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Highly Pathogenic Avian Influenza Virus H5N1 in Africa : Current Situation and Control Prospects

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ABSTRACT

Since it first appeared in poultry in Scotland in 1959, Highly Pathogenic Avian Influenza (HPAI) H5N1 has greatly impacted the global poultry industry and public health. In less than seventy years, it has spread to ninety-six countries in Asia, Europe, Africa, and America. In Africa, the first cases were reported in Nigeria in 2006. Since then, the virus has spread rapidly to around twenty African countries, becoming enzootic and raising concerns for public health. This study aims to present a review of the recent literature on HPAI H5N1 in Africa in order to contribute to understand of its epidemiology and to explore strategies for prevention, preparedness, and control of a future panzootic. The diagnosis of H5N1 HPAI in the laboratory is based on the identification and characterisation of the virus. With advances in science and technology, new rapid and less expensive diagnostic tests have been developed. However, some of these tests cross-react with H5 viruses. In Africa, efforts are still needed to better equip laboratories for the diagnosis of avian influenza. Despite the controversy surrounding the role of vaccination in controlling outbreaks of HPAI H5N1 in poultry, recent studies have shown that vaccination plays an effective role when there is a high degree of antigenic similarity between vaccine strains and wild strains. The decision to use poultry vaccination as a means of controlling the H5N1 HPAI virus is guided by the epidemiological and socio-economic context of each country.

Keywords: Africa, Avian influenza, Epidemiology, Poultry, Zoonosis.

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INTRODUCTION

Highly pathogenic avian influenza is a highly contagious viral disease affecting domestic poultry, ornamental birds, and wild birds **(Lean *et al.*, 2022; Tammiranta *et al.*, 2023; Krammer *et al.*, 2025).** This infection is caused by avian influenza viruses, which are classified into two groups based on their pathogenicity to susceptible birds: low pathogenic viruses, causing few or no clinical symptoms, and highly pathogenic viruses, leading to severe symptoms and mortality rates of up to 100% in flocks within less than 48 hours **(O'Brien *et al.*, 2021; Charostad *et al.*, 2023; Krammer *et al.*, 2025).**

Highly pathogenic avian influenza H5N1 poses a significant threat to the global poultry industry. The damage it has caused is estimated at more than 500 million birds worldwide **(WOAH, 2023),** and its impacts on livelihoods, food security **(Subedi *et al.*, 2024)** and the economy **(Gashaw, 2020)** are disastrous. Recently, the HPAI H5N1 virus has been involved in numerous outbreaks in domestic poultry and wild birds, and threatens to spread to mammals **(Peacock *et al.*,**

2025). The HPAI H5N1 virus has been isolated from various terrestrial (both domestic and wild) and marine mammal species, including humans, cows, minks, sea lions, seals, grizzly bears, and others **(Tammiranta *et al.,* 2023; Webby and Uyeki, 2024; Airey and Short, 2024).** This raises serious concerns about the potential for cross-species transmission and long-lasting human-to-human spread **(Graziosi *et al.,* 2024; Parums *et al.,* 2025).**

The HPAI H5N1 virus has a genome made up of a negative single-stranded RNA molecule divided into eight segments and exhibits a relatively high rate of nucleotide substitution **(Sonnberg *et al.,* 2013).** Over time, significant mutations have been observed in the HA, PB2, M1, and NS1 proteins of HPAI H5N1 isolates, resulting in decreased cross-reactivity among viruses from different hosts and increased virulence in mammals **(Nooruzzaman *et al.,* 2024).** The accumulation of random mutations across the eight genome segments, driven by natural selection and host immune responses, leads to variability in antigenicity, infectivity, and virulence **(Pfeiffer *et al.,* 2011).**

