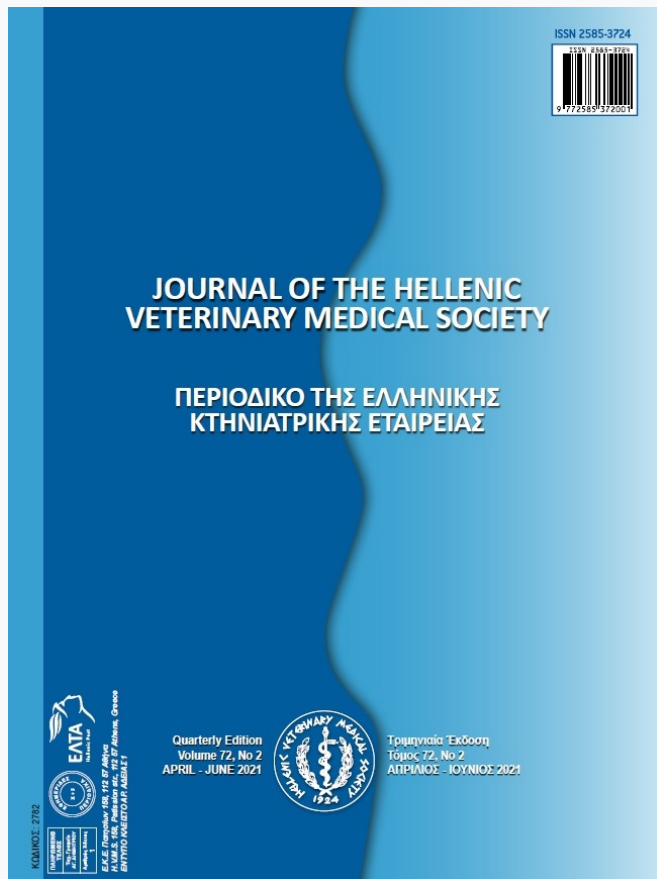


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The Role of Poultry Farms and Wild Birds During 2016-2017 Avian Influenza Epizootic in Europe

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ABSTRACT: Avian influenza is a contagious viral disease, affecting several species of birds, and poses a significant public threat. During 2016-2017, there were 2,224 high pathogenic avian influenza outbreaks in Europe, which led to the destruction of 9,663,770 birds, and 72 low pathogenic avian influenza outbreaks in 5 European countries, which caused 276,584 bird fatalities. The majority of the epidemics were in wild and backyard birds, except for France and Hungary, where the majority of outbreaks were in duck-geese farms. Notably, there were a total of 100 outbreaks in turkey farms and 37 outbreaks in layer farms, while in broiler farms there were only 10. It is indisputable that wild birds are natural hosts and reservoirs for all types of avian influenza viruses. However, the role of poultry farms on the AI intra-country epidemiology has not been fully clarified. Based on the official reports of OIE for AI, this study indicates that poultry farms, especially fattening turkey and layer chicken farms, are high-risk factors concerning the introduction of the disease into an area and its spread into other poultry farms.

Keywords: Avian influenza, epizootic, Europe, wild birds, poultry farms

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INTRODUCTION

Avian influenza (AI) is an infectious viral disease of substantial importance, due to the virus' rapid spread and high mortality rates in poultry flocks and its possible transmission to mammals, including humans, usually following close contact with infected poultry. During the last century, viruses originated, either entirely or partly, from avian influenza A viruses, caused most of the human influenza pandemics (Acha and Szyfres, 2003, Fouchier and Munster, 2009, Kuchipudi et al., 2014).

Besides, AI has a tremendous economic impact, due to trading restrictions and embargoes imposed on infected areas or countries. The control measures, which are enforced by legislation in the European Union as well as in other countries worldwide, usually involve the implementation of stamping-out policies with defined restriction zones and severe trade implications (Aldous et al., 2010). The cost of 2016-2017 AI epizootic in Europe is immense, although difficult to be estimated. The last devastating AI epizootic in the USA had a dramatic impact on the country's poultry sector, in both economic terms and the number of birds' losses. In particular, the cost was estimated to 1.3 billion American dollars and resulted in the death of more than 50 million birds, either by cause of the disease itself or after the stamping-out policy (Ramos et al., 2017). Two main global pandemics characterize the epizootiology of AI in the 21st century. Notably, the first epizootic started in 2004 and concluded in 2012, peaking in 2006, while the second was observed in 2013 and concluded recently (OIE Situation Report, 2018).

