# MODELLING THE SPREAD OF AVIAN INFLUENZA VIRUSES
# AMONG WILD BIRDS IN THE EBRO DELTA (SPAIN) *

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#### SUMMARY

This study presents a stochastic model to simulate the possible spread of Avian Influenza viruses (AIV) in wild birds under different scenarios. This work based on ornithological and ecological information provides a tool for identification of the species and zones in a specific area that should be targeted in a risk-based avian influenza (AI) surveillance system. The model illustrates the spatio-temporal dynamics of AIV among wild birds based on an individual susceptible-infectious-susceptible approach. It was focused on the Natural Park of Ebro Delta, which is one of the most important reserves of waterfowl in the Western Mediterranean Basin in terms of abundance and variety of species. A series of inputs related to the hosts, viruses and to the environment were included into the model as follows : the onset date of introduction, the number and type of infected bird species and their location, the different polygons according to ecological and ornithological criteria that made up the Natural Park of Delta Ebre, a list of frequent bird species divided into high risk species and intermediate species, the census of each one of these bird species by polygon and period and their patterns of dispersion, the degree of affinity among bird species, the duration of infectiousness and different rates of transmission probability. This type of model can provide the decision makers with useful information for the design and the implementation of future surveillance activities for AIV in wild birds in specific areas.

**Keywords** *:* Modelling, Avian influenza, Surveillance, Wild birds.

#### RESUME

Cette étude présente un modèle stochastique pour représenter une éventuelle propagation des virus d'influenza aviaire (AIV) chez les oiseaux sauvages à partir de différents scénarios. Ce travail fournit un outil pour identifier les espèces d'oiseaux et les zones à échantillonner dans un système de surveillance fondée sur l'utilisation des informations ornithologiques et écologiques. Le modèle représente la dynamique spatio-temporelle des AIV chez les oiseaux sauvages basée sur une approche individu susceptible-infectieux-susceptible. Il concerne le Parc naturel du Delta de l'Ebre, qui est l'une des plus importantes zones humides dans le bassin occidental de la Méditerranée de par l'abondance et la variété des espèces d'oiseaux.

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Un ensemble de paramètres liés à l'hôte, les virus et l'environnement a été inclus dans le modèle comme suit : le date d'introduction, le nombre et le type d'espèce d'oiseaux et leur emplacement, les polygones que compose le parc naturel en fonction des critères écologiques et ornithologiques, une liste des nombreuses espèces d'oiseaux réparties en espèces à risque élevé et espèces intermédiaires, le recensement de chacune de ces espèces d'oiseaux par polygone et leurs modes de dispersion, le degré d'affinité entre les espèces, la durée de l'infection et les différentes probabilités de transmission. Ce type de modèle peut fournir des informations utiles pour les décideurs dans la conception et la mise en œuvre des activités futures de surveillance AIV pour les oiseaux sauvages dans des domaines spécifiques.


**Mots-clés** *:* Modélisation, influenza aviaire, surveillance, oiseaux sauvages.

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# I - INTRODUCTION

The importance of wild aquatic birds as natural reservoirs of influenza A viruses (AIV), particularly in avian orders such as Anseriformes and Charadriiformes has been well documented [Alexander, 2000; De Marco *et al.*, 2003; Fouchier *et al.*, 2003; Hinshaw *et al.*, 1980]. Since 2005 compulsory surveillance programs for AIV in wild birds have been carried out in the Member States of the European Union. The main objectives of these surveillance systems are : the early detection of H5N1 highly pathogenic AIV (HPAIV) in wild birds, the investigation of possible carriers or bridge species following an incident of H5N1 HPAIV and the baseline monitoring of the circulation of low pathogenic AIV H5 and H7 strains in wild birds [European Commission 268\2007\EC].

Currently one of the main challenges that the animal health services have to face is how to design the AIV surveillance due to the impossibility to provide a comprehensive coverage of the population and the logistical difficulties to conduct this kind of surveys.

