



Short Communication

Identification of Migratory Bird Vectors of Avian Influenza Virus (AIV) in North-East of Algeria

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Abstract | Migratory birds, especially *Anseriformes*, are a primary reservoir and the first source of the avian influenza virus (AIV) introduction. In 2016, following the first official detection of the H9N2 subtype circulation in broiler flocks in Eastern Algeria, a preliminary descriptive study is conducted to identify and enumerate in wetland areas, migratory bird species, known to carry the AIV. The Anatidae population peaked in January 2017 with a total of 8064 birds. The 6 frequent species observed are: Mallard (*Anas platyrhynchos*), Eurasian teal (*Anas crecca*), Gadwall (*Anas strepera*), Eurasian wigeon (*Anas penelope*) and Common shelduck (*Tadorna tadorna*). Our observations confirm the diversity of migratory bird species, particularly *Anatidae* infected with AIV, in the wetlands of Eastern Algeria. Molecular characterization of circulating avian influenza viruses in these wild birds will help assess the potential for spread of these viruses in poultry farms.

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Introduction

The avian influenza virus (AIV) has been detected in several migratory waterfowl, which constitute a primary reservoir of the virus. However, surveillance studies have identified ducks (family *Anatidae*, order *Anseriformes*), including dabbling ducks, including Mallard (*Anas platyrhynchos*) as the most infected. The prevalence of avian influenza infection in all combinations (H1-H16), varied by bird species, geographical location and time of year (Adlhoch et al., 2018). The identification of waterfowl species at each geographical site is essential as a prerequisite for any active surveillance of influenza viruses.

Among the 9 migration routes around the world, that of the East Atlantic (Figure 1) and that of the Mediterranean and the Black Sea (Figure 1) of

which Algeria is a part.

The reports to OIE provide the number of virus positive dead birds per species, but not the average population size of the affected wild birds species from which wild bird carcasses were obtained, let alone the number of animals at risk in these population (Wu et al., 2018) Therefore it is not possible to make an objective estimate of the mortality rate in order to assess the pathogenicity of infection with these subtype of LPAIV (low pathogenic avian influenza virus) or HPAIV (high pathogenic avian influenza virus) in wild bird populations. Some information may be gained by data on the number of carcasses of the different wild bird species that tested positive for HPAIV during surveillance activities (Zecchin et al., 2017; Zhang et al., 2017).





This preliminary descriptive study is conducted to detect and identify migratory bird species in Eastern Algeria, particularly the *Anseriformes* and *Charadriiformes*, known as potential carriers of AIV.

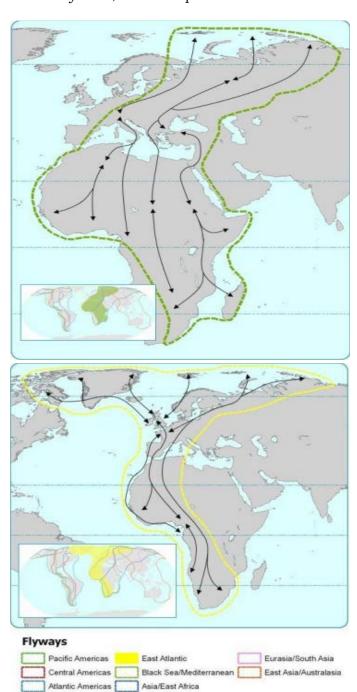


Figure 1: Flyway for migratory birds (Diego Pavon, 2017).

Materials and Methods

In order to determine their seasonal dynamics, it was proposed to identify and monitor during wintering the evolution of Anatidae numbers in the high plains of North-Eastern Algeria. This region also called "The Constantinois" is full of wild birds of the family *Anatidae*, considered the most important family of the order *Anseriformes*, with more than 150 species.

Material used

For the dismemberment of the migratory birds we used the following instruments:

- A telescope mounted on tripod (Optolyth 20×60).
- A notebook to record observations and data.
- Waterfowl Guide.
- Camera.

Counting techniques for waterfowls

Two methods were used:

- The ground count.
- The enumeration by plane: it is not feasible here in Algeria.

The choice of counting method depends on:

- The size of the site.
- The size of the bird population to be counted.
- The homogeneity of the population.

The choice of observation points: observation points are chosen according to two criteria:

- The global and dominant vision of the observation site
- The distribution of bird groups on the observation site

Sampling methods

When the group of birds are closer at a distance of less than 200 m, so close to our observation point and whose size does not exceed 200 subjects, the counts are based on an individual count. In the opposite case, groupings involving several thousand birds, it is impossible to count them one by one. Therefore, a quantitative estimate of the number of birds must be made (Lamotte et Boureliere, 1969).

A difference between the number of birds observed and that actually present always exists. The margin of error of this method is of the order of 5 to 10%.

Dates and frequencies of counts

Our study conducted during the year 2016/2017. It is based on censuses every two weeks, from September 2016 to April 2017.

