



NATIONAL VETERINARY RESEARCH
INSTITUTE, VOM, NIGERIA



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

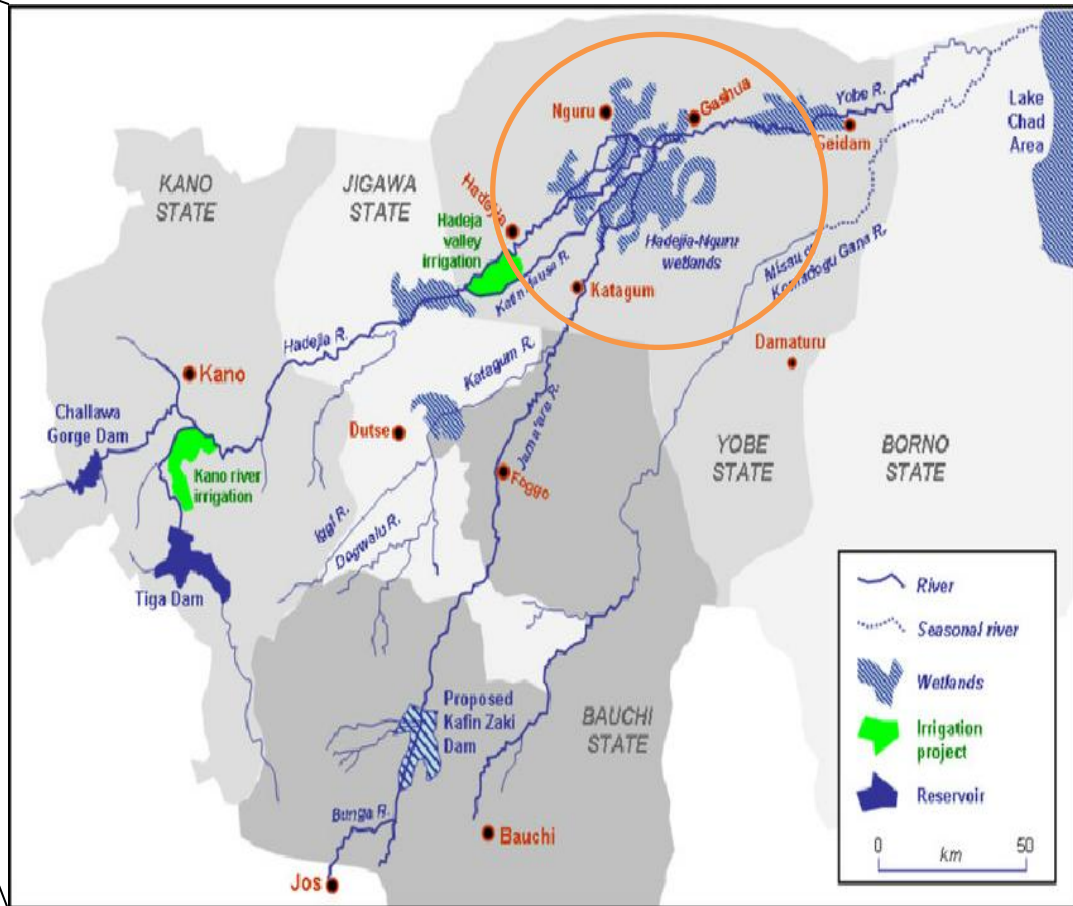
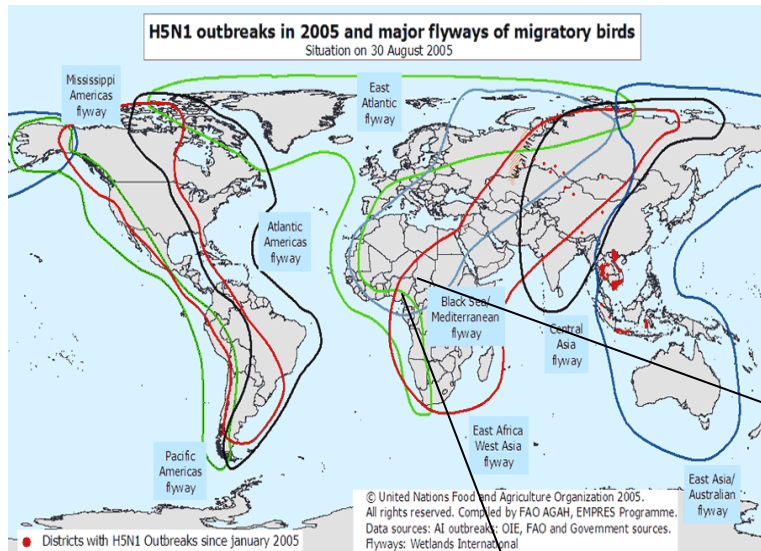
Ismaila SHITTU

National Veterinary Research Institute, Vom
Nigeria

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.
- The PB2, the

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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