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Mini-review

Avian influenza situation report—Africa

Celia Abolnik

Department of Production Animal Studies, Faculty of Veterinary Science, University of Pretoria, Onderstepoort 0110, South Africa

Corresponding author: **Celia Abolnik** (email: celia.abolnik@up.ac.za)

Abstract

Africa's vast geographic and climatic diversity makes it a critical region for the ecology and spread of avian influenza viruses, particularly due to its role as a wintering ground for Palearctic migratory waterbirds. The continent has experienced multiple waves of clade 2.3.4.4b A/H5Nx high pathogenicity avian influenza (HPAI), which has caused widespread outbreaks in poultry and wild birds since 2017. From 2023 to mid-2025, clade 2.3.4.4b A/H5N1 outbreaks were reported across West and Southern Africa, with severe impacts on poultry production and conservation of endangered wild bird species. Concurrently, South Africa and Mozambique battled an unprecedented A/H7N6 HPAI epizootic in 2023, leading to the culling or loss of over 6.8 million chickens. Additionally, the A/H9N2 subtype, particularly G5.5 sublineage strains, continues to circulate in North, West, and East Africa, with reassortant viruses with A/H5Nx viruses reported in Egypt. Underreporting and limited surveillance hamper accurate epidemiological assessment. Despite these challenges, advancements in noninvasive environmental sampling offer promising tools for early detection. Strengthening regional cooperation and surveillance is essential for mitigating future outbreaks and protecting both animal and public health.

Key words: clade 2.3.4.4b A/H5Nx high pathogenicity avian influenza, A/H9N2, A/H7N6, Africa

Introduction

Africa is the second-largest continent, covering approximately 30.2 million km^2 and stretching over 8000 km from north to south. Due to its vast size and location straddling the equator, Africa experiences a wide range of climates. The Sahara Desert in the north, measuring around 2000 km longitudinally, is the largest hot desert in the world. The Sahel region to its south transitions into savannas and tropical rainforests near the equator, where rainfall is abundant and temperatures are consistently warm. Central Africa has a humid equatorial climate, while Southern Africa features a mix of semi-arid regions, Mediterranean-type climates near coastal areas, and temperate zones at higher elevations (Beck et al. 2023). Each year, several hundred Palearctic waterbird species that breed across Europe and Asia migrate to Africa, crossing the Sahara Desert via four main routes, namely the East Atlantic Flyway, the Black Sea–Mediterranean Flyway, the East Africa–West Asia Flyway, and the Central Asian Flyway to overwinter in the continent's wetlands, lakes, and coastal zones (Deboelpaep et al. 2022).

Wild waterfowl of the orders *Charadriiformes* and *Anseriformes* are the natural reservoirs of low pathogenicity avian influenza (LPAI) virus subtypes, encompassing all combinations of H1 to H16 plus H19 hemagglutinin (H) and N1 to N9 neuraminidase (N) surface antigen types (Fereidouni et al. 2023). High pathogenicity avian influenza (HPAI) viruses emerge from time to time in gallinaceous poultry from A/H5Nx and A/N7Nx LPAI precursors (Webster et al. 1992), but the Goose/Guangdong (Gs/GD) A/H5 HPAI lineage, which first appeared in East Asia in the 1990s, is unique in that it spilled back into wild bird populations and began to spread globally along migratory flyways. Gs/GD sublineages diversified over time and many became extinct, but sublineage Gs/GD clade 2.3.4.4b A/H5Nx HPAI viruses are now endemic in the northern latitudes with year-long persistence in Europe (Fusaro et al. 2024*a*) and are translocated along with LPAI viruses in the southward seasonal migrations of waterfowl (Khomenko et al. 2018; Abolnik et al. 2022). Viruses shed into the environment of the sub-Saharan wetlands infect sympatric Afrotropical duck populations. The southward dissemination of avian influenza viruses with Afrotropical ducks is associated with rainfall and food availability rather than seasonal temperatures, but unlike birds breeding in the Palaearctic zone that display synchronized annual breeding and congregations, breeding frequencies of Afrotropical ducks are higher, and waterfowl movements are much less predictable in sub-Saharan Africa (Khomenko et al. 2018).

Thus, the Gs/GD lineage clade 2.3.3.4b A/H5Nx HPAI strains have made their way to the southernmost tip of the African continent in cyclical waves since 2017. Direct or indirect contact with wild birds and their contaminated excretions in the environment caused massive and devastating outbreaks in the continent's poultry sectors, and impacted on endangered wild bird species, especially coastal seabirds, as detailed in numerous studies (Abolnik et al. 2019; Letsholo et al. 2022; Makalo et al. 2022; Abolnik et al. 2023; Molini et al. 2023; Roberts et al. 2023). This report provides an overview of the

Fig. 1. African countries affected by avian influenza outbreaks from 2023 to 2025.

clade 2.3.4.4b A/H5N1 HPAI | A/H7N6 HPAI | A/H9N2 G5

status of avian influenza in the African continent from 2023 to 2025.