Most avian influenza viruses (AIVs) cause only mild disease in poultry and are called low pathogenic avian influenza viruses (LPAIVs). Highly pathogenic avian influenza viruses (HPAIVs) evolve from H5 and H7 LPAI viruses after their introduction and circulation in poultry flocks. HPAI viruses can kill up to 90-100% of the flock, and cause epizootics that may spread rapidly, devastate the poultry industry and result in severe trade restrictions (OIE Avian Influenza Review, 2016).

It is well known that wild birds are the main vehicle for AIVs long distance spread, such as between countries since they are natural hosts and reservoirs for all types of avian influenza viruses (Fouchier and Munster, 2009, Hill and Runstadler, 2016). However, the intra-country AI epidemiology and the role of poultry farms have not been fully clarified. Therefore,

the objective of this study is to highlight the role of poultry farms and wild birds during the 2016-2017 AI epizootic in Europe as well as to estimate the number of bird losses per country and totally in Europe.

MATERIALS AND METHODS

This study registers and categorizes AI outbreaks in several European countries, based on the official reports of epidemiological data submitted by those countries to the World Organisation for Animal Health (OIE) between January 1, 2016, and December 11, 2017. The data from each country were summarized and classified according to birds' species, farming system, number of outbreaks and number of destroyed birds. The study is in full compliance with all relevant codes of experimentation and legislation.

RESULTS

During this period, there were 2,224 HPAI outbreaks in 29 European countries, which led to the death of 9,986,136 birds, as a result of either disease mortality or stamping-out measures (Table 1). The top 10 countries, in terms of bird losses, were Italy, Hungary, France, Germany, Poland, Bulgaria, Sweden, The Netherlands, UK and Czech Republic. The top 10 countries, in terms of the number of outbreaks, were France, Hungary, Germany, Romania, Poland, Italy, Switzerland, Bulgaria, Czech Republic and The Netherlands.

The majority of the outbreaks were in wild and backyard birds, except France and Hungary, where the outbreaks were mostly observed in duck-geese farms. It is worth mentioning that among 10 European countries whose reports came from farms of Galliformes birds, there were 100 HPAI outbreaks in fattening turkey farms and 37 in layer farms, while in broiler farms there were only 10 outbreaks, closely related to turkey and/or duck-geese farms. More specifically, in Italy, there were 40 HPAI outbreaks in turkey farms, 16 in layer farms and 4 in broiler farms in a total of 60 HPAI outbreaks. In Germany, there were 49 HPAI outbreaks in turkey farms, 4 in layer farms, 2 in turkey breeder farms and 1 in a breeder farm in a total of 56 HPAI outbreaks. In France, there were 6 HPAI outbreaks in layer farms, 5 in broiler farms, 2 in breeder farms and 1 in a turkey farm, while there were 34 outbreaks in birds' farms, as the breeding category in the reports was unclear, in a total of 48 HPAI outbreaks. In Hungary, there were 6 HPAI outbreaks in turkey farms, 4 in layer farms and 1 in a broiler farm in a total of 11 HPAI outbreaks. In The Netherlands,

there were 3 HPAI outbreaks in layer farms and 2 in breeder farms in a total of 5 HPAI outbreaks. In the UK, there were 3 HPAI outbreaks in turkey farms and 1 in a breeder farm, in a total of 4 HPAI outbreaks. In Sweden, there were a total of 2 HPAI outbreaks in layer farms. Finally, in Greece and Luxemburg, there

was one reported HPAI outbreak in a layer farm, and in Austria in a turkey farm. Overall, regarding HPAI outbreaks of Galliformes, 52.91% were in turkey farms, 19.58% in layer farms, 5.29% in broiler farms, 3.17% in broiler breeder farms and 1.06% in turkey breeder farms.

