

OFFLU contributions to the WHO Vaccine Composition Meeting (WHO VCM)

Amelia Coggon - OFFLU Scientist

Frank Wong – Chair of OFFLU Avian Influenza TA & OFFLU Executive Committee



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OFFLU VCM coordinators and contributors

WOAH: Gounalan Pavade (OFFLU Secretariat)

Crick/RVC: Nicola Lewis (Activity Lead)

USDA: Amy Vincent (Swine coordinator)

FAO: Amelia Coggon (OFFLU Scientist)

Antigenic data

ACDP (Frank Wong); APHA (Joe James, Ashley Banyard);
IZSve (Francesco Bonefante); USDA-ARS (Tavis Anderson)

Genetic Data

ACDP, ANSES, APHA, ARRIAH, CAN, ICAR, IZSve IZSVL,
Ghent University, NIAH, Institut Pasteur, SSI, USDA-APHIS
NVSL, USDA-ARS NADC RVC, WUR, GenBank, GISAID,
CEIRR

Countries:

Albania, Austria, Australia, Bangladesh, Belgium, Benin, Bulgaria, Burkina Faso,
Canada, China, China Hong Kong SAR, Croatia, Czechia, Denmark, Egypt, Estonia,
Finland, France, Germany, Greece, Hungary, India, Indonesia, Iraq, Ireland, Israel,
Italy, Japan, Republic of Korea, Kosovo, Lao PDR, Latvia, Lesotho, Lithuania,
Luxembourg, Mali, Republic of Moldova, Netherlands, Niger, Nigeria, Norway,
Poland, Portugal, Romania, Russian Federation, Senegal, Slovakia, Slovenia, Spain,
Sweden, Switzerland, United Kingdom of Great Britain and Northern Ireland, United
States of America, Viet Nam

Other report Contributors

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WHO bi-annual Vaccine Composition Meeting

- Seasonal influenza vaccines are updated
- Northern hemisphere in February
- Southern hemisphere in September
- Coordinated by the WHO global influenza surveillance and response system (GISRS)
- Candidate Vaccine Viruses (CVVs) are also developed for Pandemic preparedness
- CVVs are viruses which are prepared for the potential use in vaccine manufacturing, they are a recommendation

WHO VCM Participants

- OFFLU attendance since 2011
- WHO Collaborating Centres
- WHO Essential Regulatory Laboratories (ERLs)
- National Influenza Centres (NICs)
- WHO H5 Reference Laboratories

Zoonotic influenza

- Important context to specific human cases caused by zoonotic influenza
- Providing epidemiological context
- Avian Influenza
 - Low pathogenic H3, H7 anhui lineage, H9 and H10 viruses
 - Highly pathogenic H5 and H7 viruses
- Swine Influenza
 - H1 and H3 subtypes



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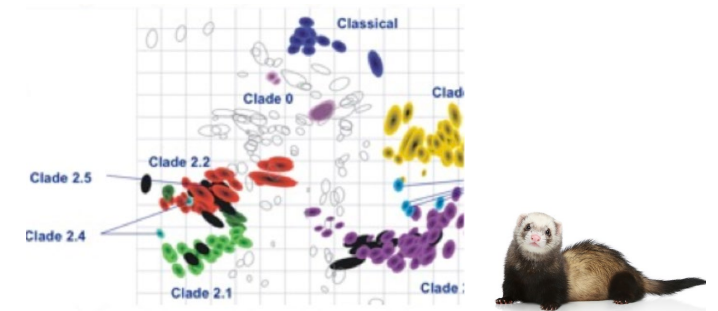
World Health
Organization



OFFLU VCM reports



Evaluation of genetic changes of significance compared to candidate vaccine viruses (CVV) for pandemic preparedness