Clade 2.3.4.4b A/H5N1

Years 2023 and 2024 saw the tail end of the previous clade 2.3.4.4b A/H5Nx HPAI epizootic that commenced on the African continent in December 2020, with Europe pinpointed as the source of two different incursions of A/H5N8 (genotype EA-2020-A) A/H5N1 (genotype EA-2020-C) (Fusaro et al. 2024*a*). In West Africa, The Gambia, Guinea, Niger, Nigeria, and Togo all reported sporadic cases in poultry or coastal seabirds in 2023 (Fasina et al. 2025) (Fig. 1). Relatively fewer outbreaks were reported in this region in 2024, in Burkina Faso, Gabon, Niger, and Nigeria (Fasina et al. 2025). Meanwhile in South Africa, a distinctive coastal seabird sublineage that emerged during the 2021–2022 outbreaks was still being sporadically detected until July 2023, and in April 2023 a new wave of A/H5N1 outbreaks in commercial poultry in the Western Cape and KwaZulu Natal provinces, which were rapidly controlled, was associated with another distinctive clade 2.3.4.4b sublineage (Abolnik et al. 2024*a*).

In the current wave of clade 2.3.4.4b A/H5N1 HPAI outbreaks (for the period starting 1 October 2024), the following West African countries reported cases in commercial poultry: Niger (Niamey region) at the beginning of February 2025; Nigeria (Federal Capital Territory, Kaduna, Kano, Katsina, Plateau, and Zamfara), with 18 outbreaks in chickens, domestic ducks, guinea fowl, or turkeys from mid-March 2025; four outbreaks in Togo (Centre and Maritime regions) in March 2025; Liberia (Bong region) in April 2025; and in June, Ghana reported an outbreak in commercial layers (FAO 2025).

Then, on 21 and 25 June 2025, clade 2.3.3.4b A/H5N1 HPAI virus-associated outbreaks broke out in commercial broiler breeders near Tswaing, North West province of South Africa, and 400 km away near Mkhondo, Mpumalanga province, respectively. No further outbreaks in poultry were reported until early July, when three domestic ducks in a flock of 250 birds in Paarl, Western Cape province, which died with neurological symptoms, tested positive for the virus. Coastal seabirds including African penguins (*Spheniscus demersus*), Hartlaub's gulls (*Chroicocephalus hartlaubii*), Great White pelicans (*Pelecanus onocrotalus*), Cape cormorants (*Phalacrocorax capensis*) as well as Sacred ibis (*Threskiornis aethiopicus*), and a hawk (species unknown) at various locations in the Western Cape province have also since tested positive for clade 2.3.4.4b A/H5N1 HPAI. Further cases in wild birds in the Western Cape, Gauteng, and Limpopo provinces, as well as a broiler breeder chicken farm in the Western Cape, a commercial farm in the Eastern Cape province, and layer chickens in the Delmas region of Mpumalanga province were confirmed since August. Preliminary genome sequencing and phylogenetic analysis results confirmed that the new clade 2.3.4.4b A/H5N1 HPAI virus from the 2024/2025 season in Europe, genotype EA-2024-DI, had arrived in South Africa.

On 25 July 2025, the Botswanan government reported a new H5N1 outbreak in a backyard chicken flock in Satau village, Chobe District, near the northern border. Fifteen out of 70 birds had died (WOAH 2025). All live poultry movement and export bans were immediately enforced. Detailed molecular epidemiological studies are set to commence as soon as genome sequences for this and other African clade 2.3.4.4b A/H5N1 HPAI viruses become available.

A/H7N6 HPAI in South Africa and Mozambique

In May 2023, an A/H7N6 HPAI virus emerged in a smallholder chicken flock in the Mpumalanga province of South Africa and quickly spread to two nearby commercial egg producers. Clinical signs included general lethargy and feed refusal, with some birds developing cyanotic combs and facial oedema. No obvious respiratory, enteric, or neurological signs were seen. The intravenous pathogenicity index of the virus isolate was 1.67. Full genome sequencing and phylogenetic analysis determined that the virus was related to various H7N1, H11N6, and H6N2 LPAI strains circulating in Southern African wild birds, and the HA0 cleavage site had been derived from a nonhomologous recombination event with the *Gallus gallus* 28S ribosomal RNA gene (Abolnik et al. 2024*b*). The H7N6 HPAI virus was deemed to be of low zoonotic potential since the viral protein sequences contained few molecular markers of any significance, e.g., those associated with increased binding to human receptors.

