



# OFFLU Annual Report 2016

In 2016, avian influenza (AI) outbreaks continued to threaten both animal health and public health worldwide. More than 50 countries within Asia, Africa, Europe and North America experienced highly pathogenic avian influenza (HPAI) virus outbreaks during 2016 and strains of AI subtypes H5N1, H5N2, H5N3, H5N5, H5N6, H5N8, H5N9, H7N1, H7N3, H7N7 and H7N8 were detected. Also H7N9 which was circulating in China in low pathogenic form since 2013 has recently mutated to become HPAI H7N9.

In response to these HPAI outbreaks, the OFFLU network experts participated in various teleconferences and meetings to share epidemiological and experimental data and diagnostic protocols that are needed to inform surveillance and control policies, and in building technical partnerships with Member Countries. OFFLU and WHO have been in regular communication to share both public and animal health data so that risk assessments can be continually updated and to discuss issues related to the animal-human interface, including pandemic preparedness.

## Contribution of avian influenza data for pandemic preparedness

Every six months OFFLU coordinates inputs from OIE/FAO Reference Centres and national veterinary laboratories to provide animal virus data for consideration during the WHO Vaccine Composition Meeting. These data are needed to update pre-pandemic candidate vaccine viruses for human vaccines against zoonotic viruses of concern, and contribute to the WHO biannual report of “[Antigenic and genetic characteristics of zoonotic influenza viruses and development of candidate vaccine viruses for pandemic preparedness.](#)”

In the February 2016 meeting, OFFLU contributed genetic data from clade 2.3.2.1c H5N1 viruses from reported poultry outbreaks in China, Vietnam, Burkina Faso, Ghana, Ivory Coast, Niger and Nigeria; clade 2.3.2.1a viruses in India; and clade 2.2.1.2 viruses in Egypt. A new candidate vaccine virus strain was proposed from a poultry-origin virus isolate from Vietnam representing one of the currently circulating clade 2.3.4.4 H5 HPAI lineages.

In the September 2016 meeting, OFFLU contributed 85 new H5Nx HA sequences from Cameroon (H5N1), China (H5N6), Egypt (H5N1), Ghana (H5N1), India (H5N1), Iran (H5N1), Lebanon (H5N1), Niger (H5N1), the Republic of Korea (H5N8), the Russia Federation (H5N8), Taiwan Province of China (H5N8), and Vietnam (H5N1). The majority of these were additions to the recent H5Nx virus sequence data generated by OFFLU Reference Laboratories that have been deposited in the public domain. Additionally, 50 HA sequence data on H9N2 viruses of avian/poultry host origins were shared. These were reported from six different countries, including China, Egypt, India, Myanmar, Vietnam and the Republic of Korea. More limited data of historical significance from wave three

H7N9 viruses from poultry in China, and H9N2 from Egypt was contributed. Furthermore, OFFLU contributed HPAI H5Nx and H5N1, and LPAI H9N2 antigenic data, characterized using the WHO ferret antisera panel, from poultry outbreaks reported in Vietnam, Cameroon, Ghana, Niger, Iran, India, Myanmar and Lebanon.

In the February 2017 meeting, sequence data for 248 H5, H7, and H9 were contributed by OFFLU from 32 animal health laboratories in 24 countries representing Europe, Asia, Africa, and the Americas. The contributing countries include Egypt, Morocco, Niger, Nigeria, Togo, Chile, USA, Bhutan, China, India, Japan, Korea, Laos, Myanmar, Taiwan, Vietnam, Austria, France, Germany, Italy, Netherlands, Romania, Russia and UK. Antigenic data for H5 clades 2.3.4.4 and 2.3.2.1, and H9 Y280 lineage viruses were contributed by three of the OFFLU reference laboratories (Istituto Zooprofilattico Sperimentale delle Venezie in Italy, the Animal and Plant Health Agency in the UK and the Australian Animal Health Laboratory, Australia).

The OFFLU VCM team would like to specifically acknowledge the OFFLU network laboratories and Member Countries involved in the significant contribution of HPAI genetic data for the year 2016 - 2017.