Due to its virulence and disastrous impact on the global poultry industry, avian influenza virus subtype H5 has been classified as an "A" influenza virus to be reported to the World Organisation for Animal Health **(WOAH, 2025).** The HPAI H5N1 virus is also listed on the World Health Organisation's (WHO) updated list of emerging pathogens likely to cause a future pandemic **(Ukoaka *et al.,* 2024).** In January 2025, the WHO reported 964 human cases of HPAI H5N1 in 24 countries, resulting in 466 deaths—a mortality rate of nearly 50% **(Parums et al., 2025).**

The present review aims to update our understanding of the HPAI H5N1 virus in Africa and to explore new approaches to its control. The documentary research was carried out in the WHOA and Elsevier databases, and on Google Scholar and PubMed search engines to obtain relevant data and scientific articles. The present study focused on a summary of research on the virus's organisation and structure, biological characteristics, epidemiological evolution, clinical features and lesions, diagnostic tools and limitations, as well as the impact of the disease, vaccination prospects, and aspects related to prevention, preparedness, and control.

History and distribution of HPAI H5N1 in Africa

The HPAI H5N1 virus has evolved considerably over less than seven decades, first appearing in 1959 in poultry in Scotland **(Charostad *et al.,* 2023)** and first identified in humans in Hong Kong in 1997 **(Neumann *et al.,* 2010; Suarez, 2010).** Since then, it has spread to ninety-six (96) countries across Asia, Europe, Africa, and the Americas, except Australia **(WOAH, 2025; Krammer *et al.,* 2025).** According to **Sonnberg *et al.,* (2013),** wild avifauna—including various species of swans, ducks, geese, gulls, and grebes—were involved in spreading the HPAI H5N1 virus of the Qinghai lineage from China to central and northern Africa between late 2005 and 2006. The introduction of HPAI H5N1 to Africa has occurred at least three times, involving three sub-lineages (II, IV, I) previously identified in Europe **(Cattoli *et al.,* 2009).**

The first documented outbreak in Africa dates back to January 2006, when isolates were detected in Nigeria following an outbreak in poultry in the northern part of the country **(Fasanmi *et al.,* 2017).** The infection quickly spread throughout Nigeria and to neighbouring West and Central African nations such as Niger, Cameroon, Burkina Faso, and Côte d'Ivoire in the same year **(Breiman *et al.,* 2007; Fasina *et al.,* 2009; Sonnberg *et al.,* 2013).** A human case was confirmed in Nigeria a year later. Genetic analysis showed these isolates to be similar to the H5N1 clade 2 strain from China, Indonesia, Japan, South Korea, and other countries **(Breiman *et al.,* 2007).**

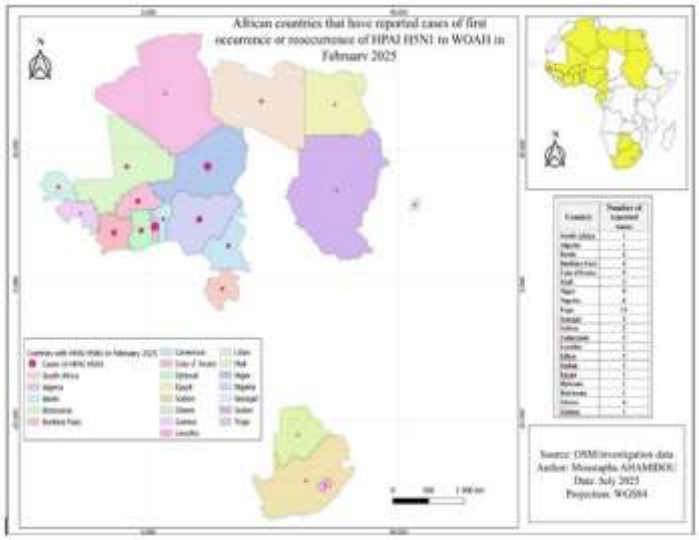

Fig.1 : Map of African countries having notified cases of HPAI H5N1 to the WOAH in February 2025.

