	2.3.2.1a	H5N1	South Asia		4.8	4.8	5.6	3.9	2.7	7.5	6.6	7.2	6.2
2023	2.3.2.1a	H5N1	South Asia		6.3	6.4	7.2	5.0	3.8	8.3	7.5	8.0	7.0
2023	2.3.2.1a	H5N1	South Asia		5.3	4.8	5.8	2.9	2.3	7.0	6.5	6.4	6.2
2023	2.3.2.1a	H5N1	South Asia		4.6	3.9	4.8	2.5	1.1	4.9	4.1	3.9	4.0
2023	2.3.4.4b	H5N1	Africa		5.1	5.1	5.3	5.5	4.1	1.1	0.8	1.9	1.1
2023	2.3.4.4b	H5N1	Africa		5.9	5.9	6.5	5.4	3.3	3.7	3.1	4.0	2.8
2023	2.3.4.4b	H5N1	Africa		6.2	5.8	6.1	6.0	5.2	2.0	2.3	1.0	2.9
2023	2.3.4.4b	H5N1	Africa		6.0	6.3	6.9	6.0	3.7	4.0	3.4	4.7	2.9
2023	2.3.4.4b	H5N1	Africa		4.8	4.9	5.5	4.3	2.0	4.3	3.5	4.3	3.1
2023	2.3.4.4b	H5N1	Americas		5.1	5.7	6.1	6.0	3.5	4.0	3.3	5.1	2.6
2023	2.3.4.4b	H5N1	Americas		4.7	4.9	5.4	4.8	2.6	3.4	2.6	3.8	2.2
2023	2.3.4.4b	H5N1	Americas		5.0	5.3	5.7	5.7	3.7	2.4	1.7	3.6	1.1
2023	2.3.4.4b	H5N1	Americas		5.2	5.5	5.9	5.8	3.8	2.3	1.7	3.5	1.2
2023	2.3.4.4b	H5N1	Europe		5.0	5.3	5.7	5.5	3.5	2.4	1.7	3.4	1.2
2023	2.3.4.4b	H5N1	Europe		5.1	5.1	5.7	4.5	3.0	2.8	2.1	3.0	1.8
2023	2.3.4.4b	H5N1	Europe		4.7	4.8	5.1	5.3	3.7	1.5	0.7	2.4	0.7
2023	2.3.4.4b	H5N1	Europe		5.5	5.8	6.2	5.8	3.9	2.6	2.0	3.6	1.5
2023	2.3.4.4b	H5N1	Europe		4.9	5.0	5.4	5.2	3.4	3.0	1.3	2.6	1.1
2023	2.3.4.4b	H5N1	Europe		5.1	5.3	5.8	5.2	3.1	3.1	2.4	3.7	1.9
2023	2.3.4.4b	H5N1	Europe		5.0	5.1	5.4	5.6	4.0	1.3	0.6	2.5	0.6
2023	2.3.4.4b	H5N1	Europe		4.9	5.1	5.5	5.2	3.2	2.4	1.7	3.2	1.3
2023	2.3.4.4b	H5N1	Europe		5.0	5.4	5.8	5.6	3.5	2.7	2.0	3.8	1.4
2023	2.3.4.4b	H5N1	Europe		5.1	5.1	5.3	5.5	4.1	1.1	0.6	1.9	1.1
2023	2.3.4.4b	H5N1	Europe		5.1	5.3	5.7	5.6	3.7	2.1	1.4	3.1	1.0
2023	2.3.4.4b	H5N1	Europe		5.3	5.4	5.8	5.2	3.3	2.6	2.9	3.1	1.7
2023	2.3.4.4b	H5N1	Europe		4.5	4.0	4.9	5.2	3.6	1.5	0.7	2.3	0.8
2023	2.3.4.4b	H5N1	South Asia		4.6	4.4	4.9	4.3	2.7	2.6	1.8	2.3	1.8
2023	2.3.4.4b	H5N1	Southeast Asia		4.8	4.4	4.7	4.7	3.9	2.2	1.9	0.9	2.4
2023	2.3.4.4b	H5N1	Southeast Asia		4.9	5.5	5.8	6.2	4.2	2.1	1.5	3.8	0.8
2023	2.3.4.4b	H5N6	Europe		5.8	5.7	6.1	5.5	3.6	2.6	2.0	3.2	1.7

