



28 March 2014

OFFLU summary report of WHO VCM February 2014

Dear OFFLU Network Members,

The WHO Consultation on the Composition of Influenza Virus Vaccines for the Northern Hemisphere 2014-2015 was held on the 17-19 February 2014 in Geneva, Switzerland. I attended together with Filip Claes as the OFFLU representation at this meeting. Firstly, I would like to thank OFFLU for the opportunity to represent the network in this important activity and also to the WHO for the invitation to participate at the Vaccine Composition Meetings (WHO-VCM). I would also like to express my personal gratitude, as well as those on behalf of the OFFLU network, for the work and tremendous contributions of Giovanni Cattoli (IZSVe, Italy) who represented OFFLU at the WHO-VCMs over the past few years. Giovanni's ongoing support and advice towards this activity remain greatly appreciated and have provided a smooth transition to my participation. Thanks also to Stephanie Sonnberg (St Judes-CRH, USA) and Isabella Monne (IZSVe) for their assistance in the collation and analysis of virus data submitted by the OFFLU network laboratories for the current and past meetings. The invaluable support from Richard Webby (St Judes-CRH) and Ruben Donis (CDC, Atlanta) from the WHO Collaborating Centres for Influenza (USA), in the production of A(H5N1) antigens and ferret antisera, and their distribution to the OFFLU international reference labs for use in antigenic analysis, continues to be greatly appreciated and acknowledged.

The epidemiological and molecular data on zoonotic influenza viruses for the period 23 September 2013 to 10 February 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, Bhutan and Nepal representing clade 2.3.2.1a, and clade 2.2.1 viruses from Egypt. Data from avian origin G1-like lineage A(H9N2) viruses from Bangladesh, Egypt, India, Libya and Saudi Arabia; and Australian lineage high

pathogenic A(H7N2) from Australian poultry were also received by OFFLU and presented at the meeting. The detailed report of the OFFLU contribution is appended, and the pandemic preparedness outcomes from the antigenic and genetic characterisation of zoonotic influenza viruses arising from the February 2014 WHO-VCM have been posted on the WHO website (http://www.who.int/influenza/vaccines/virus/201402_h5h7h9h10_vaccinevirusupdate.pdf).

On behalf of OFFLU, I would like to specifically acknowledge the national and regional veterinary laboratories of the abovementioned countries in recognition of their important timely submissions of avian influenza virus samples to their respective collaborating OFFLU Reference Labs for virus characterisation towards the global zoonotic influenza surveillance effort. I would also like to acknowledge and thank the following OFFLU Reference Laboratories for their timely contributions of A(H5N1) and A(H9N2) genetic data towards the February 2014 WHO-VCM round:

- (i) The National Laboratory for Veterinary Quality Control on Poultry Production (NLQP), Giza, Egypt.
- (ii) The High Security Animal Disease Laboratory, Indian Veterinary Research Institute, Bhopal, India.
- (iii) Istituto Zooprofilattico Sperimentale delle Venezie (IZSVe), Padova, Italy.

Avian influenza data was also presented by CDC-Atlanta, St Judes CRH-Memphis, CNIC-Beijing, and Hong Kong University (HKU), with obvious focus on zoonotic A(H7N9) China. Other interesting data included the first North American human case of A(H5N1) that was due to an infection from China imported into Canada in December 2013 and characterised as a divergent and reassortant clade 2.3.2.1c virus (HKU), and description of a novel reassortant A(H10N8) virus isolated from two human cases in China (CNIC-Beijing).