In March 2006, outbreaks of HPAI H5N1 associated with human cases were reported in poultry in Egypt, resulting in the deaths of 15 peoples. The same year, cases were also identified in several North and East African countries, including Sudan and Djibouti **(Breiman *et al.,* 2007; Sonnberg *et al.,* 2013; Fasanmi *et al.,* 2017).**

By 2007, Benin, Ghana, and Togo had reported cases to WOAH **(Sonnberg *et al.,* 2013; WOAH, 2025).** From the initial reports of HPAI H5N1 in Africa

until February 2025, approximately twenty African nations have notified either first-time or re-occurrence cases to WOAH. Of the 629 cases reported in February 2025, 10% were from Africa, with West African countries reporting the highest number of cases **(WOAH, 2025).** The distribution of HPAI H5N1 outbreaks across Africa notified to WOAH is shown in the accompanying figure.

Taxonomy, organisation and structure of the H5N1 virus genome

HPAI H5N1 viruses belong to the species Alfainfluenza virus influenzae, formerly influenza A virus, to the genus Alfainfluenzavirus and to the family Orthomyxoviridae **(Schoch et al., 2020; Walker *et al.,* 2022).** This family comprises five genera: Influenza A, Influenza B, Influenza C, Isavirus and Thogotovirus **(Yassine *et al.,* 2010; Neumann *et al.,* 2010; Sonnberg *et al.,* 2013).** Influenza A viruses are divided into subtypes based on two surface glycoproteins: haemagglutinin (HA) and neuraminidase (NA). To date, 16 HA subtypes and 9 NA subtypes have been identified. This represents a possible combination of 144 subtypes between the two proteins **(Lebarbenchon *et al.,* 2010; Gonzales *et al.,* 2018; Zhang and Lei, 2024).**

HPAI H5N1 viruses are enveloped viruses containing a single-stranded RNA genome with negative polarity and a length of 13.5 Kilobases **(Neumann *et al.,* 2010; Charostad *et al.,* 2023).** They exhibit helical symmetry and a diameter ranging from 80 to 120 nm **(O'Brien *et al.,* 2021).** Genomic RNA is composed of eight distinct segments, each of which encodes specific proteins that play an essential role in the virus's life cycle. These proteins include basic polymerase 1 (PB1), basic polymerase 2 (PB2), acidic polymerase (PA), haemagglutinin (HA), nucleoprotein (NP), neuraminidase (NA), matrix protein 1 (M1), matrix protein 2 (M2) and non-structural proteins (NS1 and NS2) **(Sangsiriwut *et al.,* 2018; O'Brien *et al.,* 2021; Charostad *et al.,* 2023).**

Resistance, virulence, pathogenicity and host range restriction of HPAI H5N1

HPAI H5N1 viruses can remain infective up to 6 months in surface water **(Keeler *et al.,* 2014).** They can persist at low temperatures in the environment up to 13 days and can also survive in bird faeces at 4°C for at least 35 days and at 37°C for six days **(Wood *et al.,* 2010).** HPAI H5N1 viruses are rapidly inactivated by low pH and bile acids **(Hirose *et al.,* 2016).** However, mucus can protect the virus from inactivation in the gastrointestinal environment **(Hirose *et al.,* 2016).** Also, water can be used as a diluent to lower the pH of the stomach to allow passage of the virus **(Han *et al.,* 2019).**

Neumann *et al.,* (2010) reported in their study that HA, PB2, NS1 and PB1-F2 of H5N1 influenza viruses play a key role in virulence, pathogenicity and host range restriction. However, a comparative pathogenicity study of eight single-gene reassortant viruses derived from HPAI H5N1/duck/Yokohama/aq10/2003 (DkYK10) and H5N1 A/chicken/Yamaguchi/7/2004 viruses played a role in increasing pathogenicity in chickens **(Tada *et al.,* 2011). Liang (2024)** indicated in his work that the pathogenesis of severe influenza is not only due to the direct cytopathic effects of the virus, but also to the exacerbation of the host's inflammatory responses.