Major gaps – information sharing request

Food and Agriculture Organization of the United Nations

World Organisation for Animal Health

What we need from you

- Updates from the field
- Stakeholder engagement

Information on vaccine seed strains which are in use (sequence data, viral isolate)

Comprehensive information and viral isolates from vaccine breakdown

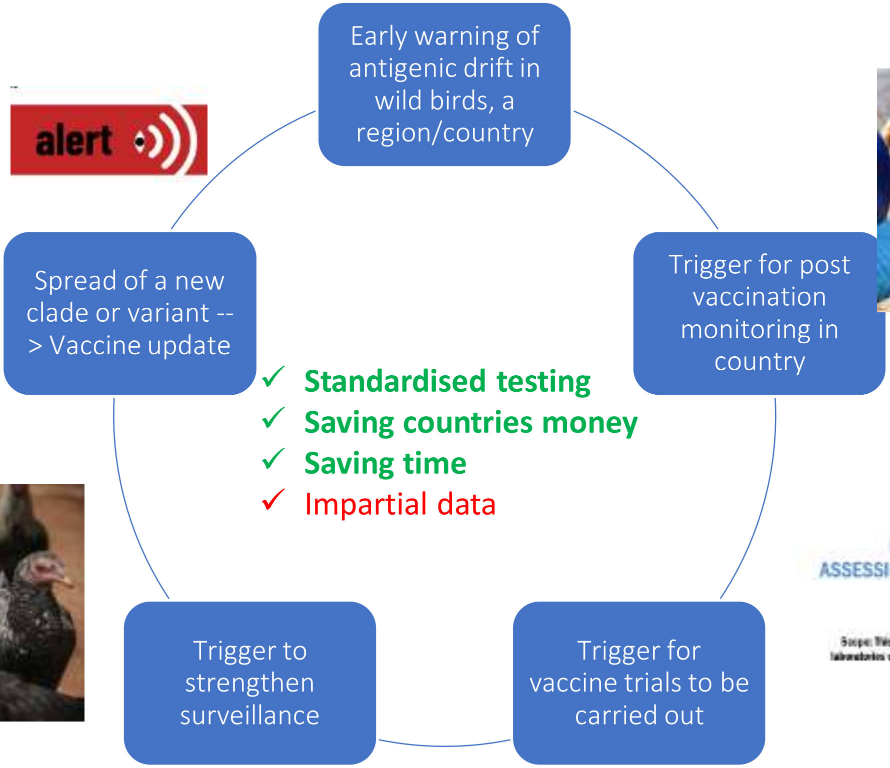
MEASURING UNIT

Animal

Species		Susceptible	Cases	Deaths	Killed and Disposed of	Slaughtered/ Killed for commercial use	Vaccinated
Birds (DOMESTIC)	NEW	53952	49048	94	53858	0	15098
	TOTAL	415932	[illegible]	554	415378	0	15098