Table 1. HPAI outbreaks in poultry farms, backyard flocks and wild birds in European countries during 2016-2017 Avian Influenza Epizootic.

Country	Broiler farms	Layer farms	Breeder farms	Turkey farms	Turkey breeder farms	Duck/goose farms	Backyard farms	Multi-farms	Wild birds	Unidentified	Total outbreaks	Destroyed birds
France	5	6	2	1	0	358	16	19	55	56	556	1,413,897
Hungary	1	4	0	6	0	195	30	0	67	3	308	1,972,341
Germany	0	4	1	49	2	11	19	6	200	0	292	1,192,215
Romania	0	0	0	0	0	0	46	0	90	0	136	1,452
Poland	0	0	0	0	0	0	25	0	71	39	135	1,008,896
Italy	4	16	0	40	0	5	15	3	14	0	99	2,803,589
Switzerland	0	0	0	0	0	0	0	0	94	0	94	0
Bulgaria	0	0	0	0	0	0	19	0	14	43	77	582,188
Czech Rep.	0	0	0	0	0	3	33	2	34	0	72	74,928
Netherlands	0	3	2	0	0	5	0	0	59	0	69	230,049
Slovakia	0	0	0	0	0	0	9	0	60	0	69	210
Denmark	0	0	0	0	0	0	1	1	51	0	53	69
Sweden	0	2	0	0	0	0	3	1	37	0	43	258,894
Austria	0	0	0	1	0	0	0	0	33	0	34	21
UK	0	0	1	3	0	0	5	2	19	0	32	106,603
Serbia	0	0	0	0	0	0	4	0	21	0	25	243
Croatia	0	0	0	0	0	0	8	0	11	3	22	492
Slovenia	0	0	0	0	0	0	0	0	21	0	21	0
Belgium	0	0	0	0	0	0	0	0	5	13	18	4,861
Finland	0	0	0	0	0	0	0	1	16	0	17	29
Greece	0	1	0	0	0	0	5	0	9	0	15	81
Spain	0	0	0	0	0	1	0	0	2	9	12	9,880
Ireland	0	0	0	0	0	0	0	0	9	0	9	2
Lithuania	0	0	0	0	0	0	0	0	5	0	5	0
Luxemburg	0	1	0	0	0	0	0	3	0	0	4	787
Bosnia and Herzegovina	0	0	0	0	0	0	1	0	2	0	3	51
Republic of North Macedonia	0	0	0	0	0	0	1	0	1	0	2	1,992
Cyprus	0	0	0	0	0	0	0	0	1	0	1	0
Portugal	0	0	0	0	0	0	0	0	1	0	1	0
Total	10	37	6	100	2	578	240	38	1,002	166	2,224	9,663,770
Total %	0.45	1.66	0.27	4.5	0.09	25.99	10.79	1.71	45.05	7.46	100	

Source: OIE, Immediate notifications and follow-up reports of highly pathogenic avian influenza

Table 2. LPAI outbreaks in poultry farms, backyard flocks and wild birds in affected European countries during 2016-2017 Avian Influenza Epizootic.

Country	Subtype	Broiler farms	Layer farms	Breeder farms	Turkey farms	Turkey breeder farms	Duck/goose farms	Backyard farms	Multi-farms	Wild birds	Unidentified	Total outbreaks	Destroyed
Germany	H5N1, H5N2, H5N3	0	0	0	0	0	2	5	1	0	0	8	3,009
The Netherlands	H5N2, H7N9	0	0	0	0	0	0	0	0	0	3	3	103,143
France	H5N1, H5N2, H5N3, H5N8, H5N9, H7	0	0	1	0	2	40	0	1	0	13	58	126,216
Denmark	H5N2, H7N7	0	0	0	0	0	2	0	0	0	0	2	4,416
UK	H5N1	0	0	0	0	0	0	0	0	0	1	1	39,800
Total		0	0	1	0	2	44	5	2	0	17	72	276,584

Source: OIE, Immediate notifications and follow-up reports of low pathogenic avian influenza

The dominant HPAI virus subtype in Europe during the 2016-2017 epizootic was H5N8. Nevertheless, other AI subtypes were also observed during that period. The H5N5 subtype was detected in Croatia, Czech Republic, Germany, Greece, The Netherlands, Serbia and Slovenia in wild birds and fattening turkey farms. H5N9, H5N1 and H5N2 subtypes were identified in France, in duck/goose farms, broiler farms, guinea fowl farm, multi-species farm and a hatchery. The H5N6 subtype was detected in a backyard farm in Greece and The Netherlands, in two outbreaks in wild birds, while the H7N7 subtype was found in Italy, in a turkey and a layer farm.