In order to increase the probability of early detection, a risk-based surveillance can be a valuable tool. This type of surveillance introduces a positive bias by focussing on the individuals that are more likely to be infected.

The purpose of this study is to provide a new surveillance tool based on a stochastic model to identify within an area at high risk the main species, sites and periods of the year where the introduction and spread of AIV through waterfowl birds are more likely. In this paper we will deal with some outputs of the model obtained during the nesting period.

This model is focussed in the Natural Park of the Ebro Delta, in Catalonia (North-Eastern Spain). This natural park is an area up to 320 km$^2$ where there are many wetlands and resting sites for migratory waterfowl in close proximity to the poultry industry. In this area there is a risk of potential transmission from wild birds to domestic poultry because waterfowl come to irrigated crop areas for feeding and may interact with domestic ducks and geese. In the same way, wild birds may contact with terrestrial poultry kept in the open or interact with other avian intermediate species.

Data collected in Catalonia between 2005 and 2007 within the avian influenza surveillance in wild birds demonstrated the circulation of different strains of low pathogenic avian influenza viruses (LPAIV) among the wild bird population in this area [Alba *et al.*, 2007].

## II - MATERIAL AND METHODS

### 1. INPUTS OF THE MODEL

The Ebro Delta Natural Park is composed of various types of ecosystems, such as rice fields, lagoons, salt marshes, bays, sandy beaches, rivers and urban areas. In order to build the model, the study area was divided into different polygons taking based on ecological and ornithological criteria. Figure 1 shows the spatial distribution of the 27 polygons and the type of ecosystem in which the Ebro Delta was divided.

**Figure 1**

**Division in polygons of the Ebro Delta based on ecological and ornithological criteria**
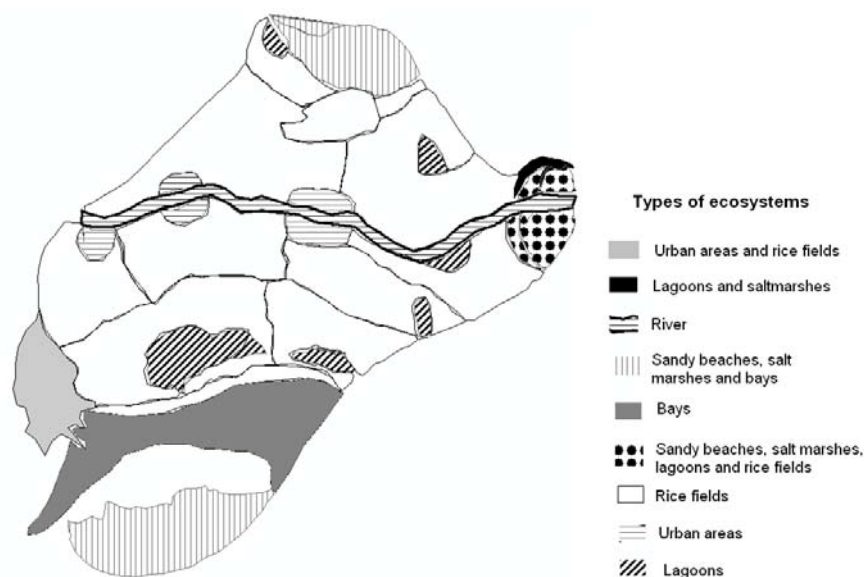


The species considered in the model, included both species most likely to introduce AIV (high risk species) and other species that may act as intermediate hosts or « bridge » species.

The high risk species were chosen based on the literature [Atkinson *et al.*, 2007 ; Pfeiffer *et al.*, 2006 ; USGS website, 2007], while their census in the area was obtained from the Department of Environment and Housing of Catalonia [official sources DMAiH, 2007]. The list of « bridge » species was determined based on their degree of affinity with the high risk species and their census [official sources DMAiH, 2007].