Seed Strain / HA Gene Source	Clade[1]	Reference	Represented
A/Goose/Guangdong/96	0*	Shi et al., 2022	No
A/chicken/Vietnam/C58/04	1*	EFSA 2023	Yes
A/Vietnam/1194/2004	1*	EFSA 2023	Yes
A/Chicken/Shanxi/2/2006	7.2*	Shi et al., 2022	No
A/Chicken/Liaoning/S4092/2011	7.2	Shi et al., 2022	No
A/chicken/Legok/2003	2.1.1	EFSA 2023	Pending
A/CK/Egypt/ME1010/2016	2.2.1.1	EFSA 2023	Pending
A/Chicken/Egypt/Q1995D/2010	2.2.1.2*	EFSA 2023	Pending
A/Chicken/Egypt/RG-173 CAL/2017	2.2.1.2	EFSA 2023	Pending
A/Duck/EGYPT/M2583D/2010	2.2.1.2*	EFSA 2023	Pending
A/chicken/West Java/Pwt-Wij/2006	2.3.1.2	EFSA 2023	No
A/duck/Sukoharjo/BBVW-1428-9/2012	2.3.2.1g[2]*	Indriani et al., 2014	Yes
A/Hubei/1/2010	2.3.2.1a[2]*	EFSA 2023	Pending
A/duck/Guangdong/S1322/2010	2.3.2.1b[2]*	Shi et al., 2022	Yes
A/chicken/Vietnam/NCVD-KA435/13	2.3.2.1c[1]/e[2]*	EFSA 2023	Pending
A/chicken/Tanggamus/031711076-65/2017	2.3.2.1c	EFSA 2023	No
A/chicken/Liaoning/SD007/2017	2.3.2.1d	Shi et al., 2022	Pending
rgCA2/2.3.2.1d	2.3.2.1d	Kang et al., 2022	No
A/duck/Anhui/SI246/2014	2.3.2.1	Shi et al., 2022	No
A/Duck/Anhui/1/2006	2.3.4*	Shi et al., 2022	Yes
A/chicken/Guizhou/4/2013	2.3.4.4/g[2]*	Shi et al., 2022	No
A/duck/Korea/ES2/2016	2.3.4.4/e[2]*	EFSA 2023	Pending
A/Waterfowl/Korea/S57/2016	2.3.4.4	Kuruppuarachchi et al., 2022	No
A/Gyrfalcon/WA/41088-6/2014	2.3.4.4c[2]*	EFSA 2023	Yes
A/chicken/Egypt/ME-2018/2018	2.3.4.4b[2]*		Yes
A/green-winged teal/Egypt/877/2016	2.3.4.4b[2]*	EFSA 2023	Yes
A/whooper swan/Shanxi/4–1/2020	2.3.4.4b[2]*	Shi et al., 2022	Yes
A/duck/Guizhou/S4184/2017	2.3.4.4h	Shi et al., 2022	Pending
A/duck/Fujian/S1424/2020	2.3.4.4h	Shi et al., 2022	Pending
rgES3/2.3.4.4h	2.3.4.4h	Kang et al., 2022	No
A/duck/Guanzou/S4184/2017	2.3.4.4h	Shi et al., 2022	Pending
A/Duck/VietNam/QB7412	unknown	EFSA 2023	No

Stakeholder application of OFFLU AIM outputs



- Early warning of antigenic drift in wild birds, a region/country
- Trigger for post vaccination monitoring in country
- Trigger for vaccine trials to be carried out
- Trigger to strengthen surveillance
- Spread of a new clade or variant --> Vaccine update

✓ **Standardised testing**
✓ **Saving countries money**
✓ **Saving time**
✓ Impartial data

OFFLU AVIAN INFLUENZA MATCHING (OFFLU AIM) GUIDE TO ASSESSING ANTIGENIC CHARACTERISTICS OF AVIAN INFLUENZA VIRUSES

Updated June 2024

Scope: This report provides information for national/sub-national level laboratories on how to assess antigenic characteristics of avian influenza viruses.

OFFLU Guide for countries

Where do I find the documents?

https://www.offlu.org/index.php/offlu-aim-background-documents/

- www.offlu.org
- OFFLU AIM

OFFLU summary report for the WHO vaccine composition meeting September 2024

Updated OFFLU statement on HPAI in dairy cows

OFFLU statement on HPAI in dairy cows

OFFLU summary report for the WHO vaccine composition meeting February 2024

OFFLU call to discuss AI in the Latin America and Caribbean region

Flu Global Net article: Preliminary Genomic Analysis of H5N1 HPAIV from South Georgia

Updated joint FAO/WHO/WOAH assessment of recent influenza A(H5N1) viruses in animals and people

FAO publication A(H5N1) influenza in dairy cattle in the United States of America

OFFLU global technical meeting Agenda

Diagnostic guidance: HPAI dairy cattle

OFFLU annual report 2023

OFFLU-WHO VCM February 2024 full report (Avian influenza)

OFFLU-WHO VCM February 2024 full report (Swine influenza)

Scan the QR code to give your feedback on OFFLU AIM and sign up for future updates

