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# **ROMANIAN AVIAN INFLUENZA OUTBREAKS DISTRIBUTION IN THE**

## **LAST 10 YEARS**

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Abstract: Avian influenza is an infectious, highly contagious disease caused by RNA viruses belonging to the genus Influenzavirus, part of the Orthomyxoviridae family. According to the WOAH, the avian influenza viruses that pose an epidemic and zoonotic risk are those belonging to the H5 and H7 types-HPAI. The aim of these researcher was to resume the outbreaks of the Avian Flu in the last decade. In Romania, after a period of epidemiological silence over six decades, avian influenza has re-emerged, with H5N1 strain. In 2015, 118 pelicans in the Danube Delta were death because of H5N1 infection. Following the evolution of avian influenza on the territory of Romania, mortality losses within the domestic poultry population reached 34,090 heads (WOAH). In domestic birds, the recorded mortality was 224,713 heads. In 2024, Romania reported 36 outbreaks of avian influenza with the H5N1 viral subtype. WOAH show that the prevalent strains of avian influenza virus on the territory of Romania belong to the H5N1 serotype. The wild reservoir is intensely active in the epidemiology of avian influenza and is a major factor of pressure on domestic populations. This epidemiological reality, to which is added scientific information that demonstrates the spill-over of the H5N1 strain to other mammalian species of economic interest - cattle - requiring monitoring of the wild reservoir and investigation of other animal species in relation to the disease outbreaks discovered in domestic birds.

#### Introduction

The transmission of HPAI strains such as H5N1, H5N8 and H7N9 has raised serious concerns worldwide (Sutton, 2018). Among the different HPAIV strains, H5N1 and H5N8 are considered the most pathogenic, with a high mortality rate in birds and humans (Kim et al., 2023). From 2003 to 14 July 2023, the World Health Organization (WHO) has documented 878 cases of HPAI H5N1 infection in humans and 458 (52%) deaths in 23 countries (WHO, 2023). The genome of the HPAI H5N1 virus consists of a negative-sense single-stranded RNA molecule, approximately 13.5 kilobases in length. The genome is segmented into eight distinct segments, each encoding specific proteins that play critical roles in the viral life cycle. These proteins include basic polymerase 1 (PB1, 757) amino acids), basic polymerase 2 (PB2, 759 amino acids), acidic polymerase (PA, 716 amino acids), hemagglutinin (HA, 568 amino acids), nucleoprotein (NP, 498 amino acids), neuraminidase (NA, 499 amino acids), matrix protein 1 (M1, 252 amino acids), matrix protein 2 (M2, 97 amino acids), as well as the nonstructural proteins NS1 (225 amino acids) and NS2 (121 amino acids) (Figure 1)(Sangsiriwut et al., 2018; Noor et al., 2022).

### Material and method

In our country, in the last decade, avian influenza has evolved with the viral subtypes H5N1, H5N8, H5N5 and H5Nx. In this study we made a retrospective view above the last 10 years of outbreaks of Avian Influenza. During 2011-2017, avian influenza was seasonal in Romania. Thus, in 2015, between March and April, 118 dead pelicans were recorded, confirmed with H5N1, in the Danube Delta. In 2016, cases of infection with the avian influenza virus subtype H5N8 were diagnosed in Constanta County, in wild birds (swans and cormorants) (WOAH). In the fourth quarter of 2016, 5 outbreaks of avian influenza were reported in Romania, all detected in wild birds and all attributed to the viral subtype H5N8, in the counties of Tulcea (1 outbreak), Constanta (3 outbreaks), Teleorman (1 outbreak), (Figura 1) (source: https://hpai.efsa.aus.vet/).

2016

Constanța Tulcea Teleorman

2016





#### **Results and discussions**

During 2021, 16 outbreaks of avian influenza were diagnosed in our country. Of these, 8 cases were infections with the H5Nx subtype, 1 with H5N5 and 7 with the H5N8 subtype (WOAH) (Figure 3). The H5N8 viral subtype was reported in the counties of Ilfov (1 outbreak in wild birds), Mureş (3 outbreaks in domestic birds in the G.P. and 1 outbreak in domestic birds on a farm), Harghita (2 outbreaks in domestic birds in the G.P.). In 2022, 19 outbreaks of avian influenza with the H5N1 viral subtype were reported to WOAH, of which 3 were recorded in domestic birds and 16 outbreaks in wild birds (Figure 4). The outbreaks reported in domestic birds were identified in the counties of Ialomita (1 outbreak in domestic birds in G.P.) and Giurgiu (2 outbreaks: 1 in domestic birds in G.P. and 1 in domestic birds on a farm). Outbreaks in wild birds were reported in the counties of Tulcea (2 in swan, mallard), Galați (2 in swan and gull), Călărași (1 in swan), Neamț (4 in swan), Cluj (3 in swan), Ialomița (1 in swan), Brăila (1 in gull) and Constanța (2 in pelican). Following the evolution of avian influenza on the territory of Romania, mortality losses within the domestic poultry population reached 34,090 heads (WOAH).

#### Conclusions

Thus, official reports (WOAH) show that the prevalent strains of avian influenza virus in Romania belong to the H5N1 serotype, wild birds, waterfowl and raptors being exposed/hosts throughout the country. The wild reservoir is intensely active in the epidemiology of avian influenza and is a major factor of pressure on domestic populations. This epidemiological reality, to which is added scientific information demonstrating the spill-over of the H5N1 strain to other species of mammals of economic interest - cattle - requires monitoring of the wild reservoir and investigation of other animal species in relation to the disease outbreaks discovered in domestic







Figura 4. Distribuția focarelor de gripă aviară în România, în 2022





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