During the same period, there were also 72 LPAI outbreaks in 5 European countries, which led to the death of 277,752 birds (Table 2). France was the country with the highest number of birds' losses, followed by The Netherlands, UK, Denmark, and Germany. Regarding the number of LPAI outbreaks, France was the country with the highest number, listing 58, followed by Germany with 8 outbreaks, The Netherlands with 3, Denmark with 2 outbreaks and the UK with 1 outbreak. The majority of LPAI outbreaks were reported in duck-goose farms (44/72 outbreaks). In breeder and turkey breeder farms were observed only 3 LPAI outbreaks, in France while there were no outbreaks in broiler, layer and turkey farms. The dominant LPAI virus subtype in Germany, The Netherlands, France, and Denmark was H5N2, which was responsible for the death of 96,598 birds in backyard, breeder, duck-goose farms and game bird farms.

The H5N1 subtype was responsible for the death of 96,349 birds of duck-goose farms and multi-species farms in the UK, France, and Germany. The H5N3 subtype was the cause of death of 17,921 birds in backyard, turkey breeder and duck-goose farms in Germany and France. Besides, France was the only country where the H5N8 and H5N9 subtypes of LPAI virus were detected in duck-goose farms. Similarly, The Netherlands was the only country where the H7N9 subtype was observed, but the affected population was not identified.

DISCUSSION

AIVs pose significant threats to avian and human health and cause severe damage to the poultry industry, concerning mortality, welfare, economic losses, and trading restrictions (Kuchipudi et al., 2014, Ramos et al. 2017). Wild birds, and especially those belonging to the orders Anseriformes (for instance waterfowl, ducks, geese, swans) and Charadriiformes (gulls, terns and shorebirds), are considered the natural reservoir hosts of the AIVs (Acha and Szyfres, 2003, Swayne, 2006). The findings of our study fully support the above mentioned results since the majority of infected wild birds during the 2016-2017 AI epizootic in Europe were ducks, geese, swans, gulls, terns and shorebirds.

Migratory birds, during their long migratory journeys, exchange viruses with other populations at staging, stopover, or wintering sites (Georgopoulou and Tsiouris, 2008, Gill et al., 2009). Shorebirds and gulls

contribute more to the AI transmission over more extensive geographic distances than ducks and geese. In particular, gulls and shorebirds play a crucial role in linking the continents, as they undertake long-distance migration, and allow a more direct route of virus transmission (Gill et al., 2009, Hill and Runstadler, 2016). In contrast, waterfowl are non-migratory birds, which fly and reside over land, stop at wetlands for food and supply, thus contributing to interspecies transmission and spread of AIV on the inside (Miller et al., 2005, Gill et al., 2009, Hill and Runstadler, 2016).

Based on the official reports of OIE during 2016-2017 AI epizootic, there were 72 outbreaks of LPAI viruses, the majority of which prevailed in duck-geese farms in France. H5N2 was the dominant LPAI virus subtype of the epizootic, while other subtypes, such as H5N1, H5N3, H5N8-H5N9, H7N7 and H7N9 were reported as well. In cases of LPAI viruses transmission from wild birds to poultry, there are three scenarios. The first scenario, the most common among the three, is the termination of the viruses' circulation. The second is the preservation of the viruses' circulation. Finally, the third scenario is the evolution of the viruses into HPAI, such as H5 or H7. However, once an AIV has been transmitted and efficiently circulated to poultry, it can rarely be re-adapted in wild birds (Swayne, 2006).