For each of these species, the following information was collected :

1. Average census in each of the polygons by period (based on data from the years 2001 to 2005),

2. Degree of affinity between the various species taking into account whether they share the same habitat, the groups of feeding or nesting and their gregariousness behaviour, and

3. Patterns of movements of these species within the Ebro Delta.

Table 1 shows the list of species that were included into the model, with their respective census in the breeding and wintering periods.

**Table 1**

**Species and total census by species considered in the model**

| Family | Species | Risk status | Wintering census | Breeding census |
|---|---|---|---|---|
| *Anatidae* | Pintail *(Anas acuta )* | High | 1807 | 0 |
| | Shoveler *(Anas clypeata )* | High | 11 455 | 12 |
| | Teal *(Anas crecca )* | High | 11 262 | 0 |
| | Wigeon *(Anas penelope)* | High | 2 242 | 0 |
| | Mallard *(Anas platyrhynchos)* | High | 42 332 | 22428 |
| | Garganey *(Anas querquedula)* | High | 0 | 6 |
| | Gadwall *(Anas strepera)* | High | 2 797 | 728 |
| | Greylag Goose *(Anser anser)* | High | 840 | 0 |
| | Pochard *(Aythya ferina)* | High | 523 | 6 |
| | Tufted Duck *(Aythya fuligula)* | High | 55 | 0 |
| | Red-crested *Pochard (Netta rufina)* | High | 3 670 | 4 428 |
| | Shelduck *(Tadorna tadorna)* | Intermediate | 204 | 206 |
| *Ardeidae* | Grey heron *(Ardea cinerea)* | Intermediate | 84 | 91 |
| *Charadriidae* | Kentish Plover *(Charadrius alexandrinus)* | Intermediate | 1 768 | 0 |
| | Grey Plover *(Pluvialis squatarola)* | Intermediate | 1 455 | 0 |
| | Lapwing *(Vanellus vanellus)* | High | 14 280 | 0 |
| *Glareolidae* | Collared Pratincole *(Glareola pratincola)* | Intermediate | 434 | 0 |
| *Laridae* | Audouin's Gull *(Larus audouinii)* | Intermediate | 20 227 | 22 064 |
| | Slender-billed Gull *(Larus genei)* | Intermediate | 340 | 1 146 |
| | Mediterranean Gull *(Larus melanocephalus)* | High | 0 | 8 |
| | Herring Gull *(Larus michahellis)* | Intermediate | 6 241 | 12 482 |
| | Black-headed Gull *(Larus ridibundus)* | High | 0 | 4 008 |
| *Phoenicopteridae* | Greater FlaminGo *(Phoenicopterus ruber)* | High | 1837 | 1 953 |
| *Podicipedidae* | Great Crested Grebe *(Podiceps cristatus)* | Intermediate | 189 | 194 |
| | Little Grebe *(Tachybaptus ruficollis)* | Intermediate | 620 | 640 |
| *Rallidae* | Coot *(Fulica atra)* | High | 19 595 | 5 940 |
| *Recurvirostridae* | Black-winged Stilt *(Himantopus himantopus)* | Intermediate | 3 056 | 3 290 |
| | Avocet *(Recurvirostra avosetta)* | Intermediate | 918 | 814 |
| *Scolopacidae* | Black-tailed Godwit *(Limosa limosa)* | High | 6 964 | 0 |
| | Ruff *(Philomachus pugnax)* | High | 937 | 0 |
| | Redschnak *(Tringa totanus)* | Intermediate | 262 | 255 |
| *Sternidae* | Whiskered Tern *(Chlidonias hybridus)* | Intermediate | 3 016 | 1 953 |
| | LittleTern *(Sterna albifrons)* | Intermediate | 681 | 672 |
| | Common tern *(Sterna hirundo)* | Intermediate | 8 447 | 9 070 |
| | Gud-billed Tern *(Sterna nilotica)* | Intermediate | 922 | 962 |
| | Sandwich Tern *(Sterna sandvicensis)* | Intermediate | 4 063 | 4452 |
| | **Total census** | | **173 523** | **97 808** |

Due to the impossibility of obtaining some inputs from published data, various probability distributions were used. The parameters in these distributions were obtained from expert ornithologists.

