Development of an active risk-based surveillance strategy for avian influenza in Cuba

E. Ferrer [a], P. Alfonso [a], C. Ippoliti [b], M. Abeledo [a], P. Calistri [b], P. Blanco [c], A. Conte [b], B. Sánchez [c], O. Fonseca [a], M. Percedo [a], A. Pérez [d], O. Fernández [a], A. Giovannini [b],*

[a] Centro Nacional de Sanidad Agropecuaria (CENSA), San José de Las Lajas 32700, Mayabeque, Cuba
[b] Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "G. Caporale", Via Campo Boario, 64100 Teramo, Italy
[c] Instituto de Ecología y Sistemática (IES), Carretera Varona, Km 6, La Habana, Cuba
[d] Instituto de Medicina Veterinaria, Calle 12 No. 355, e/15 y 17 Vedado, 10400 La Habana, Cuba

ARTICLE INFO

ABSTRACT

The authors designed a risk-based approach to the selection of poultry flocks to be sampled in order to further improve the sensitivity of avian influenza (AI) active surveillance programme in Cuba. The study focused on the western region of Cuba, which harbours nearly 70% of national poultry holdings and comprise several wetlands where migratory waterfowl settle (migratory waterfowl settlements – MWS). The model took into account the potential risk of commercial poultry farms in western Cuba contracting from migratory waterfowl of the orders *Anseriformes* and *Charadriiformes* through dispersion for pasturing of migratory birds around the MWS. We computed spatial risk index by geographical analysis with Python scripts in ESRI® ArcGIS 10 on data projected in the reference system NAD 1927–UTM17. Farms located closer to MWS had the highest values for the risk indicator p_j and in total 31 farms were chosen for targeted surveillance during the risk period. The authors proposed to start active surveillance in the study area 3 weeks after the onset of *Anseriformes* migration, with additional sampling repeated twice in the same selected poultry farms at 15 days interval (Comin et al., 2012; EFSA, 2008) to cover the whole migration season. In this way, the antibody detectability would be favoured in case of either a posterior AI introduction or enhancement of a previous seroprevalence under the sensitivity level. The model identified the areas with higher risk for AIV introduction from MW, aiming at selecting poultry premises for the application of risk-based surveillance. Given the infrequency of HPAI introduction into domestic poultry populations and the relative paucity of occurrences of LPAI epidemics, the evaluation of the effectiveness of this approach would require its application for several migration seasons to allow the collection of sufficient reliable data.

1. Introduction

Until 1996, highly pathogenic avian influenza (HPAI) viruses belonging to serotypes H5 and H7 viruses were successfully eradicated or failed to persist in nature (Salomon and Webster, 2009). However, avian influenza (AI) has

* Corresponding author. Tel.: +39 0861332240; fax: +39 0861332251.
 E-mail addresses: a.giovannini@izs.it, armando.giovannini@aol.com (A. Giovannini).

greatly enhanced its significance in the last years. It has been calculated that the impact of AI on the world-wide poultry industry from 1999 to 2004 (Capua and Alexander, 2004) involved more than 200 million animals. Today, it is unknown whether the ecology of these viruses has changed and whether highly pathogenic H5N1 viruses continue to be propagated in domestic or wild bird reservoirs.

Furthermore, some avian influenza virus (AIV) can infect humans with serious public health implications (WHO, 2013, 2014). Changes in agricultural practices, enhanced animal health surveillance, and/or virus evolution may have contributed to the apparent increase in animal influenza outbreaks reported in recent times; that turns AI into an increasing concern for veterinarians worldwide (Ducatez et al., 2008).

The surveillance and control of AI have historically focused on the detection and eradication of infections due to HPAI viruses in poultry populations. However, reports of low pathogenicity avian influenza (LPAI) viruses in poultry are recurrent, with outbreaks annually affecting several countries (WAHIS, 2014). Most of AI infections in poultry are caused by LPAI virus strains, which may belong to any serotype, including H5 and H7. These H5 or H7 LPAI viruses may circulate causing unnoticeable clinical signs, unless they mutate into HPAI viruses (Alexander and Brown, 2009). Therefore the recurrence of LPAI virus circulation is a constant risk to poultry industries throughout the world.