Several authors reported the role of the PB2 and NS1proteins in the pathogenicity of the HPAI H5N1 virus. **Hatta *et al.,* (2001)** identified the PB2 protein at position 627 as the main determinant of the pathogenicity of the HPAI H5N1 virus in mice. Highly mouse-pathogenic H5N1 influenza viruses contained the amino acid Lys at this position, while low mouse-pathogenic H5N1 influenza viruses possessed the amino acid Glu at this **location. Li *et al.,* (2005)** reported that the single substitution of Asp for Asn at position 701 of the PB2 protein confers lethality in mice, while the opposite change attenuates the virus in mice. A single amino acid change at position 92 of the NS1 gene (Asp to Glu) confers high pathogenicity in pigs **(Neumann *et al.,* 2010). Jiao *et al.,* (2008)** showed that the amino acid at position 42 of the NS1 protein affected the pathogenicity of duck H5N1 viruses in mice, and that the amino acid change affected the induction of interferon by the host cell. **Li *et al.,* (2006)** reported that modification of a single amino acid at position 149 of the NS1 protein affects pathogenicity.

HA plays a major role in host range determination because of its essential role in binding to host receptors and in membrane fusion upon virus entry. HA mutants allow viruses to extend their tissue tropism, modify receptor specificity, increase host receptor binding and optimise membrane fusion at different temperatures or pH **(Liang, 2024).** In addition, the host range restriction of influenza viruses is partly determined by the binding specificity of the HA receptor. In most cases, avian and equine viruses preferentially bind galactose-linked sialic acid via an α2,3 bonds (SAα2,3Gal), in contrast to human influenza viruses, which have a higher binding affinity with SAα2,6Gal **(Neumann *et al.,* 2010).** This difference in binding affinity is reflected in the predominance of SAα2,3Gal on duck intestinal epithelial cells, but SAα2,6Gal on human tracheal epithelial cells. However, most HPAI H5N1 viruses isolated from humans have an avian-type receptor specificity, demonstrating the ability of avian influenza viruses to infect humans.

HPAI H5N1 virus evolution

HPAI viruses are derived from Low Pathogenic Avian Influenza (LPAI) viruses through modifications of the haemagglutinin proteolytic cleavage site, i.e. mutation of multiple non-basic amino acids, duplication of basic amino acids or recombination with insertion of cellular or viral amino acids **(Lee *et al.,* 2021).** Between 1959 and 2019, out of a total of 42 natural and independent LPAI H5 (n=15) and H7 (n=27) to HPAI virus conversion events occurred in Africa (n=4). In Africa, only South Africa has experienced four HPAI emergences between 1961 and 2013, caused by H5 subtype viruses (H5N3 in 1961 and H5N2 in 2004, 2006 and 2011) **(Lee *et al.,* 2021).**

The development of large-scale commercial farming has increased the potential for influenza viruses to evolve. Repeated transmission of a low pathogenic avian influenza (LPAI) virus between susceptible chickens leads to the evolution of a highly pathogenic strain **(Fasanmi *et al.,* 2017).**

Molecularly, reassortment events occur most frequently in the three PB1, PA and HA segments of the HPAI H5N1 virus genome compared to the PB2, NA, NP, NS and MP segments **(Wei *et al.,* 2014). Nataraj *et al.,* (2024)** reported that the pairing of HA and NA subtypes of avian viruses is molecularly programmed by HA glycosylation and NA stalk length, modulating the fitness and emergence of new avian influenza viruses.

A recent phylogeny study highlighted the genetic relationship between H5N1 viruses circulating worldwide. It showed that the HA genes of 274 viruses belonging to six sub-clades (clades 2.3.2.1a to 2.3.2.1f) had acquired genetic mutations and undergone complicated reassortment to form 58 genotypes, with genotype 43 being the most dominant genotype isolated from eight Asian and African countries **(Xing *et al.,* 2024).**

Comparative analysis of influenza A (H5N1) genomic sequences from different hosts in the US and around the world revealed diversity in genome entropy per segment of PB2, PB1, PA, HA, NP, NA, M1, M2 and the NS1 region due to genome nucleotide diversity, which is linked to mutations in the RNA genome **(Chakraborty and Bhattacharya, 2024).** The same study indicated that the greatest nucleotide diversity was observed in the PB1 and HA regions.