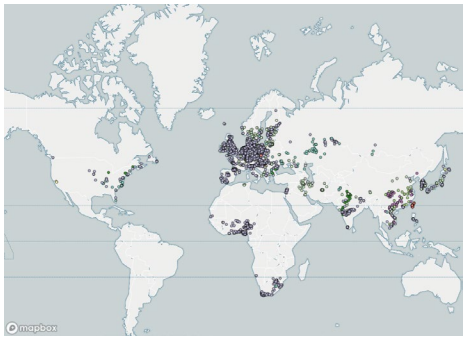
Antigenic properties of viruses quantitatively assessed using harmonized protocols in OFFLU contributing laboratories



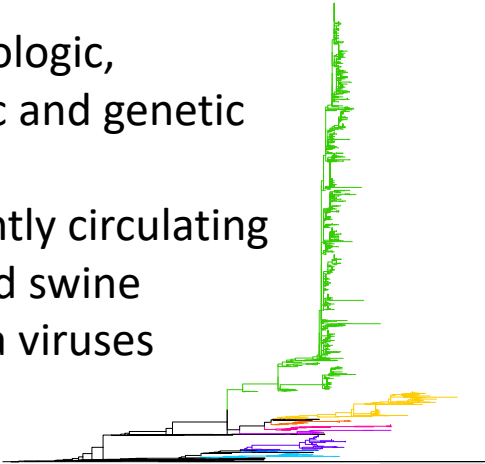
World Health Organization



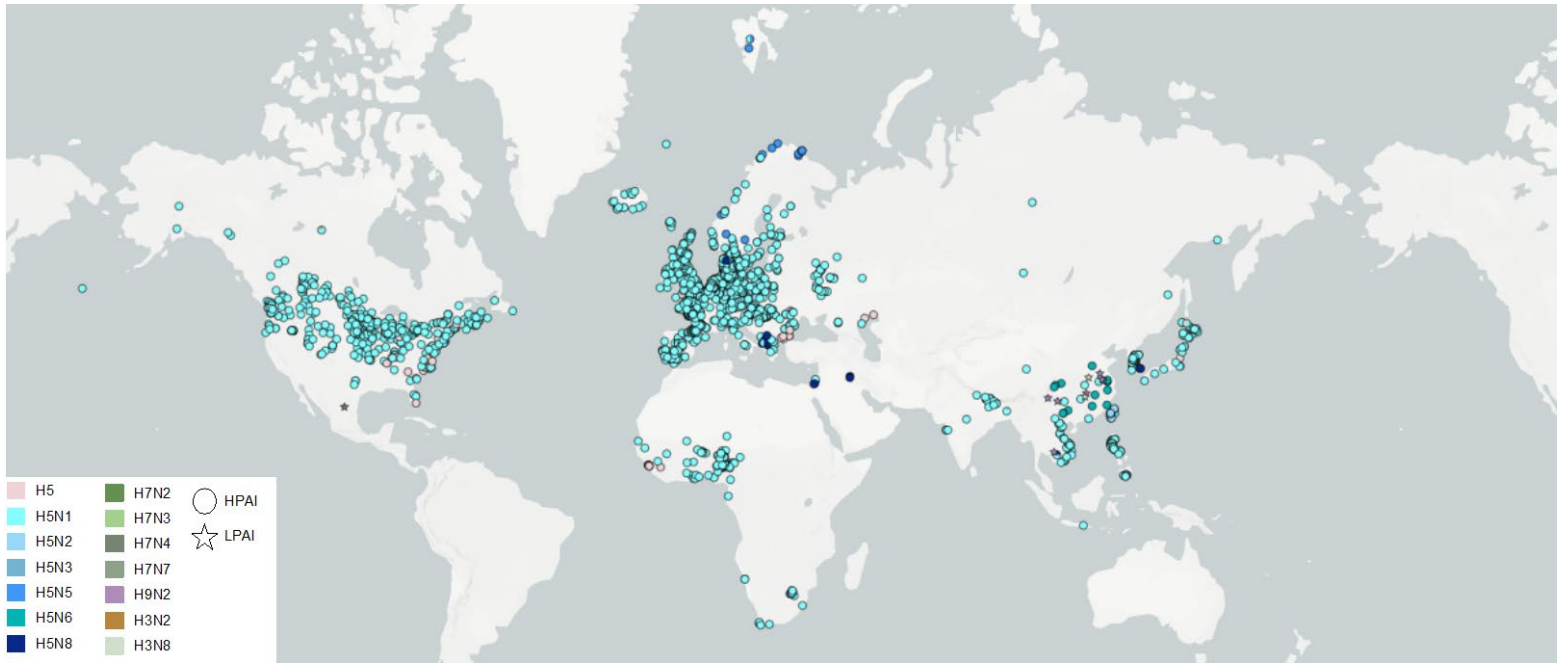
- OFFLU data package presented
- Discussed in the context of zoonotic human influenza cases
- WHO VCM zoonotic report
- Updates to CVVs