Finally, another set of crucial variables such as the period of infectiousness of the infected birds or the probability of transmission from one infected bird to another were also defined as probability distributions. The parameters for these probability distributions can be modified depending on the scenario considered.

## 2. MODELLING AND SIMULATIONS

We developed a model based on a Monte-Carlo method that simulates the dynamics of AIV spread among wild birds starting with the introduction of one infected bird. This approach allows us to represent and compare the evolution of AIV dissemination from the introduction of the infected wild birds under various scenarios.

The outputs of the model are :

1. The species and sites most likely to be affected,

2. The likelihood that the introduction of different infected species spread AIV to other birds and

3. The secondary sites and species that would be affected by the introduction of AIV.

The census by polygon for each of the high risk species considered were used to weigh the probability that one of these species would

introduce AIV and the most likely site within the Ebro Delta that would be affected. The spatial spread and the establishment of new secondary cases among different wild bird species will depend on :

1. The period of the year in which the infected bird is introduced,

2. The bird species which introduced the virus and its location,

3. The census of wild birds by polygon and period,

4. The degree of affinity among species and,

5. The probability distributions for : i) the capacity of dispersion of infected birds, ii) the period of infectiousness and iii) the probability of transmission between the same species and various species.

The model was stated in a period of one year (52 weeks) dividing the year in two different periods in which the wild bird population was regarded as stable : the period of nesting and breeding (from March to September) and a the period of wintering (from October to February).

For each of the simulated scenarios, 10,000 iterations were run and analyzed.

The model was based on a compartmental SIS approach, where the disease induced mortality was not considered.

For its implementation, the following software programmes were used : Microsoft Visual Basic 6.0, Microsoft Office Access 2003 and ArcGIS.9[®] (ESRI, Redlands, CA, USA).

## III - RESULTS

As an example of the outputs of the model, we present the results obtained after running and analysing 10,000 iterations for two scenarios during the nesting-breeding period (see table 2).

The pie graphs presented in figure 2 show the probability of AIV's spread after introduction of a single infected bird into the studied area considering the input values presented in Table 2 and varying the transmission

probability. In scenarios simulated with high T values, the probability of having an epidemic affecting 100 or more birds is 89% and only 0.2% of the infected birds introduced will not give secondary cases. Conversely, when the values of T are low, no major epidemics will occur in 75% of the cases (less than 100 secondary cases) and 25% of the cases introduced will not result in new infections.

**Table 2**

**Probability of transmission during the nest ng-breeding period**

| Variables | | T low | T high |
|---|---|---|---|
| Introduction's onset (week) | | 9 | |
| Lenght of the period (weeks) | | 31 | |
| Transmission probability (T) from a high risk species | to the same species | 0.4 | 0.8 |
| | to another species | 0.2 | 0.4 |
| Transmission probability (T) from an intermediate species | to the same species | 0.3 | 0.6 |
| | to another species | 0.15 | 0.3 |