Until the end of July 2023, sporadic cases of A/H7N6 HPAI were detected in layer-type birds on commercial farms in the Mpumalanga and Gauteng provinces. Failures in the State's official control program saw an explosion of >100 outbreaks from August 2023 in a highly poultry dense region spanning the Mpumalanga, Gauteng, North West, and Limpopo provinces. Mostly commercial egg-layer chickens and broiler breeder flocks were affected, with mortality rates in layer-type birds reported as ranging from 5% to 60% depending on the age and management status of the flocks. Mortality rates in broiler breeder flocks were reported as much higher. Outbreaks in distantly located layer farms in the Western Cape province in October 2024 and the Free State province in November 2024 were linked by molecular and epidemiological evidence to the purchase of infected point-of-lay pullets from a rearing farm in the North West province. No H7N6 HPAI was detected in any species other than chickens in ongoing active wild bird surveillance at the time. The disease was controlled by culling, but some commercial layer flocks were quarantined instead without enforced culling. The H7N6 HPAI epizootic in South Africa slowed towards the end of 2023, and the virus was not detected after January 2024.

In October 2023, the A/H7N6 HPAI virus was identified as the cause of death of 15 000 layer hens on a commercial farm in the Morrumbene district of Inhambane province in Mozambique. A further 30 000 birds were culled in the control measures, and genetic sequencing confirmed that the H7N6 HPAI virus spread from South Africa, via the translocation of infected chickens (Abolnik et al. 2024*b*; Monjane et al. 2024) (Fig. 1).

The 2023 H7N6 HPAI epizootic was first documented emergence of an H7Nx HPAI virus in sub-Saharan Africa, and it had the worst economic impact of any avian influenza virus strain thus far. An estimated 6.82 million chickens died or were culled in South Africa; of these, 3.97 million were commercial eggs layers and 2.85 million were broiler breeder birds. This represented about 20% of the national egg laying flock and almost 30% of the national broiler breeder flock. Egg shortages and increased prices for eggs and meat, as well as export bans resulted as a consequence. The two largest producers collectively lost $18.4 million (Abolnik et al. 2024*b*). Research is ongoing into the high infectivity and transmissibility of the virus in chickens and the transmission pathways.

A/H9N2

The A/H9N2 LPAI subtype is distributed across the globe in the wild bird reservoir, but stable lineages of the virus have established in poultry since the mid-1990s, some with zoonotic potential. A/H9N2 infections of poultry are of economic importance, leading to decreased egg production, increased mortalities, and a predisposition to secondary infections. Widespread vaccination using whole inactivated A/H9N2 viruses has driven further virus diversification in the field (Hu et al. 2025). A/H9N2 lineages are broadly classified based on the HA sequences into the Y, G, and B lineages. Y is the oldest and most widespread of the A/H9 viruses, typically but not exclusively composed of wild bird viruses. Nine sublineages, Y1 to Y9, are described (Fusaro et al. 2024*b*). A/H9N2 viruses classified as Y lineage have been detected in wild birds in Egypt, Zambia, and South Africa with sublineage Y8 A/H9N2 and A/H9N6 strains recently reported in Madagascar (Fusaro et al. 2024*b*; GISAID 2025).

The chicken-adapted G lineage first emerged in poultry in 1997 and became endemic in Asia and some African countries. G lineage is split into sublineages G1 to G5, with G5 further divided into G5.1 to G5.7 (Fusaro et al. 2024*b*). The G5.5 sublineage affects poultry across North and West African countries, with cases reported in Morocco, Algeria, Tunisia, and Libya, as well as Mali, Mauritania, Senegal, Burkina Faso, Ghana, Togo, Benin, and Nigeria (Fig. 1). In East Africa, the virus has been confirmed in poultry in Uganda and Kenya (Fusaro et al. 2024*b*; Beyit et al. 2025) and as far south as Mozambique, at Mukatine in the Matola district of Maputo province in Mozambique in August 2025. Egypt reported the presence of the G5.6 lineage (Fusaro et al. 2024*b*), and co-circulating A/H9N2 and clade 2.3.4.4b A/H5Nx strains that have reassorted. The most recent report is of a novel reassortant Egyptian A/H5N2 virus with clade 2.3.4.4b H5N1 and G1-sub-lineage A(H9N2) parental viruses, detected in domestic ducks and environmental samples (El Shesheny et al. 2025).

Conclusions and future perspectives

The incidence and prevalence of avian influenza in the African continent are certainly underinvestigated and underreported, leading to large gaps in our understanding of the epidemiology of the disease. Active and passive surveillance in the continent's 54 countries is constrained by financial and human resources, but there is also a reluctance by some African governments to test for and report avian influenza in poultry due to the political and economic repercussions. Looking forward, the successes of noninvasive environmental sampling for avian influenza in wild birds at key sites, including wetlands and live bird markets (Abolnik et al. 2022), offer opportunities to put early warning systems into place in the continent, but intra-African cooperation and collaboration need to be improved.

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Author information

Author ORCIDs

Celia Abolnik https://orcid.org/0000-0003-3044-465X

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