Various approaches have been applied for the diagnosis of AI (OIE, 2008), including techniques for the detection of the virus, its genome, antigens or antibodies. However, the antibodies to AIV, as evidence of infection, often persist for the entire production life of the infected poultry (Fouchier et al., 2003), allowing a high opportunity for long-term diagnosis. The detection of a significant increase of antibody titre allows an opportunity for early warning. Consequently, antibody detection to LPAI viruses is compulsory for several countries, e.g. in the EU countries (European Commission, 2007, 2009).

The control and eradication of AI are based on passive and active surveillance, disease notification, prevention of possible contacts, biosecurity measures, and movement restriction of live birds, poultry products, by-products and potentially infective material, and depopulation of infected farms (OIE, 2013). However, when timely disease detection fails, the stamping out as a key control measure could become ineffective because the virus could be already seriously disseminated into vast poultry populations. In such cases, the economical consequences of the outbreak could be devastating.

Wild waterfowl (particularly ducks, geese, swans, gulls and shorebirds) are considered the original source of all AIV known subtypes (Munster et al., 2007). Hence the active surveillance, aimed at early detection of the disease, in several countries or regions, has included the sampling of wild bird (Burns et al., 2012; Iglesias et al., 2010). However, wild birds are not well suited for active surveillance for a number of reasons. AI virus in wild waterfowl shows a seasonal prevalence, a very variable pattern, which can vary over time and between locations within a species (Olsen et al., 2006; Figuerola et al., 2007;

Hill et al., 2012). It is, therefore, difficult to make an initial assessment of the most important species to target on the basis of virus detection alone, which demands high sampling intensity for detecting viruses.

Furthermore, sampling of wild birds is a labour-intensive, costly, and time-consuming task that has not been exempted from discussion at the decision-making level in the European Union and other regions affected by the disease (Martinez et al., 2011). The detection of viruses in migrating birds does not necessarily mean that these viruses have been, or will be, successfully introduced into a new geographic area (Martin et al., 2009) and, consequently, resident waterfowl could be a best target to assess the establishment of AI in a geographical area. However, sampling and testing of wild birds is not required by the Terrestrial Animal Health Code to declare a country, zone or compartment free from AI (OIE, 2013).

The design of surveillance programmes has to be carefully planned, taking into consideration the local epidemiological and ecological conditions, the areas where migrating waterfowl transit and settle (Miller et al., 2009; OIE, 2013; U.S., 2007, 2008), and social and economic conditions (Alfonso et al., 2008; Fiebig, 2011; Martin et al., 2011; Stärk et al., 2006).

The geographical location of Cuba makes this island an important site along bird migration routes for resting or wintering (Blanco, 2006) (Fig. 1).

The Cuban poultry population susceptible to AIV comprises 14 million of poultry, predominantly reared for egg production, which constitute an important source of proteins of animal origin for residents.

People living in rural areas of Cuba raise poultry, mainly for own consumption rather than for commercial purposes. Details of the structure of Cuban poultry farming are reported in the Supplementary Document 1. In summary, 88% of Cuban poultry belong to commercial farms while the rest of the poultry rearing has a low average density (around 17.4 birds/km^2).

Cuban AI surveillance programme focuses on determining either the evidence or the presence of infections by subtypes H5 and H7, as those of main concern for poultry due to its ability to become highly pathogenic after transmission to alternative hosts (Martin et al., 2009). This approach is in agreement with the chapter on AI of the Terrestrial Animal Health Code (OIE, 2013). Currently, the AI surveillance in Cuba is based on a passive and an active component.

The passive surveillance is usually the most effective for early detection of exotic diseases with severe clinical forms, such as the HPAI. It is, however, less effective in detecting the LPAI strains and it requires laboratory confirmation and typing of the virus strain responsible for the outbreak. The active component is based on serology by inhibition of hemagglutination assay (IHA), which is designed to be able to detect at least a prevalence of 5% AI infected holdings, with 30% infected animals within an infected holding (IMV, 2006). These values of target prevalence can lead to missing the presence of infection or delay in its detection, depending on the dynamics of the infection in the population (Gonzales et al., 2010). However, the sensitivity of active surveillance can