[http://www.who.int/influenza/resources/documents/characteristics\\_virus\\_vaccines/en/](http://www.who.int/influenza/resources/documents/characteristics_virus_vaccines/en/)

[http://www.who.int/influenza/vaccines/virus/201703\\_zoonotic\\_vaccinevirusupdate.pdf?ua=1](http://www.who.int/influenza/vaccines/virus/201703_zoonotic_vaccinevirusupdate.pdf?ua=1) [http://www.who.int/influenza/vaccines/virus/201703\\_zoonotic\\_vaccinevirusupdate.pdf?ua=1](http://www.who.int/influenza/vaccines/virus/201703_zoonotic_vaccinevirusupdate.pdf?ua=1)

## OFFLU avian influenza virus characterization meeting

In March 2017, OFFLU organized an avian influenza virus characterization technical meeting at FAO Headquarters, Rome, comprising experts from OIE-FAO Reference Centres for avian influenza, national veterinary laboratories and public health laboratories. The meeting served as a platform to discuss and promote sharing of genetic and antigenic data relating to avian influenza with the purpose of establishing a methodology for monitoring genetic and antigenic changes among the circulating strains. The experts also discussed the production of chicken sera by OFFLU labs against the main circulating viruses. The ultimate goal of this activity is to provide detailed data on genetic and antigenic properties of

virus, and the associated immunology in animals, to scientifically support countries in developing optimal control strategies, including potential use in selecting poultry vaccine seed strains against circulating low and high pathogenicity avian influenza viruses. The Reference Centres experts also agreed to participate in a proficiency testing exercise to ensure mechanisms of harmonization of the various diagnostic methods employed and avian influenza virus characterization. The meeting provided an opportunity for the network of Reference Centres to agree to processes and procedures to meet these requirements.

## Guidance on Influenza A cleavage sites

OFFLU experts updated a guidance document that provided information about influenza A (avian) cleavage sites for assistance in differentiation of low pathogenicity and high pathogenicity AI viruses through molecular analyses. This document included molecular sequences for consistent multi-basic cleavage sites of HPAI H5N1 viruses from Asia, Africa and Europe; previously reported multi-basic cleavage sites of other HPAI viruses (H5 and H7); and a list of 2-3 residue multi-basic cleavage sites. The document was updated in December 2016

taking into account the recent HPAI outbreaks for the past year. Considering the importance of this information, the document has been referenced in the avian influenza chapter of the OIE *Manual of Diagnostic Tests and Vaccines for Terrestrial animals*.

[http://www.offlu.net/fileadmin/home/en/resource-centre/pdf/Influenza\\_A\\_Cleavage\\_Sites.pdf](http://www.offlu.net/fileadmin/home/en/resource-centre/pdf/Influenza_A_Cleavage_Sites.pdf)

## OFFLU Swine influenza virus group activities

The OFFLU swine influenza group met for the sixth annual technical meeting in March 2017 at the FAO Headquarters, Rome and shared data about influenza in global pig populations including regional and country-specific reports from Australia, Japan, Thailand, Vietnam, South Korea, Europe, USA, Canada, Brazil, Chile, Guatemala, Colombia, Argentina and Africa. Participants included scientists conducting influenza surveillance and/or performing influenza research or diagnoses in swine and at the human-swine interface.

The members of the group published a paper on the global antigenic diversity of swine influenza A viruses. The study characterized the antigenic diversity of H1 and H3 viruses circulating in both swine and humans on a multi-continental scale within and between different regions of the world where swine influenza viruses (SIV) surveillance data were available. There is considerable diversity in both H1 and H3 influenza viruses circulating in swine. The current global antigenic diversity of SIV creates substantial risks for both human and swine populations. The antigenic divergence of SIV to seasonal influenza viruses circulating in humans may be a major contributor to the risk of outbreaks and pandemics of SIV in humans.