Diagnosis of HPAI H5N1

The clinical diagnosis of HPAI is based on the observation of specific and varied signs in birds **(Spickler *et al.,* 2008).** However, a definitive diagnosis can only be made once the viral ribonucleic acid (RNA) antigen has been identified and the virus characterised **(Philippa, 2008).** Infected chickens are sometimes found dead with few or no clinical signs **(Spickler *et al.,* 2008).** The main clinical signs observed generally involve nervous, circulatory, respiratory, integumentary, musculoskeletal, gastrointestinal and reproductive systems. However, other signs may also be observed. These signs range from nasal discharge to dyspnoea, coughing, sneezing, diarrhoea, hyperaemia and haemorrhage of hock, inability to stand, ataxia and torticollis. In layers, egg structural abnormalities are most commonly associated with angioedema and facial and subcutaneous oedema **(Akanbi and Taiwo, 2014; Akanbi *et al.,* 2020).**

Lesion diagnosis is based on the observation of macroscopic and histopathological lesions in affected birds. The main lesions observed are marked oedema of the head, and more specifically on the crest, barbs and around the eyes. Petechial lesions may be observed on the mucous membranes, serous membranes, heart, proventriculus and muscles. The liver, spleen, pancreas and lungs often show signs of congestion or necrosis, with hypertrophy of the spleen (van den **Brand *et al.,* 2015; Lean *et al.,* 2022; Lee *et al.,* 2025).** Neurological signs may be observed in some birds and correlate with brain lesions such as encephalitis and cerebral congestion. These lesions vary depending on the species bird, the strain of virus and the progression of the disease **(van den Brand *et al.,* 2015; Akanbi *et al.,* 2020; Krammer *et al.,* 2025).**

For laboratory diagnosis, conventional ELISA and PCR methods are still in use, despite the development of new rapid diagnostic techniques **(Alexander, 2008; Moulick *et al.,* 2017).** With advances in technology, new diagnostic tests that are less expensive and faster have been developed **(Moulick *et al.,* 2017).** These include: viral antigen detection tests, the development of an optimised dual-target qPCR method for the H5 subtype that covers the various viruses in clade 2.3.4.4b and maintains high sensitivity for the H5 avian influenza virus in the different clades, the replacement of Sanger sequencing with next-generation sequencing, which has the advantage of detecting new variants by providing more comprehensive sequence information.

In serology, it is important to note the replacement of the traditional neutralisation test with a microneutralisation test for the detection of specific infections by avian influenza virus in humans and certain animal species. For the rapid detection of AIV in clinical settings, a rapid test based on reverse transcription and isothermal polymerase chain reaction (RT-RPA) dual technology , which detects HA and M2 genes at a low concentration of 1 × 10-7ng/µL (13.72 copies/µL), has been developed **(Niu *et al.,* 2025).**

However, some nucleic acid amplification tests and rapid antigen detection tests cross-react with H5 viruses **(Pinsky and Bradley, 2024).**

In Africa, routine diagnosis of HPAI is usually carried out in molecular biology laboratories. An initial screening diagnosis is carried out using conventional PCR or real-time PCR on tracheal or cloacal swabs taken to detect type A avian influenza viruses. This is followed by another subtyping diagnostic to detect H5N1 avian influenza viruses. For confirmation diagnosis and genomic sequencing, PCR-positive samples are sent to PADOU reference laboratory in Italy. In West Africa, only a few laboratories, such as those in Dakar (Senegal) and Accra in Ghana, have sequencers. Haemagglutination inhibition (HIA) tests are used for inter-laboratory testing.