**Figure 2**

**Likelihood of AIV spread from the analysis of 10,000 iterations, assuming the introduction of a single infected bird in the Ebro Delta during the nesting-breeding period considering various probabilities of transmission**
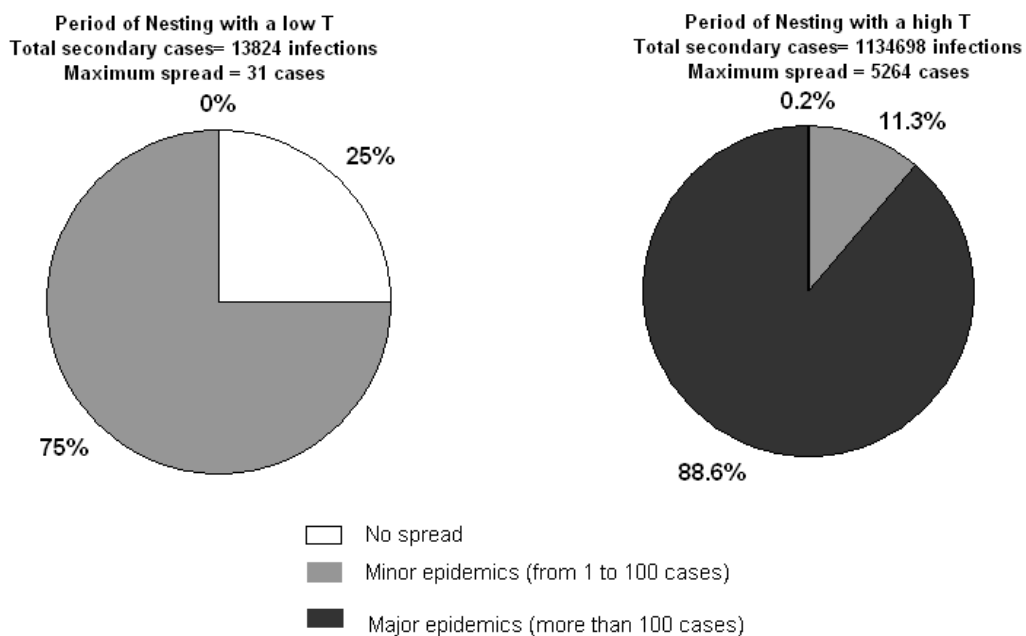


The comparison of these graphs suggests that the values for the probability of transmission (T) affect significantly the evolution of the epidemic. According to AIV epidemics in wild birds experienced in recent years in diverse European countries, it seems that the probability of transmission between different species is low.

According to the model, table 3 shows the four main species regarded as the most likely introducers of AIV in the nesting-breeding period and the proportion of these birds introduced that can infect other birds.

**Table 3**

**Main species for the introduction of AIV in the nesting-breeding period and likelihood
of dissemination for different values of the transmission (T) probability**

| Most likely introducers during the nesting-breeding period | Number (%) of introductions in 10,000 iterations | Spread with a low T | | | Spread with a high T | | |
|---|---|---|---|---|---|---|---|
| | | Number (%) of spread cases | Number of secondary cases | Ratio : Secondary cases/ Introduced cases | Number (%) of spread cases | Number of secondary cases | Ratio : Secondary cases/ Introduced cases |
| Mallard *(Anas platyrhynchos)* | 5,486 (55%) | 2,198 (40%) | 7,639 | 3.5 | 4,450 (81%) | 446,512 | 100.3 |
| Coot *(Fulica atra)* | 2,239 (22%) | 864 (39%) | 2,854 | 3.3 | 1,811 (81%) | 225,273 | 124.4 |
| Red crested Pochard *(Netta rufina)* | 1,144 (11%) | 443 (40%) | 1,529 | 3.5 | 907 (79%) | 111,280 | 122.7 |
| Black-headed Gull *(Larus ridibundus)* | 966 (10%) | 425 (42%) | 1,537 | 3.6 | 781 (81%) | 334,652 | 428.5 |

Figures 3, 4 and 5 show the types of ecosystems that would be more likely infected than other areas by the introduction of infected species. These zones are the lagoons or areas such as « Illa de Buda », a patchwork of different ecosystems of lagoons, salt marshes, sandy beaches and rice fields. Conversely, areas such as rice fields would only be affected if the probability of transmission between different species was high.

Regarding the families, Figures 6 and 7 shows that the species belonging to *Anatidae* and *Rallidae* are significantly more affected than other families. Nevertheless, there are families such as *Laridae, Sternidae, Recurvirostridae* or *Podicipedidae* that may play an important role as intermediate species if the probability of transmission were high.