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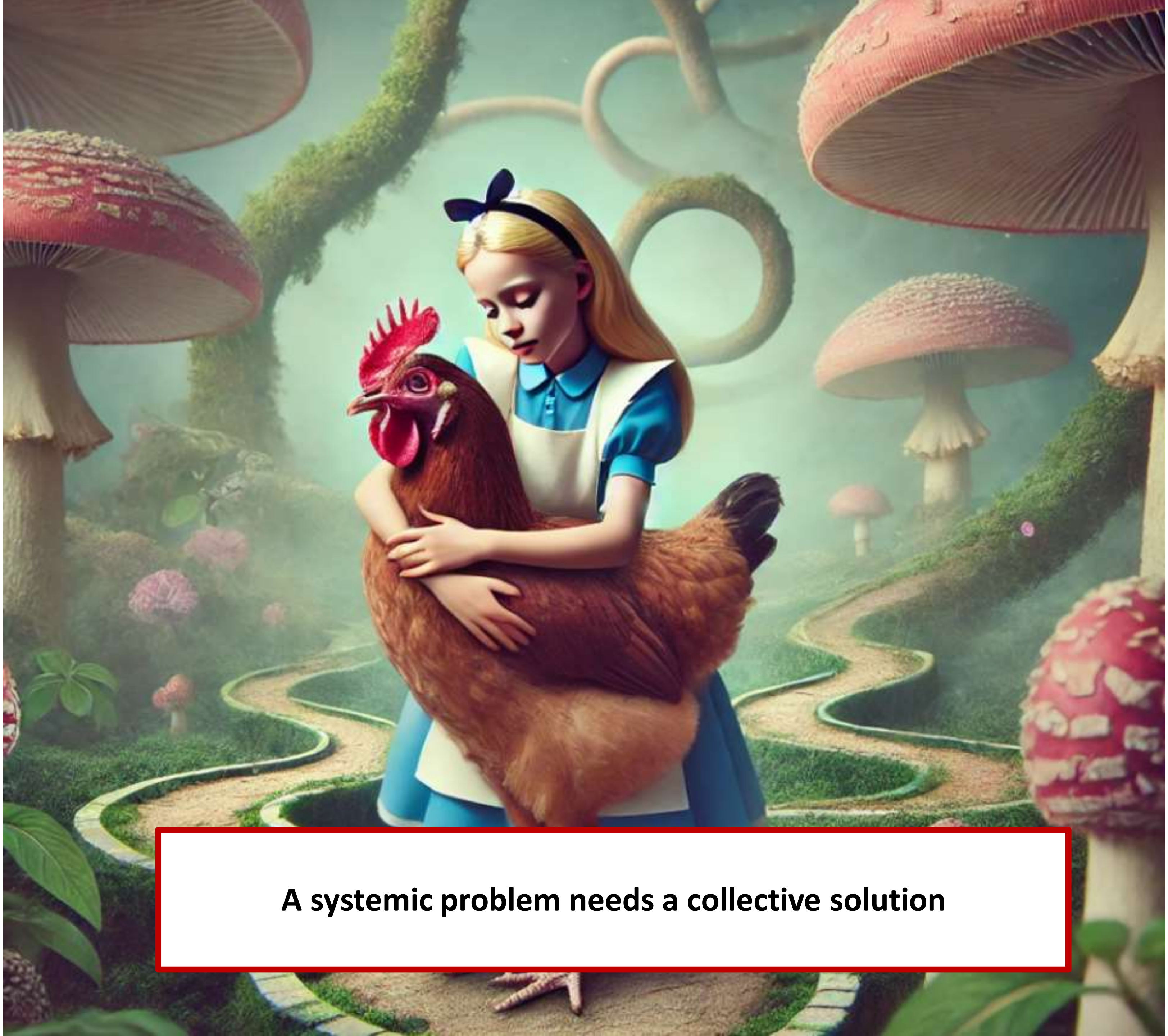
The OFFLU website has regular updates on OFFLU and parent organisations' publications, technical advice, protocols and many other useful links. Please visit: www.offlu.org for more information

- For any questions please contact: secretariat@offlu.org



A systemic problem needs a collective solution

Conclusions and future requirements

- Dealing with this impressive and dynamic diversity is paramount to **monitor in real time the HPAIV evolution** in its multiple hosts and its multiple geographical contexts;
- Adopting a comprehensive, **globally coordinated approach** to surveillance and vaccine updates is vital;
- We need all to assist initiatives such as OFFLU AIM to enhance the data sets and validate the outcomes;
- The outputs can only ever be as good as the data that its based on.

Acknowledgements

The authors, originating and submitting laboratories of the sequences from GISAID's EpiFlu™ Database.

World Organisation for Animal Health
Founded as OIE

Food and Agriculture Organization of the United Nations

Acknowledgements

offlu
WOAH FAO
network of expertise on animal influenza

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All countries sharing viruses and information with the International Reference Laboratories for Avian Influenza.

Thank you
for your attention