Ecology, epidemiology and risk factors for transmission of the HPAI H5N1 virus

The ecology of HPAI H5N1 has changed considerably in recent years. It has gone from isolated outbreaks in terrestrial poultry to more sustained circulation in terrestrial and aquatic poultry, and is even threatening to spread to mammals **(Sonnberg *et al.,* 2013; Chakraborty and Bhattacharya, 2024).** Epidemiological data have shown a complex interaction between wild birds and domestic poultry species in different ecological systems where the virus has caused epidemics **(Sakoda *et al.,* 2012).** The epidemiological characteristics of the virus, namely host variety, survival virus in the environment, minimum infectious dose, pathogenicity virus and viral excretion rates, seem to justify the endemicity of the disease in certain ecosystems **(Pfeiffer *et al.,* 2011).**

In order to gain a better understanding of the ecology and epidemiology of the HPAI H5N1 virus during its transcontinental spread, **Salzberg *et al.,* (2007)** carried out a major sequencing and analysis of 36 isolates of the HPAI H5N1 virus from birds in Europe, North Africa and South-East Asia. The results of this work indicated that the isolates belonged to three distinct lineages, including a new Euro-African lineage responsible for several fatal human infections in Egypt and Iraq in 2006.

HPAI viruses mainly infect domestic poultry through wild birds or contact with their by-products, and sporadically transform into highly virulent strains **(Lebarbenchon *et al.,* 2010).** However, since March 2024, there has been changed in the ecology and epidemiology of HPAI, with the detection of the H5N1 HPAI virus in dairy cows and its transmission to humans in the United States **(Garg *et al.,* 2024).** The current intense circulation of the HPAI H5N1 virus in cattle increases the risk of its adaptation to mammals and possible spread to other farm animals and humans **(WOAH, 2024).**

The introduction and spread of HPAI H5N1 in Africa are attributable to globalisation, international trade (legal and illegal) in poultry, the development of large-scale commercial farming, the virus's ability to survive, its ability to evolve into other subtypes through genetic reassortment, lack of compliance with biosecurity measures in live bird markets and on poultry farms (rearing methods, multi-species farms), vaccination of poultry, continuous shedding of the virus and the carriage of the virus by transcontinental migratory birds **(Tian and Xu, 2015; Fasanmi *et al.,* 2017; Harvey *et al.,* 2023).**

Aquatic birds are natural hosts and can transmit HPAI H5N1 viruses **(Lebarbenchon *et al.,* 2010).** But the mallard duck in particular is capable of transmitting the virus over long distances **(Keawcharoen *et al.,* 2008 ; Krammer *et al.,* 2025).** A study conducted by **Salaheldin *et al.,* (2018)** in Egypt indicated that ambient temperature during the winter period influences the spread of the A/H5N1 virus in different geographical areas. These same authors also reported the role of Peking ducks as a reservoir in the spreading of H5N1 virus.

Raw milk from infected cows is also a potential risk factor for transmission of the virus through consumption **(Zulli *et al.,* 2025).** In addition, there is the possibility of horizontal transmission of the virus from infected suckler cows to other animals, including cows, cats and poultry **(WOAH, 2024).**

Impact of HPAI H5N1 on food safety, the economy and public health in Africa

The HPAI H5N1 virus is a major threat to the biosecurity of poultry farms, the economy and public health. HPAI H5N1 outbreaks cause direct and indirect losses. These losses are linked to reduced production, high mortality, culling of sick birds, replacement of sick birds, loss of customer confidence, local and international trade losses due to trade restrictions, the cost of biosecurity, the cost of compensation and the cost of control and eradication **(Gashaw, 2020).** The most damaging effects most often occur in poor rural and peri-urban areas, affecting small and medium-sized farms. For example, sales of eggs, chickens and poultry feed could fall by 80%, leading to job losses and a significant drop in chicken consumption **(Breiman *et al.,* 2007; Otte *et al.,* 2008).** In endemic countries in Africa, HPAI H5N1 outbreaks have a significant negative impact on village women, who are the main poultry producers, and lead to food and nutritional insecurity at the household and community level **(Alders *et al.,* 2013).** Although it is difficult to establish the losses associated with HPAI H5N1 outbreaks in

low-income, chronically food-deficient countries, the direct costs associated with loss of production, mortality, stamping out of birds and disinfection can be estimated at hundreds of millions of dollars, depending on the country **(Otte *et al.,* 2008).**

