

14/03/2016

## **OFFLU summary report of WHO VCM February 2016**

Dear OFFLU Network Members,

The WHO Consultation on the Composition of Influenza Virus Vaccines for the Northern Hemisphere 2016-2017 took place in Geneva, Switzerland on the 22-24 February 2016. The meeting gathered about 45 participants from the WHO Collaborating Centres for influenza (CCs), WHO Essential Regulatory Laboratories (ERLs), National Influenza Centres and WHO H5 Reference Laboratories, WHO Collaborating Centre for Modelling, Evolution, and Control of Emerging Infectious Diseases and from OFFLU. The OFFLU contribution on zoonotic influenza viruses was presented by Frank Wong from the CSIRO Australian Animal Health Laboratory (AAHL) and Gwenaelle Dauphin from the OFFLU Executive Committee. We would like to thank Gounalan Pavade (OFFLU Secretariat), and Filip Claes and Ahmed AlNaqshbandi (FAO) for their valuable assistance in data collation towards this OFFLU contribution.

The epidemiological and molecular data on zoonotic influenza viruses for the period 22 September 2015 to 22 February 2016 that were gathered by the OFFLU network laboratories were presented at the meeting. We thank all of the reference laboratories and influenza experts that had contributed virus data and analysis used in the consultation, including the AAHL, Australia; National Centre for Foreign Animal Disease (NCFAD), Canada; Harbin Veterinary Research Institute, China; Laboratory of Avian Disease Surveillance, Qingdao, China; Regional Laboratory for Quality Control on Poultry Production (RLQP), Egypt; National Institute of High Security Animal Diseases (NIHSAD), India; Instituto Zooprofilattico Sperimentale delle Venezie (IZSVe), Italy; Hokkaido University, Japan; Animal

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and Plant Health Agency (APHA), United Kingdom; and the Southeast Poultry Research Laboratory National Avian Influenza Reference Laboratory (SPRL), USDA.

Since there were only few human A(H5) infections in the current reporting period, the information based on viruses in poultry was all the more crucial for the evaluation of candidate virus strains. Compared to the previous period, the number of reported outbreaks of HPAI from Europe and North America was substantially lower with none reported for clade 2.3.4.4 H5 viruses, and this was reflected in the absence of new virus data. However, clade 2.3.4.4 H5 viruses, and this was reflected in the absence of new virus data. However, clade 2.3.4.4 H5N6 HPAI remains a concern for zoonotic risk and poultry outbreaks in China and Southeast Asia with virus sequence data from China indicating genetic drift of these viruses. Additionally, new genetic data from clade 2.3.2.1c H5N1 viruses from reported poultry outbreaks in China, Vietnam, and 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 were presented by OFFLU. Clade 2.3.2.1c virus data from the North and West African poultry epidemics and clade 2.3.2.1a virus data from India, were valued contributions. The need for continued efforts toward antigenic surveillance by HI testing against the WHO reference ferret antisera was highlighted by the WHO for these viruses.

In contrast to the increased number of virus data submissions from the network over the 2015 year including the timely sharing of viruses to the OFFLU reference HI testing laboratories for antigenic analysis using ferret sera, the number of contributions submitted in time for the current VCM round was unfortunately significantly lower. In particular, OFFLU was not able to present any antigenic (HI) data this time due to the lack of viruses submitted to the relevant antigenic analysis. The absence of antigenic data for clade 2.2.1.2, 2.3.2.1a and 2.3.2.1c H5N1 viruses that are causing ongoing outbreaks in poultry in various affected regions, continues to present crucial gaps in timely surveillance for the current process for evaluating selected candidate vaccine viruses for pandemic preparedness. This highlights the ongoing issue of the general low level of phenotype (antigenic) characterisation data for circulating animal influenza viruses that are generated from, or shared by, the global animal health and veterinary lab networks. This is particularly concerning since relevant animal influenza virus surveillance directly by the animal and agricultural sectors should be the keystone for zoonotic influenza risk analysis and pandemic preparedness. OFFLU through a committed network, should have the strongest contribution in this regard, but in reality this remains challenging as have been repeatedly highlighted in

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previous reports. Data from zoonotic influenza viruses of animal origin are also presented by the WHO collaborating Centres including CDC-Atlanta, SJCRH-Memphis, CNIC-Beijing, and The University of Hong Kong (HKU). The absence of any virus information from Cambodia, Indonesia, and Chinese Taipei, which have had continuing reports of serious H5 HPAI outbreaks in poultry is of great concern to OFFLU and the WHO.

The pandemic preparedness outcomes from the antigenic and genetic characterisation of zoonotic influenza viruses arising from the 2015 WHO-VCMs have been posted on the WHO website:

## http://www.who.int/influenza/vaccines/virus/201602 zoonotic vaccinevirusupdate.pdf.

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. This selection is a result of a good animal health-public health interaction, FAO supported surveillance activities in Vietnam, and the sharing of virus samples from NCVD (National Centre for Veterinary Diseases) with the CDC WHOCC.

Both poultry and swine viruses are scrutinized during the WHO VCM. At the current meeting, concerns were raised about the potential zoonotic risk of H1N1 viruses with Eurasian lineage genes that are circulating in pigs in China, against which human immunity is thought to be low. The global OFFLU network should thus maintain its vigilance and surveillance rigour for related and other emergent or novel swine origin influenza A viruses.

Finally on behalf of OFFLU network, we would like to thank the WHO for the invitation to participate at the vaccine composition meetings and for its ongoing support of the OFFLU representation in this important technical activity.

The OFFLU VCM Team

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