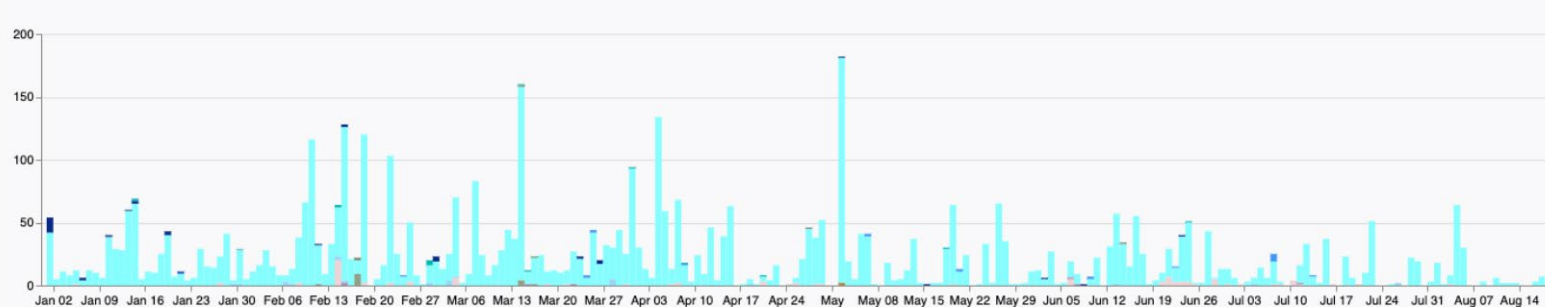
Epidemiologic, antigenic and genetic analyses of currently circulating avian and swine influenza viruses