**Figure 3**

**Spatial distribution of the areas at high risk of being affected during the nesting
and breeding period assuming**

**Figure 4**

**Number of infected birds introduced (first figures written in black) and secondary cases
(t) figures written in grey in the different types of ecosystem in the nesting and breeding period
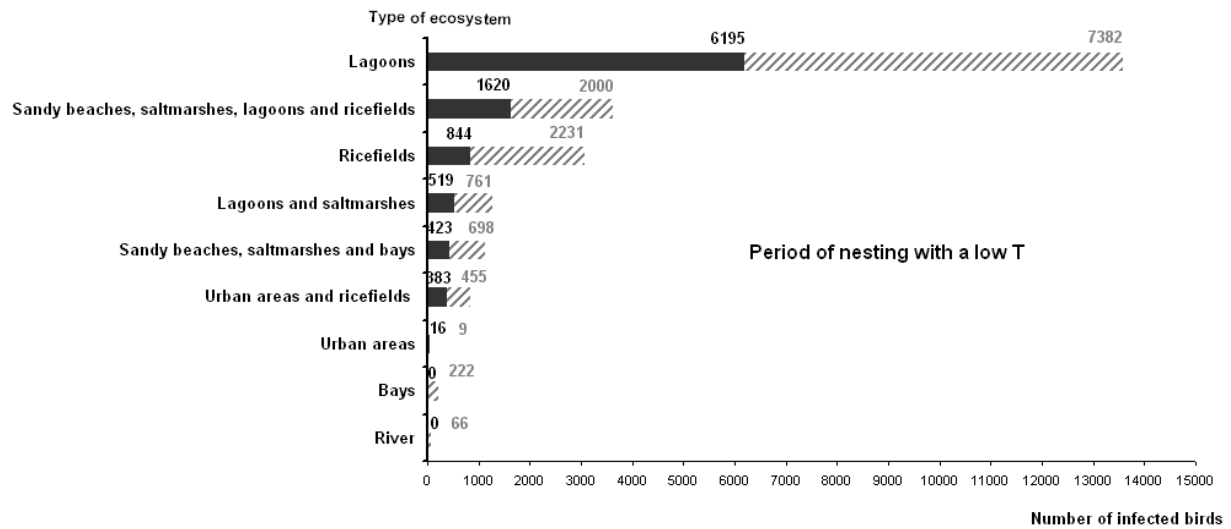considering a low probability of transmission between species**



**Figure 5**

**Number of infected birds introduced and secondary cases in the different type of ecosystems
during the period of nesting and breeding considering values of high probability
of transmission between species.**

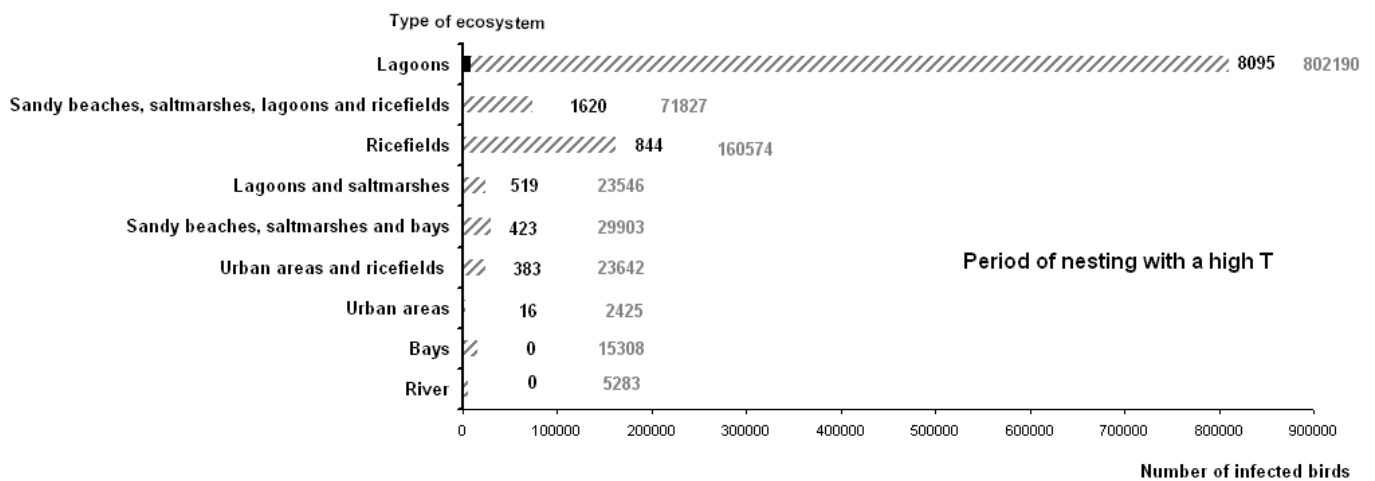The figures in black and in grey indicate the introduced and secondary cases, respectively.

