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OFFLU summary report of WHO VCM September 2014

Dear OFFLU Network Members,

The WHO Consultation on the Composition of Influenza Virus Vaccines for the Southern Hemisphere 2014 was held on the 22–24 September 2014 at the WHO in Geneva, Switzerland. Frank Wong (AAHL) and Filip Claes (FAO) presented the OFFLU contribution on zoonotic influenza viruses.

The epidemiological and molecular data on zoonotic influenza viruses for the period 18 February to 15 September 2014 that were gathered by OFFLU network laboratories were presented at the meeting. These included new data from avian origin high pathogenic A(H5N1) (HPAI) viruses from Bangladesh and Nepal belonging to clade 2.3.2.1a, from Lao People's Democratic Republic (clade 2.3.2.1c viruses), and from Libya and Egypt (clade 2.2.1 viruses). New unpublished data for emergent variant clade 2.3.4-origin (so-called clade 2.3.4.6) H5N6 HPAI viruses in China and Lao PDR were also presented by OFFLU. The emergence and current circulation of these viruses in the animal sector was of particular interest to WHO and key data was presented by OFFLU on A(H5N6) and A(H5N8) at this VCM. The need for expedient formal clade nomenclature assessment of these variant H5 HPAI viruses by WHO/OIE/FAO was also recognised at the VCM. The H5 HPAI virus data for China, Egypt, Libya and Lao PDR were connected to recent avian influenza events/outbreaks that have occurred within the VCM reporting period (source: FAO EMPRES-i), highlighting the timeliness and relevancy of data in this OFFLU contribution. Some new A(H7N9) and G1-like lineage A(H9N2) data from China and Egypt respectively, were also presented in the OFFLU package. Crucially, antigenic data was also able to be presented by OFFLU on recent 2013 A(H5N1) including circulating clade 2.3.2.1a viruses in Bangladesh and clade 2.2.1 viruses in Egypt; as well as for the recently emerged 2014 clade 2.3.4-origin A(H5N6) in Lao PDR. The latter virus was antigenically divergent from previously characterised clade 2.3.4 H5N1 viruses including the reference antigens represented in the current WHO ferret antisera panel, and the need to generate relevant two-way HI data for these divergent H5 HPAI viruses was identified as a matter of priority. The detailed OFFLU data package is appended, and the pandemic preparedness outcomes from the antigenic and genetic characterisation of zoonotic influenza viruses arising from the September 2014 WHO VCM have been posted on the WHO website (http://www.who.int/influenza/vaccines/virus/201409_zoonotic_vaccinevirusupdate.pdf?ua=1).

Zoonotic influenza data was also presented by CDC-Atlanta, St Judes CRH-Memphis, CNIC-Beijing, and Hong Kong University (HKU), with focus on A(H5N1) and A(H7N9).

OFFLU specifically acknowledges the national and regional veterinary laboratories of Bangladesh, China, Egypt, India, Lao PDR, Libya and Nepal for their important timely submissions of avian influenza virus samples and data for this meeting and towards the ongoing global zoonotic influenza surveillance effort. I would also like to acknowledge and thank the contributing OFFLU Reference Laboratories for their work towards the September 2014 WHO VCM, including the (i) National Laboratory for Veterinary Quality Control on Poultry Production (NLQP), Giza; (ii) High Security Animal Disease Laboratory, Indian Veterinary Research Institute, Bhopal; (iii) National Avian Influenza Reference Laboratory, Harbin Veterinary Research Institute, Harbin; (iv) Istituto Zooprofilattico Sperimentale delle Venezie (IZSve), Padova; (v) Animal Health and Veterinary Laboratories Agency, Addlestone, Weybridge; and (vi) CSIRO Australian Animal Health Laboratory, Geelong.

WHO participants also expressed their appreciation and specifically recognised the OFFLU efforts toward this consultation. Zoonotic H5, H7 and H9 subtype animal influenza viruses remain global, regional and national threats for animals and humans. These viruses continue to be dynamic with ongoing evolution and new reassortments detected, as highlighted by the emerging circulation of variant clade 2.3.4-origin HPAI viruses in China and the surrounding region. The need and importance for continued close monitoring using an internationally harmonised platform for virus characterisation and global virus data interpretation such as that provided by the WHO VCM consultations are ongoing.

On behalf of OFFLU network, we would like to thank the WHO for the invitation to participate at the Vaccine Composition Meetings (VCM) and for its ongoing support of the OFFLU representation in this important activity. The associated support from Richard Webby and colleagues from the WHO Collaborating Centre for Influenza at St Judes Children's Research Hospital on the production of reference influenza virus antigens and ferret antisera and their distribution to the key OFFLU reference labs for use in antigenic analysis is again greatly appreciated and acknowledged.

The OFFLU VCM team