Recent and unpublished genetic data from the poultry origin avian influenza viruses from Bhutan and Nepal (H5N1), and India and the Middle East (H9N2) were uniquely contributed by the OFFLU network. The WHO again expressed their appreciation and acknowledged the importance of the OFFLU contribution of global zoonotic influenza data to the WHO-VCM discussions at this meeting. However, the September 2013 to February 2014 reporting period unfortunately represented the lowest number of viruses contributed by the OFFLU network since formal participation at the WHO-VCMs, with new data from only seven A(H5N1) viruses and eleven A(H9N2) viruses able to be analysed and reported at the WHO-VCM. Although this may be in small part due to an overall decrease in the number of reported HPAI

outbreaks in poultry, a more alarming trend observed among those endemic countries with known and ongoing A(H5N1) outbreaks is the dramatic decrease in the number of avian influenza virus samples submitted to international/OFFLU reference labs for virus isolation and full genetic and antigenic characterisation. This may also be exacerbated by a decrease in the timely response and contribution of any available virus characterisation data to the WHO-VCM activity by some members of the OFFLU network. This is of great concern to OFFLU given the persistence of HPAI poultry outbreaks in some affected countries, and the increasing global awareness of emergent novel avian influenza subtypes with panzootic and zoonotic/pandemic potential such as China A(H7N9) that are linked closely with the live poultry market industry. Significantly and of greatest concern was that no antigenic data could be contributed by the OFFLU network to the February 2014 WHO-VCM. The OFFLU international reference laboratories received fresh stocks of updated reference ferret reagent panels just prior to the February 2014 VCM, although in most cases these were received too late to generate new data in time for the meeting. HI data that will be generated using these reagents will be shared at the next WHO-VCM. However, the ability of the OFFLU network to collect timely harmonised antigenic data from recently circulating viruses from many of these countries remains particularly challenging due to the lack of suitable samples submitted for culture amplification of live virus at the key OFFLU national and international reference labs containing requisite BSL3 facilities. At the VCM, WHO had expressed an interest in the antigenic picture and possible divergence of clade 2.3.2.1a A(H5N1) viruses causing 2013-2014 poultry outbreaks in Nepal and the OFFLU lab network labs should continue to pursue the generation of relevant HI data from any of these viruses where possible.

Another observation was that none of the available genetic data shared by the OFFLU network at the February 2014 WHO-VCM corresponded with those countries that had reported poultry outbreaks within the relevant reporting period, highlighting a potential lag of six or more months between the incidence of recorded outbreaks and the time required for virus characterisation to be performed by OFFLU network laboratories. Some of the possible issues have already been revised by Giovanni in his report for OFFLU from the September 2013 WHO-VCM, and steps toward solving some of these issues are progressing. OFFLU should continue to investigate strategies around the advocacy of securing agreements for sample/virus transfers between the governing animal health bodies of different affected countries and to facilitate support for international shipments from developing countries to expedite this process. As can be seen in the recent VCM data presented from both the poultry and human health sectors, H5, H9 and H7 subtype avian influenza viruses remain global,

regional and national threats for animals (livestock) and humans. These viruses remain very dynamic with ongoing evolution and new reassortments detected, again highlighting 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.

Finally I would like to remind OFFLU network members of the importance of their continued relevant contributions to the WHO-VCM process in creating a timely global surveillance and virus data repository of recently circulating animal outbreak influenza viruses for the purpose of not only pandemic preparedness against zoonotic strains, but also for informing epidemic and epizootic mitigation strategies in the animal livestock industry sectors. OFFLU's advocacy for the timely and coordinated sharing of regional disease outbreak information, and genetic and antigenic data of virus strains through its network of Reference Labs and Collaborating Centres is crucially important because it is impossible for any one country to perform its own monitoring in isolation due to the rapid cross boundary movements of influenza viruses regionally and around the world. Information on viruses circulating in different regions of the world such as that gathered by the WHO-VCM consultation process, will enable every country to have ready access to the relevant molecular epidemiological information, but this process will only work if countries share their information (or viruses to produce the info) in a real time or most timely manner. In this way, countries across the OFFLU network would benefit from the contribution of other countries (in particular regional neighbours), to be better prepared for any new incursion(s), and to gain diagnostic experience and knowledge in disease outbreak and virus identification and monitoring.

Regards,

Frank Wong

Australian Animal Health Laboratory, Geelong, Australia

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