The psychosis is linked to the potential for intra- and inter-species transmission of the virus, its presence in the food chain through its detection in dairy cattle and its capacity for transmission to humans. However, the risk of human-to-human transmission remains low **(Sanchez-Rojas *et al.,* 2025).** Cases of human infection result in a wide spectrum of disease severity, ranging from conjunctivitis or mild respiratory illness to severe and fatal pneumonia **(Webby and Uyeki, 2024).**

Prevention, control and preparedness for HPAI H5N1 pandemics

The overall strategy for the prevention and control of HPAI H5N1 is based on a holistic approach. It focuses primarily on establishing an effective surveillance system, improving biosecurity processes, increasing the use of vaccines, rapid notification of cases and technical assistance, rapid and effective diagnostic tools, trade restrictions, import controls, culling of infected animals, cleaning and disinfection, compensation and inter-sectoral collaboration **(FAO and World Organisation for Animal Health, 2025).** In a Nigerian study, **Fasanmi *et al.,* (2018)** reported that regular surveillance and control of H5N1 HPAI is 68 times more cost-effective than inaction in developing countries.

The role of vaccination in controlling outbreaks of HPAI H5N1 in poultry is controversial **(Swayne *et al.,* 2014),** mainly due to fears of silent spread with viral mutation **(Peyre *et al.,* 2009)** and expansion to humans **(Islam *et al.,* 2023).** However, a recent study evaluating the efficacy of vaccines against HPAI H5N1 mortality in poultry has shown some efficacy. This argue in favour of reassessing the role of vaccination in the policy to control HPAI H5N1 in poultry **(Tseng *et al.,* 2024).** Another study analysing vaccine trials found that antigenic similarity between vaccine strains and field strains increased the efficacity of protection, reduced viral shedding and improved haemagglutination inhibition titres **(Kovács *et al.,* 2025).**

According to the **WOAH (2023)** in its guidance note, the use of vaccination of poultry against HPAI H5N1 must be adapted to the specific epidemiological and socio-economic context, as well as to the needs and capacities of each country or region. However, **Raphael *et al.,* (2025)** indicated that while vaccination against avian influenza can reduce long-term financial losses and stabilise poultry production, certain challenges must be addressed, such as high implementation costs, trade restrictions and disparities in access.

As part of the overall strategy for vaccinating poultry against HPAI, it is essential to first update the vaccines to be used so that there is a match between the vaccine strains and those present in the field. Next, it is necessary to select the most appropriate type of vaccine and vaccination schedule. At this stage, a distinction must be made between two types of vaccination : emergency protective vaccination and preventive vaccination, which prioritises achieving the highest possible level of protection, especially in the most susceptible species in areas at high risk of transmission (EFSA Panel on **Animal Health and Animal Welfare *et al.,* 2023**).

From a rational perspective of HPAI vaccination in Nigeria, a controlled vaccination approach has been proposed which involves monitoring vaccine application, the ability to differentiate vaccinated from infected flocks, assessment of seroconversion, simultaneous surveillance of avian influenza virus circulation and analysis of isolates obtained from surveillance to determine whether there is genetic and/or antigenic concordance with vaccine strains **(Meseko *et al.,* 2023).**