**Figure 6**

**Number of infected birds introduced and secondary cases by family during the nesting
and breeding period for in case of low probability of transmission between species.**

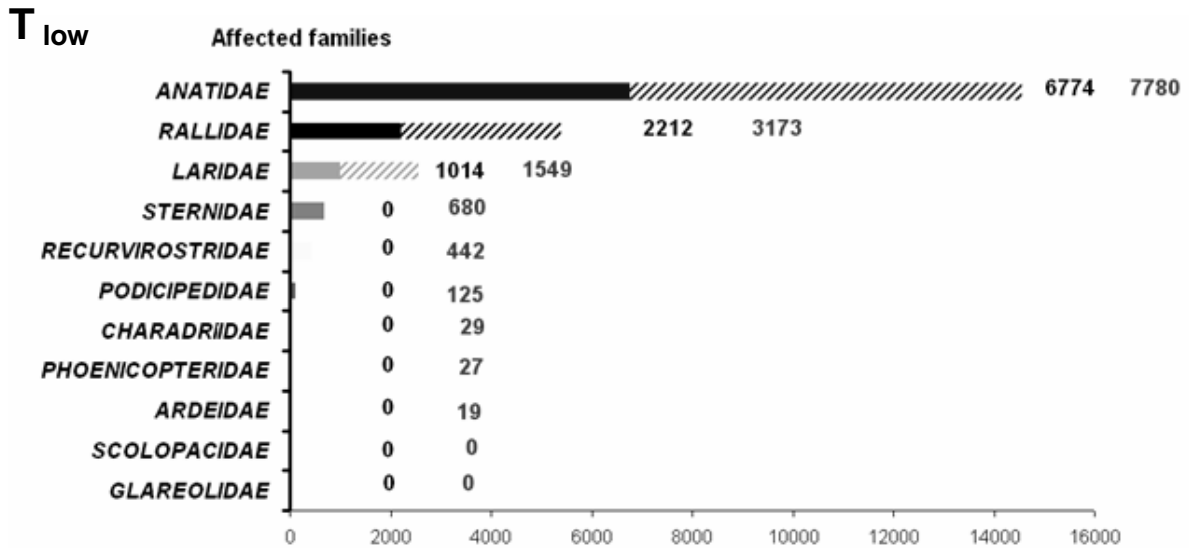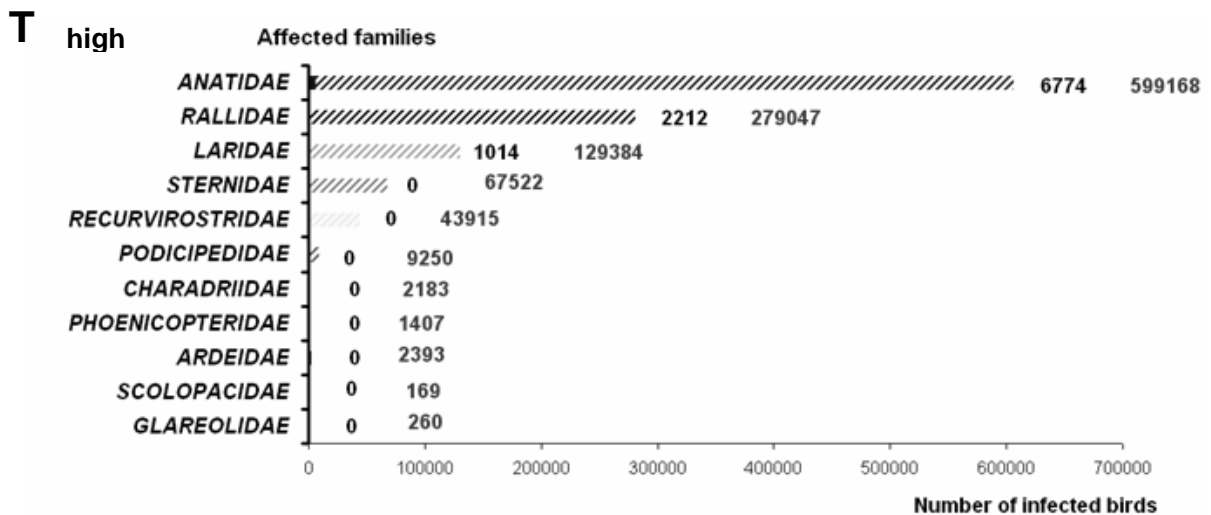Solid colours : Introduced cases. Colours with lines : secondary cases.



