



NATIONAL VETERINARY RESEARCH
INSTITUTE, VOM, NIGERIA



Genomic characteristics of the first avian influenza (H5N8) virus isolated from poultry in Nigeria

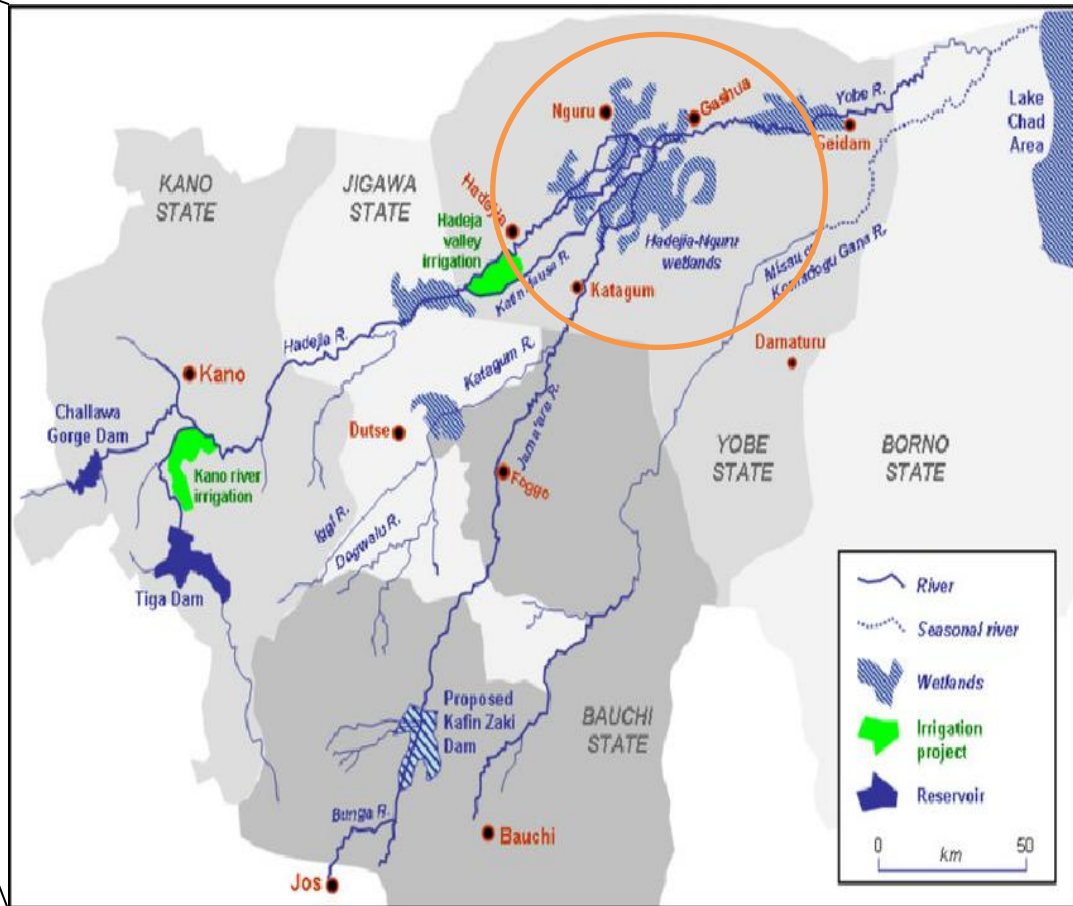
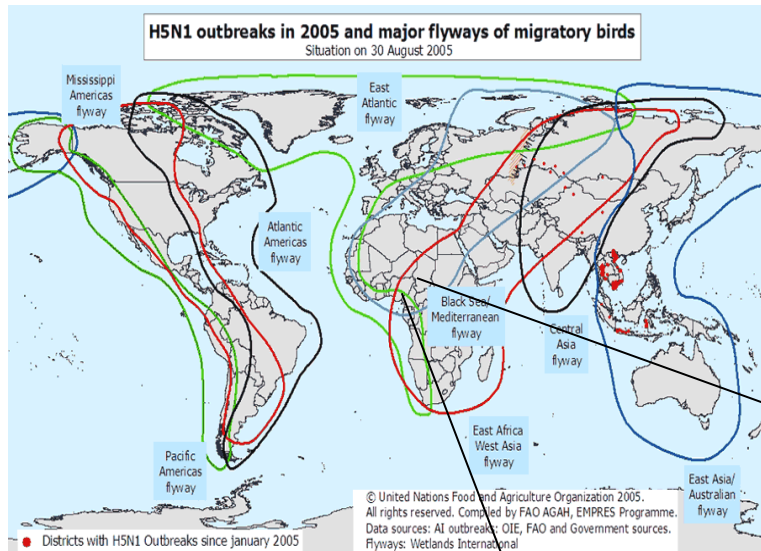
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Background

- The First reported incursion of highly pathogenic avian influenza (HPAI) subtype H5N1 into Nigeria was in 2006 (clade 2.2)
 - In July, 2008 a new strain (clade 2.2.1) was detected in live bird market (LBM) during surveillance
 - In late 2014, a resurgence with a new strain of H5N1 (clade 2.3.2.1c) was reported to OIE
 - In November, 2016 another introduction of a new strain H5N8

- Since 2010 - 2014, H5N8 has been in circulation in migratory waterfowls and poultry in Asia, Europe, Middle East and North America (OIE, 2010, 2014).
- In 2016, it spreads to Africa with Egypt being the first to report to OIE (OIE, 2016)
- No infection of humans was reported with this subtype but several birds were killed and destroyed (OFFLU, 2016)



Map of major flyways of migratory birds
 Source: FAO, 2005

Aim

- To gain insight into the genomic characteristic of the newly introduced H5N8

Approach

- The index case of H5N8 was reported in a poultry farm with **mixed specie** located in Dan bare, **Kano state**
- Outbreak started when a **new live animal** sourced from a nearby **LBM** was introduced into the flock
- Carcasses were collected and tested by realtime RT-PCR and isolation attempted in embryonated chicken eggs
- Isolate subjected to Next Generation Sequencing at IZSVe, Padova, Italy

Findings

- The virus was detected, isolated and identified as H5N8
- On analysis of the HA gene, multiple basic amino acid typical of HPAI was found at the cleavage site.
- No potential additional glycosylation sites
- Mutations associated with increased pathogenicity was absent

Findings CONT'D

- Mutations (Gln222Leu and Gly224Ser) on the HA proteins responsible for preference to avian host cell receptor as against human receptor were absent.
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Findings CONT'D

- Phylogenetic analysis of HA and NA gene sequences showed clustering with contemporary clade 2.3.4.4b specifically isolate from India (A/duck/India/10CA01/2016) with a similarity of 99.4%
- The other genes have higher similarity to H5N8 viruses previously isolated from Asia



Phylogenetic tree constructed by Maximum Likelihood of the **HA gene**. The H5N8 virus from Nigeria analysed here is marked in red.



Phylogenetic tree constructed by Maximum Likelihood of the NA gene. The H5N8 virus from Nigeria analysed here is marked in red.

Conclusion

- Trans continental incursion of H5N8 clade 2.3.4.4
- No considerable changes observed in the genes
- Enhanced monitoring of high risk areas

ACKNOWLEDGEMENT



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