HPAI and LPAI viruses have been frequently isolated in commercial poultry farms of chickens, turkeys, ducks, geese, and ratites, as well as in pigeons and cage birds. However, the sensitivity and the clinical manifestation of the disease in birds vary between avian species. For example, pigeons appear to be relatively resistant to infection compared to poultry (Swayne, 2006). Similarly, the high mortality in chickens and simultaneously the absence of clinical disease in ducks after AIV challenge, indicate that there are differences in the innate immune response among avian species (Kuchipudi et al., 2014).

An interesting observation during the 2016-2017 AI epizootic, according to the official reports of the World Organization for Animal Health, was the type of Galliformes farms which were mostly affected by HPAI viruses. In particular, 52.91% of the outbreaks occurred in turkey farms, 19.58% in layer farms, 5.29% in broiler farms, 3.17% in breeder farms and 1.06% in turkey breeder farms.

Regarding that, the higher sensitivity of fattening turkeys to AI compared to that of broiler chicks could

be the reason for the higher prevalence of AI outbreaks in turkey farms (Aldous et al., 2010). In particular, turkeys were 10-fold more susceptible to infection than chickens, with the cases concerning turkey farms being 4.5% of the total cases, while in broiler farms the rate was 0.45%. Likewise, turkeys are being raised for a more extended productivity period and under less strict biosecurity measures since occasionally they have outdoor access, e.g. for scratching and grazing. Similarly, layer hens are being raised for even more than a year productive period, and biosecurity gaps are more frequent since layer farms have more visits (egg transports, feed) and equipment exchange (egg trays, egg trolleys, egg tray crates), thus the infestation degree concerning layer farms equals 1.66%. These management practices increase the risk of contact with both wild birds and mechanical carriers and contribute to the higher prevalence of AI outbreaks in turkey and layer farms. Taking all the above into account, we could conclude that turkey and layer farms constitute a critical risk factor for the introduction of the disease into an area and its spread into other poultry farms.

Additionally, according to the official reports of OIE during 2016-2017, the majority of AI outbreaks were in duck-geese farms. The main reason for that higher prevalence is probably the outdoor farming system and the notably direct contact of them with the wild birds. Furthermore, the relative resistance of these species to AIV infections could lead to the shedding of large amounts of the virus to the environment and the spread of the disease to the other birds of the farm (Kuchipudi et al., 2014).

During the conduction of the present investigation, it became clear that OIE is keeping and recording a very detailed file regarding animal diseases, and that cannot be accomplished without the close collaboration of every country. It is obvious that evaluating the exact size of an endangered population is not always easy to determine, and every so often even the type of the epidemiological unit itself. This kind of work seems to be even more difficult amid a pandemic, especially in the case of a disease such as AI, whose spread can occur rapidly and dramatically. That can be seen quite clearly in the reports of countries such as Poland and Bulgaria that reported a large number of "unidentified cases". Likewise, France reported both a substantial amount of unidentified cases and plenty of outbreaks in birds' farms, without the specification of the breeding system. In this way, the study

and statistical processing of the results is made difficult, as the data from the reports seem incomplete, mainly regarding the bird species, thus not allowing a more thorough epidemiological investigation of the outbreaks.

The majority of the OIE reports claimed that the AIV infection was a result of contact, direct or indirect, between wild birds and poultry (OIE Situation Report, 2017). In particular, outbreaks linked to the dominant H5N8 subtype in Europe indicated that the sources of the infection were the contact with wild species or with infected animals when grazing or watering, through fomites (such as humans, vehicles, feed), the introduction of new live animals, via airborne spread, and, finally, via unknown or inconclusive routes. Genetic analyses of the European viruses indicate that they were introduced via wild birds to northern and central Europe from Asia (El-Shesheny et al., 2017).