The group also published a paper describing the development of a phylogeny-based global nomenclature system for SIV and an automated annotation tool for H1 hemagglutinin genes for all H1 genes available in GenBank. Phylogenetic criteria were used to establish a globally consistent nomenclature to compare swine H1 virus hemagglutinin (HA) among regions and between swine and humans. The annotation tool utilized a data set of 7,070 H1 sequences. The tool can be updated readily to include evolving nomenclature as new clades emerge. A common global nomenclature facilitates communications about the genetic relationship of influenza A viruses (IAVs) infecting humans and pigs, within and between regions.

The tool was then integrated into the Influenza Research Database (IRD) for public access and offers multiple interfaces to existing applications within IRD.

<https://elifesciences.org/content/5/e12217>

<http://msphere.asm.org/content/msph/1/6/e00275-16.full.pdf>

[https://www.fludb.org/brc/influenza\\_h1clade\\_search\\_segment.spg?method=ShowCleanSearch&decorator=influenza](https://www.fludb.org/brc/influenza_h1clade_search_segment.spg?method=ShowCleanSearch&decorator=influenza)

## Equine influenza experts update vaccine recommendations

Equine influenza (EI) is a respiratory disease of horses and has the potential to disrupt major equestrian events. EI can be controlled by vaccination but it has been demonstrated in the field that antigenic drift impacts vaccine efficacy. The Expert Surveillance Panel of EI comprised of OFFLU and WHO influenza experts met at the OIE Headquarters in March 2017 and reviewed the EI virus activity, characteristics of the viruses isolated and vaccine performance. The panel studied the

individual animal cases and outbreaks of equine influenza reported by Ireland, Sweden, UK and the USA in the past year and recommended that vaccines for the international market should contain both clade 1 and clade 2 viruses of the Florida sublineage.

<http://www.oie.int/en/our-scientific-expertise/specific-information-and-recommendations/equine-influenza/>

## OFFLU wildlife/wild bird influenza group

The experts from various continents involved in wildlife/ wild bird influenza surveillance and research met by teleconferences on various occasions to share data and provided situation updates of outbreaks in wild birds and poultry and updated guidance document on the role of wild birds in the circulation of avian influenza viruses. Guidance was provided on wild bird movements, surveillance strategies, diagnostics, reporting and response to detection in wildlife.

The group developed a concept note for a global surveillance program for avian influenza viruses in wild birds. The

overarching objective of this proposed global surveillance program for influenza viruses in wild birds is to cost-effectively and regularly monitor the changing characteristics of genomic diversity of influenza viruses and secure the benefits of such surveillance information equally for all countries through a single affordable program. The funding mechanism for this project needs to be identified.

[http://www.offlu.net/fileadmin/home/en/resource-centre/pdf/H5N8\\_OFFLU\\_Statement.pdf](http://www.offlu.net/fileadmin/home/en/resource-centre/pdf/H5N8_OFFLU_Statement.pdf)

## OFFLU applied epidemiology working group

Recognizing the need to develop integrated epidemiological approaches to avian influenza risk assessment and management at a global level, the OFFLU Steering and Executive Committee approved the formation of the Applied Epidemiology Working Group in September 2016. The experts of this group will work to identify the pathways leading to the introduction, spread and maintenance of relevant avian influenza viruses in different eco-social system settings and estimate the risks associated with these pathways. The

technical activity will also develop appropriate risk management options for relevant avian influenza viruses in different eco-social system settings, including the design of surveillance systems and its components. A technical meeting is being planned for this group at FAO Headquarters in June 2017 to agree on the terms of reference and to develop specific work plans. In addition, the experts will assess the utility of the FLURISK tools for integrated risk assessment and management of avian influenza.

## OFFLU website

The OFFLU website ([www.offlu.net](http://www.offlu.net)) was restructured to include animal influenza information on all species including avian, swine, equine and wildlife. The information related to outbreaks, OIE and FAO publications on influenza, outputs of OFFLU technical activities, diagnostic protocols, training

materials, influenza at human-animal interface were updated regularly. Please use the website and if you have any material to post or share with the worldwide network contact [secretariat@offlu.net](mailto:secretariat@offlu.net)

## Acknowledgements

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