

# Temporal and geographical comparison between two highly pathogenic avian influenza global epidemics



Tizzani P.<sup>1</sup>, Awada L.<sup>1</sup>, Noh S.<sup>1,2</sup>, Mapitse N.<sup>1</sup>, Caceres P.<sup>1</sup>

1. World Organisation for Animal Health, Paris, France [information.dept@oie.int](mailto:information.dept@oie.int)

2. Animal Disease Research Unit, USDA-Agricultural Research Service, Pullman, WA 83341, USA

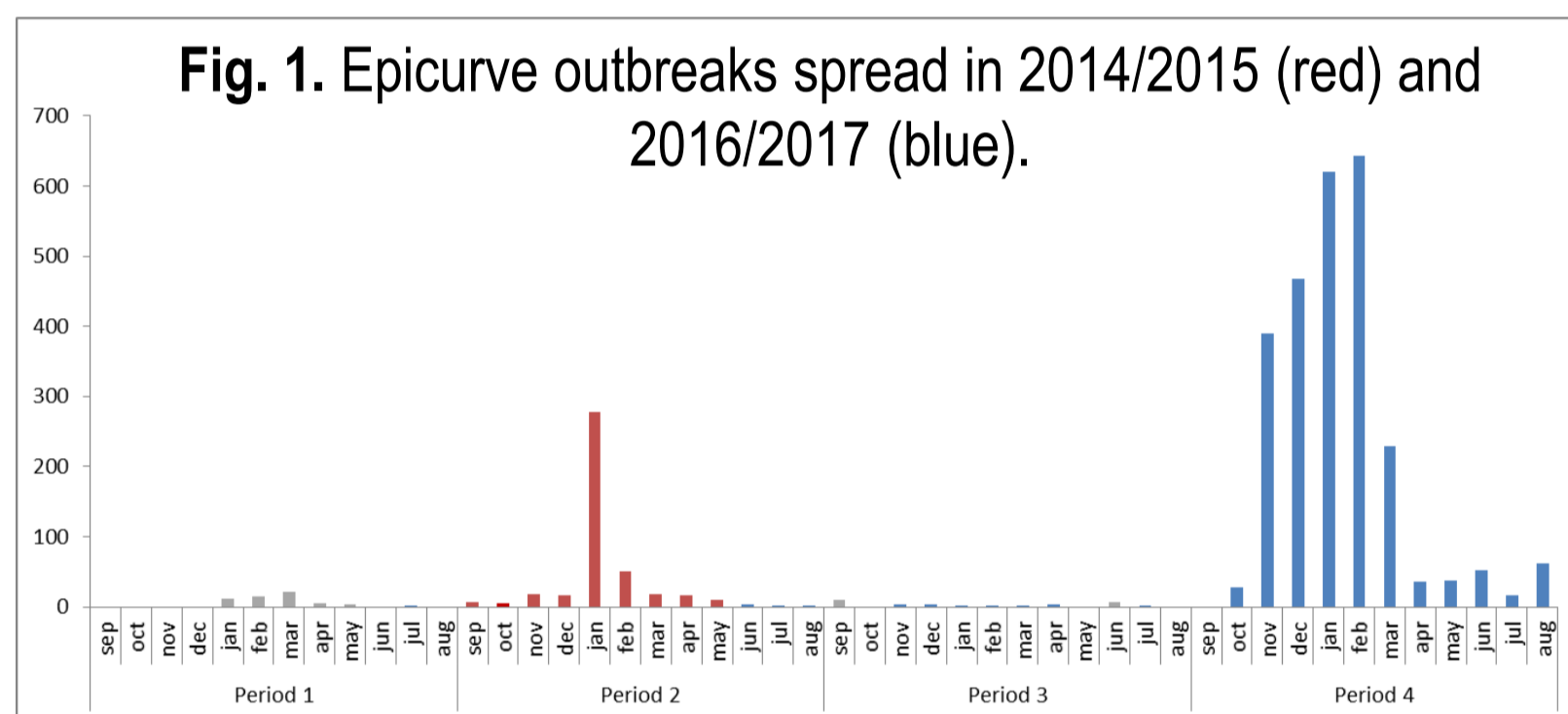
## Introduction

H5N8 is the most notified disease, in terms of immediate notifications submitted by Member Countries to the OIE since 2005, due to its significant impact on animal and public health. The following analysis focuses on two H5N8 global epidemics, subtype H5N8, which occurred in wild and domestic birds in 2014/2015 and 2016/2017, in order to show the importance of continuous surveillance for effective disease management and control. This analysis presents the similarities and differences between both epidemics in terms of epidemic curves and geographical spread, and identifies major intervention points to reduce the threat of HPAI.

