

H5N8 and spread through migratory birds



Tizzani P., Awada L., Potocnik M., Mapitse N., Caceres P.
World Animal Health Information and Analysis Department
World Organisation for Animal Health | information.dept@oie.int

INTRODUCTION

The H5N8 influenza A subtype was isolated in Ireland in 1983. After that, only sporadic findings occurred until the first outbreak officially notified in Korea (Rep. of) (January 2014). In the autumn 2014 the virus spread to Europe and the USA via migratory birds. Finally, in autumn 2016 the serotype appeared again, with a larger spread from both a spatial (area affected) and numeric (number of outbreaks and cases reported) point of view.

MATERIAL AND METHODS

The analysis was performed using data from H5N8 outbreaks notified by OIE Member Countries through WAHIS in the period 2013 - 2017 (n= 1964). The period of study was divided in four: Period 1 (P1 - Sept. 2013 - Aug. 2014), Period 2 (P2 - Sept. 2014 - Aug. 2015), Period 3 (P3 - Sept. 2015 - Aug. 2016), Period 4 (P4 - Sept 2016 - Feb 2017). The influence of the main wetlands and migratory flyways on outbreaks distribution was investigated. Kernel density estimator (KDE) was used to evaluate geographical disparities in spread of H5N8.

RESULTS

Two major H5N8 events in the last four years were identified, during P2 (422 outbreaks) and P4 (1443), while the other periods showed a limited H5N8 activity. The two events showed significantly different spatial behaviors. The mean distance from wetlands was almost five times lower in P4 (W= 459 240, p-value < 0.001) (Figure 1).

Moreover, the occurrence of the outbreaks in the flyways shows significant differences: the most affected flyways were the EAA in P2 (OR: 125, IC: 250-625), and the BSM in P4 (OR= 175, IC= 43-705) (Table 1) (OR value takes as reference the other flyways in the same period). Notably, the Kernel density areas in P4 (blue) were 54% larger than in P2 (red) (Figure 2).

CONCLUSIONS

The analysis shows that the two major H5N8 events follow different spread models. The dynamic of H5N8 constitutes an interesting case study of the potential evolution of a subtype in time, with increased threat for diffusion and impact on animal health. Considering the possibility of sudden epidemiological changes in disease characteristics, the OIE encourages its Member Countries to improve surveillance in wildlife and to continue to timely report all outbreaks information through WAHIS. Since 2017, and to avoid possible impact on trade, the OIE separated notification of HPAI in "none poultry including wild birds" from "poultry".

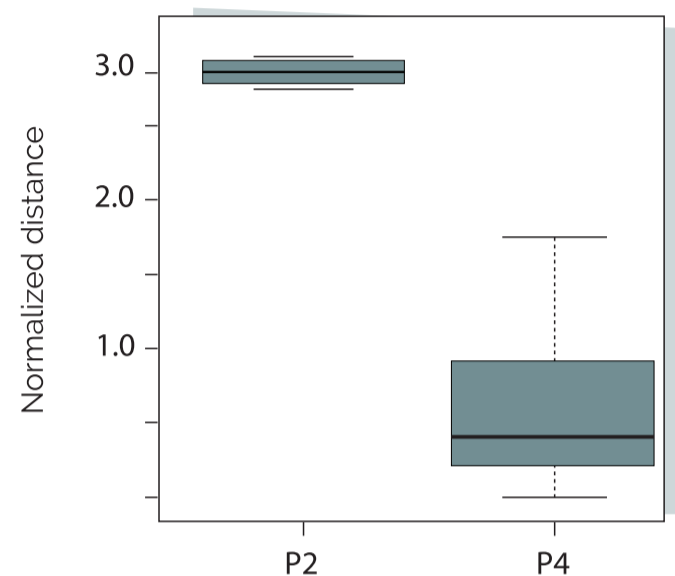


Figure 1. Distance of the outbreaks from wetlands in P2 and P4

Flyways	P2	P4
Black Sea - Mediterranean (BSM)	0.6 %	49.4 %
Central Asia (CA)	0.0 %	4.9 %
East Atlantic (EA)	3.0 %	38.9 %
East Asian - Australasian (EAA)	90.6 %	0.8 %
Mississippi Americas (MA)	3.0 %	0.0 %
Pacific Americas (PA)	2.8 %	0.0 %
West Asian - East Africa (WAEA)	0.0 %	6.0 %

Table 1. Percentage of outbreaks that occurred in the main bird flyways in P2 and P4

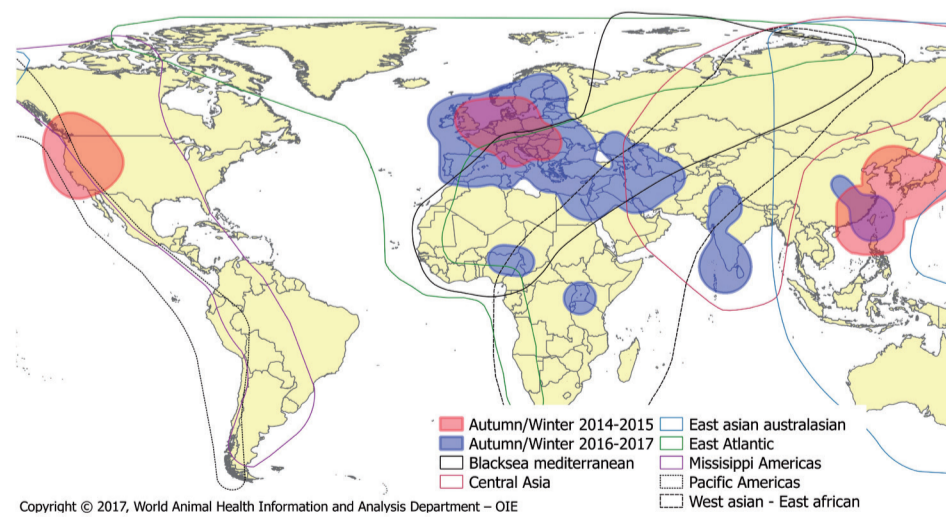


Figure 2. 95% Kernel estimation of H5N8 spread in P2 (red areas) and P4 (blue areas)



WORLD ORGANISATION FOR ANIMAL HEALTH
Protecting animals, preserving our future