



# OFFLU Annual Report 2015

In 2015, the OFFLU network entered the tenth year of operations and continued to share and offer technical advice and veterinary expertise to international organisations and Member Countries to assist in the prevention, diagnosis, surveillance and control of animal influenza including avian, swine and equine influenza. Countries of the Asian, African, European and American continents experienced highly pathogenic avian influenza (HPAI) outbreaks during 2015 and strains of avian influenza (AI) subtypes H5N1, H5N2, H5N3, H5N6, H5N8, H5N9, H7N3, H7N7 and H7N9 were encountered.

In response to the animal influenza 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 public health and animal health data so that risk assessment can continually be updated and on issues related to the animal-human interface, including pandemic preparedness.

## OFFLU technical meeting

It was particularly pleasing during 2015 to be able to bring together the OFFLU experts along with other influenza researchers and students for an OFFLU Technical Meeting. The meeting took place in April 2015 following the 9th International Symposium on Avian Influenza at University of Georgia, Athens, USA and was kindly facilitated by the organisers of the symposium. Around 100 animal influenza scientists participated in this meeting.

During the meeting, the OFFLU experts reported on the progress of various OFFLU technical activities, including WHO Vaccine Composition Meeting contributions, AI vaccination group activities, proficiency testing results, influenza research agenda, swine influenza expert group activities, equine influenza expert group activities and human-animal interface activities. The participants were updated on the OFFLU strategic plan to be progressively implemented in the coming years and presentations of new technical activities to improve diagnostic technologies, proposal for updating AI vaccines for

poultry, creation of wildlife expert group involved in influenza surveillance and research, a new epidemiology group to work on risk assessment and surveillance and a socio-economic group to understand the social and economic impact of influenza viruses in animals and their impact on humans.

Prior to the technical meeting, OFFLU circulated a questionnaire to the experts to comment on the OFFLU's purpose and mission and next five year strategy programme. Feedback from the experts revealed that OFFLU five year strategy vision reflected the views of the animal influenza research community and the network is serving as a useful and valuable platform for the interaction amongst influenza experts working on avian, swine, equine and public health.

[http://www.offlu.net/fileadmin/home/en/meeting-reports/pdf/OFFLU\\_Athens/minutes\\_\\_OFFLU\\_TECHNICAL\\_MEETING\\_2015\\_Final.pdf](http://www.offlu.net/fileadmin/home/en/meeting-reports/pdf/OFFLU_Athens/minutes__OFFLU_TECHNICAL_MEETING_2015_Final.pdf)

## 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 AI virus data to the WHO Vaccine Composition Meeting. These data are needed to update pre-pandemic candidate vaccine viruses for human vaccines in case AI viruses emerge to become disease threats in humans.

Virus data contributed by the OFFLU network over 2015 was predominated by the emergent clade 2.3.4.4 H5Nx HPAI viruses that had distributed over multiple countries in Asia, Europe and North America. In the February 2015 meeting, new data from avian origin clade 2.3.4.4 H5Nx HPAI viruses

from Canada (H5N2), China (H5N6), Lao PDR (H5N6), Italy (H5N8), Japan (H5N8), Russia (H5N8) and the USA (H5N1, H5N2, and H5N8) were shared. New data from H5N1 HPAI viruses of clade 2.2.1 in Egypt, and clade 2.3.2.1c in China, India, Nigeria and Russia were also presented. Furthermore, OFFLU contributed some data from wave three H7N9 viruses from poultry in China, and H9N2 from Egypt.

In the September 2015 meeting, new OFFLU data from avian origin clade 2.3.4.4 H5Nx HPAI viruses since February 2015 were shared by Canada (H5N1, H5N2), Hungary (H5N8), the Republic of Korea (H5N8) and Vietnam (H5N6). Additionally,

new H5N1 data from clade 2.2.1.2 viruses in Egypt, Israel and the Palestinian Authority, clade 2.3.2.1a viruses in Bhutan and India, clade 2.3.2.1c viruses in Burkina Faso, Ghana, Ivory Coast, Niger, Nigeria, Bulgaria, Romania, Russia, Turkey, India and Vietnam, and clade 2.3.4.2 viruses in Myanmar were presented. Significantly, these included real time genetic data from the emergence and re-emergence of H5N1 lineages in several countries in Eastern Europe (clade 2.3.2.1c) and West Africa (clade 2.3.2.1c) and Myanmar (clade 2.3.4.2).

The OFFLU VCM team would like to specifically acknowledge the above mentioned OFFLU network laboratories and countries for the significant contribution of HPAI genetic data for the year 2015.