Identifications of species carrying influenza viruses

Identification is based on the list of infected species (ducks, geese, swans, gulls, gulls, terns, cormorants ...etc.), cited by Olsen et al., 2006.





Table 1: Number of migratory bird species, identified in Eastern Algeria.

Order/Family	Common species	Identified species	Positive (IAV) identified species
Anseriformes Anatidae	Ducks, Geeses, Swans	9 identified species: -Northern Shoveler (Anas clypeata) -Marbled Teal (Marmaronetta angustirostris) -Common pochard (Aythyaferina) - Mallard (Anas platyrhynchos) - Eurasian teal (Anas crecca) - Northern pintail (Anas acuta) -Gadwall (Anas strepera) -Eurasian Wigeon (Anas penelope) -Common Shelduck (Tadorna tadorna)	6 infected species: - Mallard (Anas platyrhynchos) - Eurasian teal (Anas crecca) - Northern pintail (Anas acuta) - Gadwall (Anasstrepera) - Eurasian Wigeon (Anas penelope) - Common Shelduck (Tadorna tadorna)
Charadriiformes			
Laridae	Seagulls, Gulls	2 identified species: -Black headed gull (<i>Larus ridibundus</i> , <i>Chroicocephalus ridibundus</i>) - Slender-billed Gull (Chroicocephalus genei)	1 infected specie: - Black headed gull (<i>Larus ridibundus</i> , <i>Chroicocephalus ridibundus</i>)
Sterna		2 identified species: - Sterna nilotica, (Gull-billed tern) - Whiskered tern (Childonias hybrida)	
Scolopacidae	Waders or Shorebirds	4 identified species: - Little stint (Calidris minuta) - Lesser yellowlegs (Tringa flavipes): - Common redshank (Tringa totanus) - Whimbrel (Numenius phaeopus)	
Gruiformes Rallidae	Water rails Coots	2 identified species: -Common moorhen (Gallinula chloropus) -Common coot (Fulica atra)	01 infected specie -Common coot (Fulica atra)
Pelecaniformes Phalacrocoracidae	Cormorants	1 specie: - Great cormorant (<i>Phalacrocorax carbo</i>)	-Great cormorant (<i>Phalacrocorax carbo</i>)

Results and Discussion

The follow-up allowed us to identify twenty (20) species of migratory birds in the area of observation (Table 1). Nine species (09) of Anatidae (ducks, geeses, and swans) dominate this area. The Anatidae population peaked in January 2017 with a total of 8064 birds. Among the identified species, six (6) are in the list of avian taxa carrying the highly pathogenic H5N1 virus (Adlhoch et al., 2018; Olsen et al., 2006). These species are: Mallard (Anas platyrhynchos), Eurasian teal (Anas crecca), Gadwall (Anas strepera), Eurasian wigeon (Anas penelope) and Common shelduck (Tadorna tadorna). The seasonal dynamics showed that the maximum number of birds is reached in winter and composed of 1700 Mallard (Anas platyrhynchos), 650 Eurasian teal (Anas crecca), 1070 Eurasian wigeon (Anas penelope) and 3780 Common shelduck (Tadorna tadorna). As for Northern pintail (Anas acuta) and Gadwall (Anas strepera), their numbers reached a maximum in November 2016 with 600 and 150 birds respectively.

The observations found are similar to those reported

by a team of researchers in Europe (Adlhoch et al., 2018; Delany et al., 2009).

About the Charadriformes family, eleven (11) species have been identified. They are: Black-headed gull (Larus ridibundus), Slender-billed gull (Chroicocephalus genei), Sterna nilotica (Gull-billed tern), Whiskered tern (Childonias hybrida), Little stint (Calidris minuta), Common redshank (Tringa totanus), Whimbrel (Numenius phaeopus), Common moorhen (Gallinula chloropus), Common coot (Fulica atra) and Great cormorant (Phalacrocorax carbo). Among these identified species, only three (03) are in the list of avian taxa carrying highly pathogenic influenza viruses. The species are Black headed gull (Larus ridibundus), Common coot (Fulica atra) and Great cormorant (Phalacrocorax carbo). This population of waterfowl (Charadriformes) is very often located in Europe (Adlhoch et al., 2018). It is regularly infected with the highly pathogenic avian influenza virus (FAO, 2018). During winter migration, these birds are found in some southern Mediterranean countries, particularly in Algeria.





Conclusions and Recommendations

Our observations confirm the presence, abundance and above all the diversity of migratory bird species (20 identified species) within the wetland complex of the high plains of Eastern Algeria. Identification and characterization of avian influenza viruses in these potentially infected wild birds will help to clarify the risk of spread of influenza viruses to domestic poultry populations.

Authors Contributions

It is clearly stated that all author has contributed significantly to the study

Conflict of Interest

The authors declare that there is no conflict of interest exists

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