**Figure 7**

**Number of infected birds introduced and secondary cases by family during the nesting
and breeding period in case of high probability of transmission between species.**

The first and second figures indicate t introduced cases and secondary cases, respectively.

## IV - DISCUSSION AND CONCLUSIONS

The use of modelling allows us to obtain interesting information on the plausible behaviour of AIV epidemics in wild birds, and gives us some insights on the species or zones more likely to be affected.

The results based on currently available information, suggest that mallards, coots, red crested pochards and black headed gulls would be the species at highest risk of acting as introducers in the Ebro Delta Natural Park during the nesting period and that the lagoons would be the areas where more than 80% of the infected birds would be introduced.

In addition our model provides information about the plausible evolution of epidemics under various scenarios and the specific role that *Anatidae* and *Rallidae* families may play in the spreading of the AIV in diverse areas. Whereas other groups such as *Laridae, Sternidae, Recurvirostridae* or *Podicipedidae* may become important as intermediate species if the probability of transmission were high.

Obviously the conclusions that may be drawn from the developed model are mainly limited by the lack of understanding of the mechanism involved in the spread of AIV and the limited knowledge on the input parameters.

The complexity of the processes to be modelled was dealt with by including only those parameters which are more influential. However, diverse external environmental factors such as temperature, winds, rainfall, type of soil, anthropic disturbances and other, that may affect bird behaviours and the dynamics AIV circulation, were not considered in the present study.

The parameters related to the species heterogeneities (such as the affinity between species) were associated to a high degree of uncertainty and/or variability, which was dealt with by using probability distributions based on expert opinion. Similarly, there was no available information for some crucial inputs such as the duration of infectiousness for all bird species. Nevertheless, the model allowed these values to be easily modified by the modeller which makes the model a flexible tool that can be adapted to new situations, or when new data becomes available. Furthermore, the use of different values for a given parameter (either by using probability distributions or by changing its value) allows us to assess the effect of this parameter on the transmission of AIV. This assessment is exemplified from the results by the comparison of the scenarios varying the values of transmission probability where it may be observed whether these parameters affect significantly the epidemics' evolution. According to AIV epidemics in wild birds experienced in recent years in diverse European countries [European Commission ADNS, 2006, 2007, 2008, 2009], it seems that the probability of transmission between different species is low.

The aim of the model is not to represent accurately the reality, but to provide a useful tool to help decision makers in the design and the implementation of surveillance for AIV in wild birds in specific areas where ornithological and ecological information are available.

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