From 2007 to 2014, vaccinated poultry in Egypt suffered from antigenic drift variants of clade 2.2.1.1 and in 2014/2015, an unprecedented recrudescence of clade A/H5N1 2.2.1.2 was observed in poultry and humans **(Salaheldin *et al.,* 2018).** At the same time, an Egyptian phylogeny study conducted between 2006 and 2011 reported cases of HA antigenic drift. These results showed that phylogenetically divergent H5N1 viruses, which did not show antigenic cross-reactivity, were circulating in Egypt. This indicates that it is problematic to use a single influenza virus strain as a starting virus to produce an influenza vaccine in Egypt **(Watanabe *et al.,* 2012).** However, **Ibrahim *et al.,* (2015)** reported that the amino acid mutation (G140R, Y144F, I190L, K192Q, D43N) in the haemagglutinin gene of HPAI H5N1 virus exhibited increased cross-reactivity which can be effectively used as a tool to develop broadly reactive influenza vaccines to cope with the continuous antigenic evolution of viruses.

If HPAI H5N1 is confirmed by laboratory tests, the infected farm is depopulated. This includes the systematic slaughting of all poultry on the infected farm, the safe disposal carcasses, litter, products and any potentially contaminating material by burial, the cleaning and disinfection of buildings and equipment and the observance of a sanitary vacuum of at least 21 days before any repopulation. Although depopulation has contributed to the eradication of HPAI in some countries, it should be remembered that it is a very costly method and can affect the livelihoods of small-

scale African farmers. Particular attention must be paid to compensate producers who have been victims of HPAI, to help them rebuild their flocks and to encourage them to report cases of infection.

Recent changes in the ecology and epidemiology of HPAI H5N1 have negative impacts on human and animal populations, farms and communities **(Koopmans *et al.*, 2024).** This new situation highlights the need to adopt an integrated control approach, by emphasising on multi-sectoral and multi-disciplinary collaboration between the animal health, human health and environmental health sectors. Integrated molecular surveillance targeting adaptive mutations using genomic sequencing in animals and humans is therefore essential for the early detection of zoonotic avian influenza and the effective implementation of control **measures (Alvarez *et al.*, 2025).** To cope with an HPAI H5N1 pandemic, actions must focus on strengthening human, animal and environmental epidemiological surveillance and on building laboratory capacity. In addition, the role of avian vaccines needs to be reassessed and redefined **(Breiman *et al.*, 2007).**

CONCLUSIONS

The HPAI H5N1 virus is a major threat to the global poultry industry, to biodiversity and to public health, due in particular to its virulence, the evolution of its ecology and its characteristics of adaptation to mammals and humans in particular. In with view to control it, attempts to vaccinate with a single strain of influenza virus proved ineffective when phylogenetically divergent H5N1 viruses with no antigenic cross-reactivity co-circulated. However, the increased cross-reactivity revealed by amino acid mutation in the haemagglutinin gene can be effectively used as a tool to develop broadly reactive influenza vaccines to cope with the ongoing antigenic evolution of viruses. In addition, a controlled vaccination approach has to be advocated in endemic countries in Africa to monitor genetic and antigenic concordance between circulating vaccine and wild strains. The new situation regarding the adaptation of the HPAI H5N1 virus to mammals and its transmission to humans highlights the need to adopt an integrated approach to pandemic prevention, control and preparedness, with particular emphasis on genomic surveillance, laboratory capacity building and multisectoral and multidisciplinary collaboration between the animal health, human health and environmental health sectors.

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Authors' contributions

This work was carried out with the contribution of all authors. Ahamidou MOUSTAPHA drafted the manuscript. Adamou AKOURKI, Ibrahim ADAMOU KARIMOU, Amadou MOROU MADOUGOU, Alima MAINA, Moumouni OUSSEINI and Essodina TALAKI revised the manuscript. All authors read and approved the final version of the manuscript.

Competing interests

The authors have not declared any conflict of interest.

Ethical consideration

The authors of the current study checked for ethical issues, including plagiarism, consent to publish, misconduct, double publication and/or submission, and redundancy.

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Data availability and materials

Data from the study are available upon a reasonable request.

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