According to another OIE Situation Report for avian influenza, published on 18/09/2017, HPAI H5N8 caused 277 outbreaks in poultry, 51 in wild birds and led to the destruction of 427,081 poultry. HPAI H5N8 subtype is a complex reassortant virus carrying genes from A (H5N1) as one of its parental viruses. It was firstly reported in China in 2010, while later on, following further virus evolution via reassortment, several outbreaks with HPAI virus A (H5N8) viruses occurred in aquatic migratory birds, chicken, geese and ducks in China, Japan, Republic of Korea and Europe (Hill et al., 2015, El-Shesheny et al., 2017). The HPAI virus A (H5N8) virus pathogenicity varies among avian species. Particularly, during infection, mass mortality is observed in turkeys and chickens, while it has yet to be correlated with acute illness or excessive mortality rates in mallards (Adlhoch et al., 2014). The transmission of avian influenza A(H5N8) virus to humans has not been reported so far worldwide, and no human cases have been reported (Brown et al., 2017).

The epidemiologic investigation of outbreaks linked to the H5N1-H5N2 subtypes in France claimed that the source of infection either was the introduction of new live animals or was unknown/inconclusive. Based on the OIE reports on AI in 2017, the HPAI H5N1 is enzootic in Asia and Africa and causes outbreaks in poultry and sporadic human infections. Since wild birds are most frequently implicated in the transmission, all affected countries should focus on applying biosecurity measures and on avoiding contact of wild birds with poultry. HPAI H5N1 led to 17

ongoing worldwide outbreaks in poultry and the destruction of 131,168 birds, whereas HPAI H5N2 led to 182 ongoing outbreaks in poultry and 1 in wild birds and therefore led to the destruction of 1,617,816 birds (OIE Situation Report, 2017).

Greece and The Netherlands were the only European countries to be reported with the H5N6 subtype of AIV. However, this subtype is considered the result of genetic reassortment from the H5N8 European subtype (OIE Update on Avian Influenza, 2018). H5N6 affected three countries worldwide and caused 358 outbreaks in poultry. The data shows that it has outnumbered the H5N8 AIV, concerning the amount of poultry destroyed after the application of control measures by the veterinary authorities (25,096,648 birds). The Asian lineage H5N6 causes severe clinical signs in poultry and associated mortality. Migratory birds could be the vectors of HPAI H5N6 transmission outside Asia. According to reports of WHO since 2014, this group of H5N6 viruses has been related to 24 laboratory-confirmed outbreaks of human infection, including 7 deaths in China (WHO, 2020).

The Netherlands was the only European country where outbreaks associated with H7N9 AIV, which were detected in ducks and neighboring broiler farms. Although the source of the infection was unknown or inconclusive, OIE stands by the fact that live bird markets pose a significant risk factor for H7N9 virus spreading among poultry and from poultry to humans. This virus, based on phylogenetic analysis, is not the same as the China H7N9 virus that has a significant impact on poultry and human infections in Asia. Since its origin in 2013, the H7N9 virus remained LPAI in poultry mainly in China but caused over 1,562 human infections (as of September 13, 2017). However, OIE reported recently that the LPAI H7N9 virus has mutated to an HPAI H7N9 virus. According to OIE Situation Report for Avian Influenza on 18/09/2017, the H7N9 virus is the cause of 22 additional worldwide outbreaks and led to the destruction of 831,087 birds.

Finally, yet importantly, the H5N5 virus affected several European countries. The source of the infection was either the contact with wild species or unknown/inconclusive. According to the OIE update on AI in 2018, H5N5 AIV affected only 2 countries worldwide and is the cause of 2 ongoing outbreaks concerning wild birds. There were no outbreaks in poultry, and no poultry was destroyed due to the control measures.

CONCLUSION

Poultry farms play a crucial role in the spread of AI into an area, although wild birds are known to be the source for the infection of domestic poultry and humans. The introduction of AI in poultry farms leads to severe damages and trade restrictions, which have a global impact on the market. Therefore, it is of grand necessity to eliminate the exposure of poultry to wild birds through a plethora of preventive measures, such as strict biosecurity measures and rearing restrictions. Still, the particular type of poultry farms should be considered for the implementation of biosecurity protocols, since fattening turkey and layer chicken farms pose a crucial risk factor for an AI outbreak. The es-

tablishment and application of surveillance systems, diagnostic methods for early detection of AIV and harmonized restriction and control measures are only some fundamental actions that need to be administered to restrain the distribution, prevalence and introduction pathways into Europe and for the control of AI.

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