Importantly, OFFLU also contributed with antigenic data for HPAI H5N1 viruses, providing information on isolates recently detected in various countries. The characterization performed by OIE/FAO Reference Centres, using ferret antisera provided by WHO Collaborating Centres, assessed antigenic divergence of isolates from the animal health sector and compared them with available human vaccine seed strains.

[http://www.who.int/influenza/vaccines/virus/201502\\_zoonotic\\_vaccinevirusupdate.pdf?ua=1](http://www.who.int/influenza/vaccines/virus/201502_zoonotic_vaccinevirusupdate.pdf?ua=1)

[http://www.who.int/influenza/vaccines/virus/201509\\_zoonotic\\_vaccinevirusupdate.pdf?ua=1](http://www.who.int/influenza/vaccines/virus/201509_zoonotic_vaccinevirusupdate.pdf?ua=1)

[http://www.offlu.net/fileadmin/home/en/human-animal-interface/pdf/OFFLU\\_WHO\\_VCM\\_2015report.pdf](http://www.offlu.net/fileadmin/home/en/human-animal-interface/pdf/OFFLU_WHO_VCM_2015report.pdf)

## Guidance on Influenza A cleavage sites

OFFLU experts updated a guidance document that provided information about influenza A cleavage sites for assistance in differentiation of low pathogenicity and high pathogenicity A viruses through molecular analyses. This document included molecular sequences for consistent multibasic 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 multibasic cleavage sites. The document was updated in year 2015 taking into account the

clade 2.3.4.4 HPAI outbreaks for the past two years. 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)

## Swine influenza experts update surveillance data, research data, antigenic cartography map and move towards establishing a global phylogenetic cluster naming system

The OFFLU swine influenza group met for the fifth annual technical meeting in December 2015 at the OIE Headquarters, Paris and shared data about the global swine influenza situation in pig populations by providing regional and country-specific reports. Participants included scientists conducting influenza surveillance and/or performing influenza research or diagnosis in swine.

The group generated antigenic cartography maps illustrating the antigenic relationship between different swine influenza viruses within and between different regions of the world where SIV surveillance data were available. The current global antigenic diversity of swine influenza viruses 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 swine viruses in humans.

The group is working to develop a global phylogenetic cluster naming system based on criteria adapted from avian influenza

H5 genetic diversity to be suitable for the global influenza A virus genetic dataset from swine and humans. Clades were designated for H1 genes using 6611 unique published sequences for 1A lineage (classical swine), 1B lineage (human seasonal) and 1C lineage (European avian-like) and clade designation for H3 subtype using 1989 unique published sequences for 3A and 3B lineage was presented. It was evident some of the lineages need more data for finalization and efforts will be made to collect it from the regions concerned. At the end of the analyses the group will publish a manuscript on the global phylogenetic cluster naming system to harmonise communication about the genetic relationship between influenza A viruses circulating in swine among different geographic regions and also between swine and human seasonal influenza A viruses.

<http://www.offlu.net/?id=330>

## 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 on vaccine efficacy. The Expert Surveillance Panel of EI comprising OFFLU and WHO influenza experts met at the OIE Headquarters in March 2015 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 France, Germany, Ireland, Sweden, the 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 launches OFFLU wildlife/wild bird influenza group

In 2015 OFFLU established a new technical activity comprising a mix of wildlife experts, ecologists, people who work with influenzas in wildlife, as well as a bit of lab expertise to provide a platform for discussion, coordination, and data sharing between key wildlife experts involved in influenza surveillance and research. The main objective of the group include expertise and up to date input when influenza outbreaks or emergencies occur, regular review of the wild birds section in the OFFLU Research Priorities on Avian

Influenza, develop/coordinate a low-cost targeted wild bird surveillance strategy at a global level accounting for existing surveillance programmes. The group met through teleconferences to share the wild bird surveillance data in 2015, mode of operation, use of outputs from the group activities and database needs. In future the group will work towards developing a strategy for monitoring global influenza diversity in wild birds and its utility.

## Changes in the OFFLU management Committees

The new appointments in 2015 for the OFFLU Executive Committee include Prof. Jiming Chen (China Animal Health and Epidemiology Center), Dr Nicola Lewis (University of Cambridge, UK) and Ms Tianna Brand (World Organisation for Animal Health). Taking this opportunity, OFFLU would like to

thank the past Executive Committee members Dr Hualan Chen, Dr Kristien Van Reeth and Dr Keith Hamilton and OFFLU Scientist Dr Filip Claes for their valuable role and contributions in the smooth functioning of the network activities.

## Acknowledgements

OFFLU expresses its sincere gratitude to all OFFLU experts for their exceptional efforts and enthusiasm and the Chief Veterinary Officers of countries who support these experts and share data for the global health benefits. OIE and FAO would also like to thank the donors of OFFLU who have and are supporting the OFFLU activities.



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