

# Detection of Clade 2.3.4.4 Highly Pathogenic Avian Influenza H5 Viruses in Healthy Wild Birds in the Hadeji-Nguru Wetland, Nigeria, 2022

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## Abstract

**Background** The introduction of multiple avian influenza virus (AIV) subtypes into Nigeria has resulted in several poultry outbreaks purportedly linked to trade and wild birds. The role of wild birds in perpetuating AIV in Nigeria was, therefore, elucidated. **Methods** A cross-sectional study was conducted among wild aquatic bird species at the Hadejia-Nguru wetlands in northeastern Nigeria between March and April 2022. A total of 452 swabs (226 cloacae and 226 oropharyngeal swabs) were collected using a mist net to capture the birds. These samples were tested by RT-qPCR, followed by sequencing. **Results** Highly pathogenic AIV of the H5N1 subtype was identified in clinically healthy wild bird species, namely African jacana, ruff, spur-winged goose, squared-tailed nightjar, white-faced whistling ducks, and white stork. A prevalence of 11.1% (25/226) was recorded. Phylogenetic analysis of the complete HA gene segment indicated the presence of clade 2.3.4.4b. However, these H5N1 viruses characterized from these wild birds cluster separately from the H5N1 viruses characterized in Nigerian poultry since early 2021. Specifically, the viruses form two distinct genetic groups both linked with the Eurasian H5N1 gene pool but likely resulting from two distinct introductions of the virus in the region. Whole genome characterization of the viruses reveals the presence of the mammalian adaptive marker E627K in two Afro-tropical resident aquatic ducks. This has zoonotic potential. **Conclusion** Our findings highlight the key role of surveillance in wild birds to monitor the diversity of viruses in this area, provide the foundations of epidemiological understanding, and facilitate risk assessment.

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