Avian VCM report September 2022



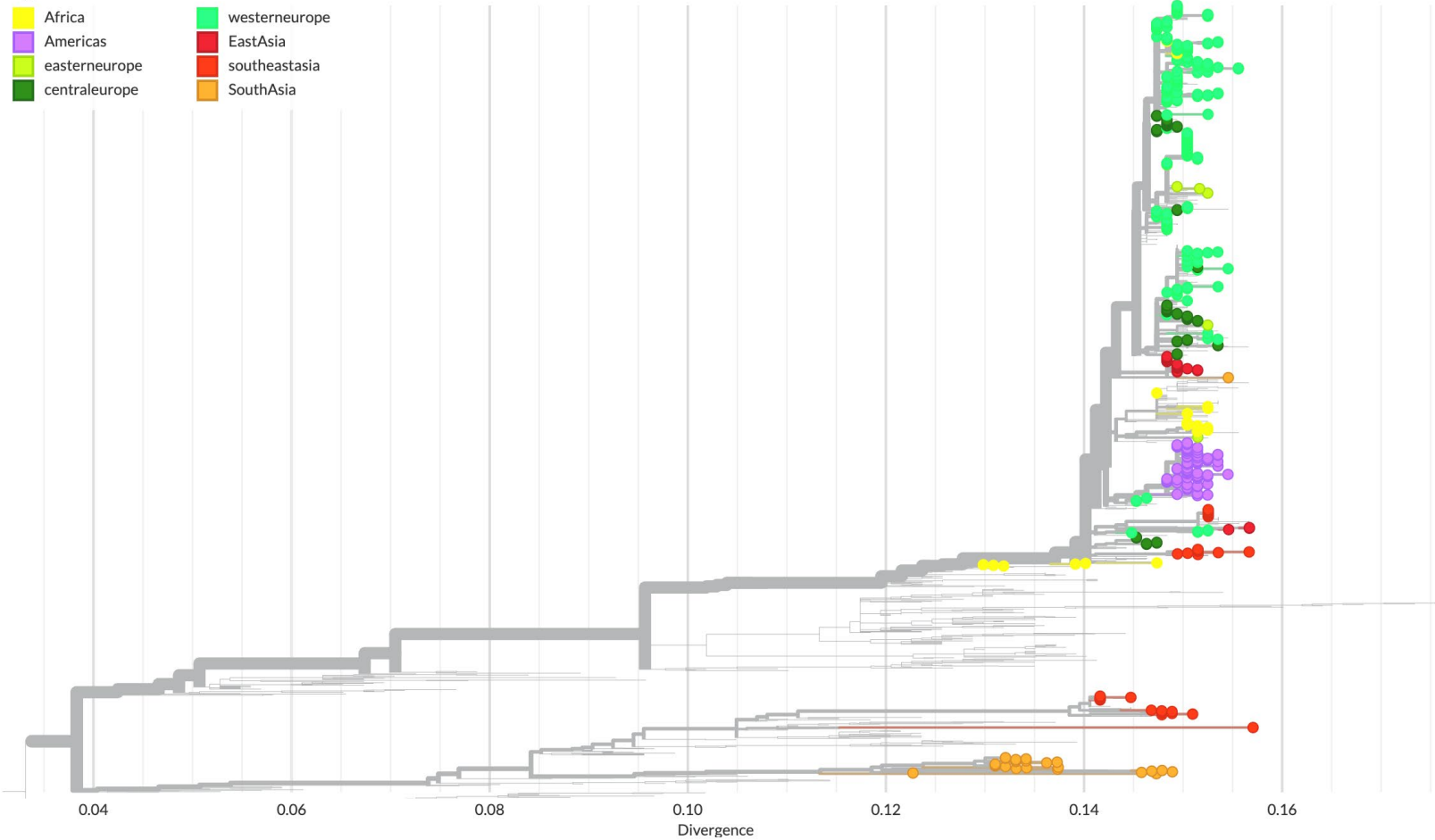
- Global spread of H5Nx viruses
- Outbreaks in poultry
- Detections in wild bird