## Material and Methods

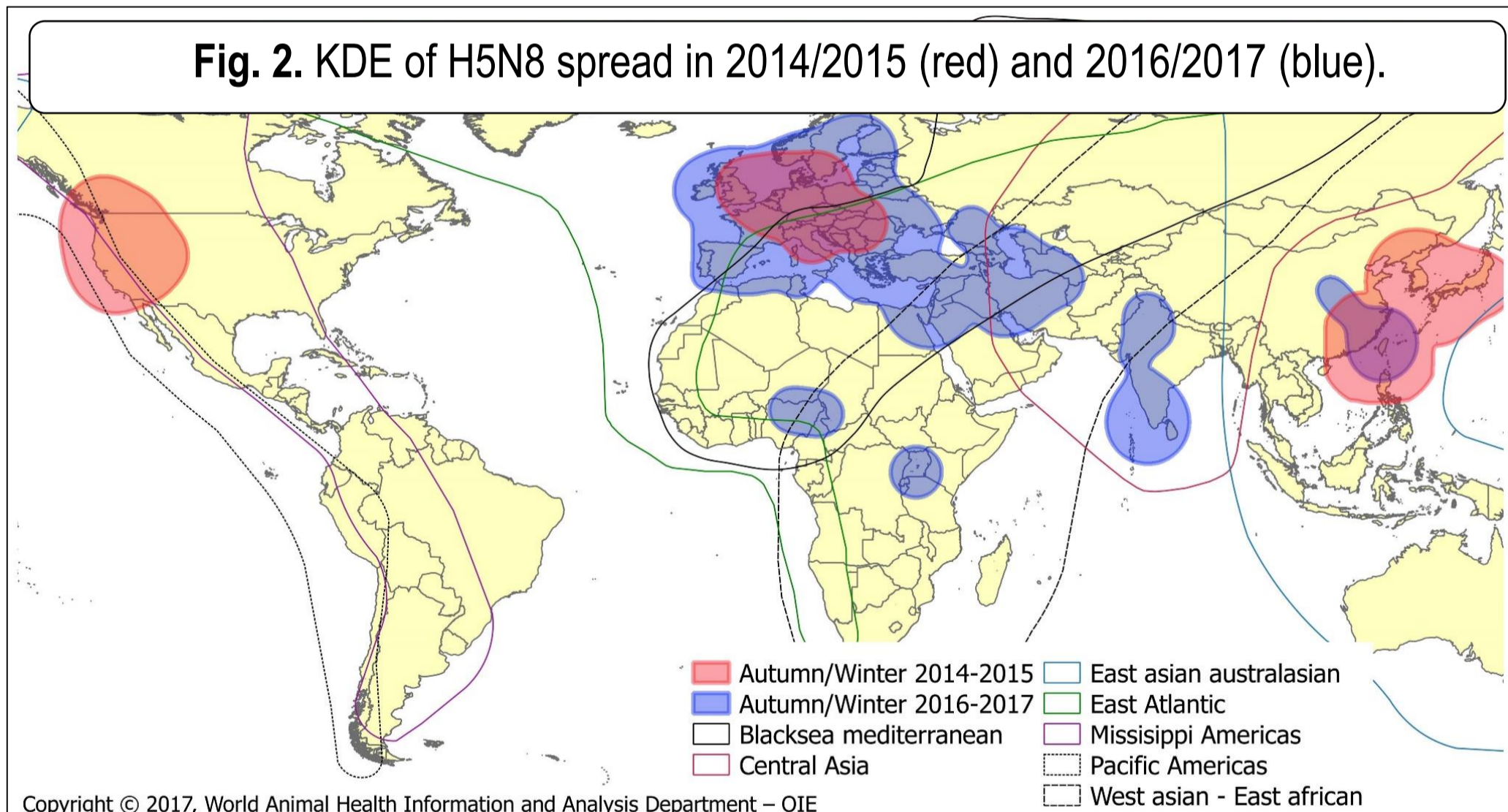
The analysis was carried out using data from H5N8 outbreaks notified through WAHIS during the two epidemic periods (n= 3092). An epidemic curve was plotted using monthly outbreak incidence and a Kernel density estimator (KDE) was used to evaluate geographical disparities between both epidemics.

## Results



The size of the 2016/2017 epidemic was significantly bigger ( $p < 0.001$ ) than the previous epidemic in 2014-2015, with an increase by 6 times in the number of outbreaks (Fig. 1). Additionally, the 2016/2017 epidemic started earlier (October) than the 2014-2015 epidemic (January).

The spatial analysis by the use of KDE showed that the geographical spread (surface affected) of the 2016/2017 epidemic was 66% larger than the 2014/2015 epidemic. The overlap between spread and bird flyways is shown on the map (Fig.2). East Asia acted as the source of the infection in both epidemics, but the disease spread more towards Europe in 2016/2017, and towards the USA in 2014/2015.



## Discussion

This analysis shows that, although both epidemics were caused by the same genotype and had the same geographical origin, their size and behavior were rather different. For an effective control of the disease, a better understanding of the causes of these differences is essential, exploring in particular the role of wild birds in its long-distance spread. This epidemic data indicates that East Asia was the source of both epidemics, reinforcing the need for continued efforts to improve early reporting of the disease in this region. In spite of increased efforts of Veterinary Services toward preparedness, the spread of the 2016/2017 epidemic highlights global weaknesses in the implementation of policies and practices to prevent HPAI transmission to animals and humans.