Avian H5 viruses

Region ^

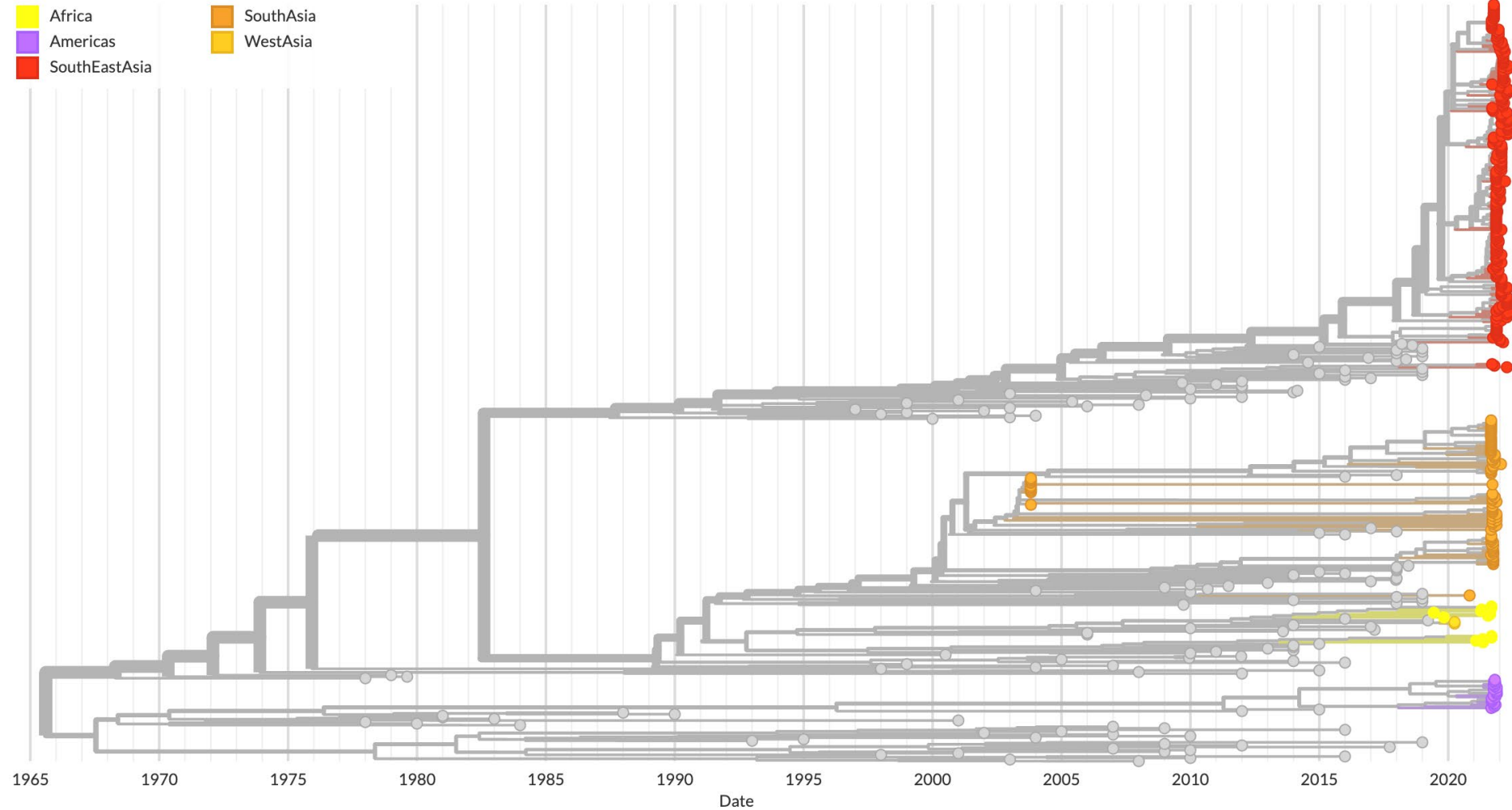
- Africa
- Americas
- easterneurope
- centraleurope
- westernurope
- EastAsia
- southeastasia
- SouthAsia



Avian H9 viruses

Region ^

- Africa
- Americas
- SouthEastAsia
- SouthAsia
- WestAsia



Highlights- September 2022

- New Clade 2.3.4.4b candidate vaccine virus proposed
- New H3N8 candidate vaccine virus proposed
Based on information from 2 human cases in China
Exposure to poultry
New virus of avian origin with Eurasian and Pacific Flyway lineage HA and NA genes, respectively. The remaining gene segments were most similar to A(H9N2) viruses.
Related viruses were detected in samples from live bird markets in China.

Highlights – Data sharing

- Sequence sharing:
588 HPAI H5, 60 LPAI H7 and 89 LPAI H9 avian sequences 345 H1 and 116 H3 swine sequences
- Antigenic Characterisation- Avian :
23, H5 2.3.4.4b
four, H5 2.3.2.1a
two H9 G2
- Antigenic Characterisation- Swine:
10, H1A
4, H1B
7, H1C
4 H3

Challenges

- Getting geographically representative data of the current situation
- Insufficient/inconsistent resources for surveillance and sequencing
- Many independent surveillance projects for which data isn't shared through official channels
- Timely sharing of whole genome sequence data to publicly available repositories such as GISAID
- Lack of surveillance data on non-notifiable subtypes such as H9 or H3s
- Trade implications
- Virus sharing is important and shipment of live samples can take time and are costly
- Benefits to sharing aren't clear for the animal health sector

Thank you for your attention

OFFLU would like to thank colleagues and contributors for continued support to OFFLU and to all contributors and countries for their kind and generous contributions of genetic material and information for the OFFLU VCM packages

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



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