SCIENTIFIC RESEARCH POSTER TITLE

Co-circulation of two genotypes and serogroups of African swine fever virus in Nigeria

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Conference Name

Rome |28/4/25

1 Introduction

African swine fever (ASF) is one of the most important diseases of domestic and wild pigs, threatening food security globally. The disease is associated with severe socio-economic consequences that threaten the livelihood of small-scale farmers and the profitability of large-scale farmers in Nigeria. The virus has been characterized into 24 genotypes based on p72 genotyping, and all are found in Africa. The genome size ranges between 170 – 194kb, with more than 150 structural proteins. Genotype I was first reported in Nigeria in 1997 and remained the dominant circulating genotype until 2020 when genotype II was reported from a pig farm settlement in Lagos that eventually spread to other parts of the country through panic and emergency sales. Therefore, continuous surveillance for a better understanding of the epidemiology and dynamics of the circulating viruses is relevant to the control and future eradication programme.

Summary/Key Points

- African swine fever virus
- Co-circulation

2 Methods/Approach

Diagnosis

All suspected samples submitted to the laboratory were subjected to molecular detection starting with DNA extraction using Qiagen DNA mini kit, specific gene primers for B606L (p72) for detection and other genes such as EP402 (CD2v), E183L (p54) for genotyping. Positive amplicons were purified and submitted to LGC Genomics® Berlin, for sequencing

Genome alignment

Assembled sequences were compared against the reference NCBI sequence using BLASTn, accessed on April 01 2025, and closely related sequences were retrieved for comparison against the assembled sequences.
Sequence alignment was carried out using MAFFT v7 online version accessed April 01 2025. clean up the sequence alignment and also remove poorly aligned sequences trimAl v1.42 was used with option –automated1, which helps to obtain clean, good and accurate data for downstream analysis.

Phylogenetic analysis

to understand the clear relationship between the assembled sequences and the reference sequence, a phylogenetic tree was constructed using Maximum Likelihood (ML) method ModelFinder was used to determine the most suitable substation model base on the Bayesian Information Criterion (BIC). IQTREE v 1.6.12 was used to build the tree applying the best fit model identified by the modelFinder. The Phylogenetic approach allowed the robust estimation of the genetic relationship among the sequences.

3 Results (Graphs, Tables, Figures)

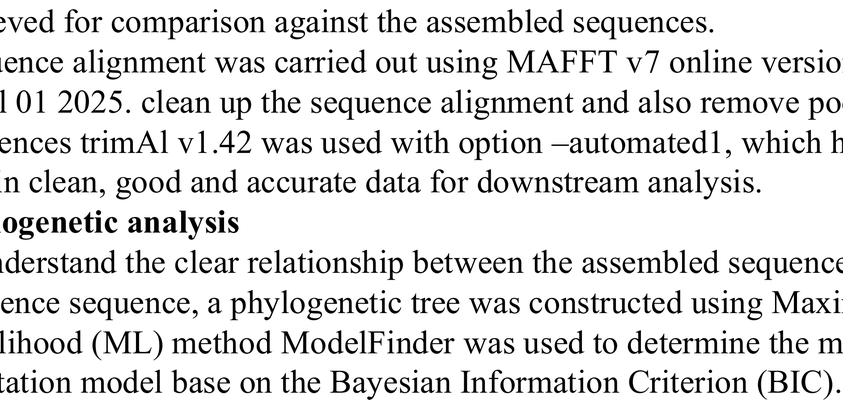


Figure 1: The B646L gene of the viruses were utilized to delineate circulating genotypes. The result obtained showed that of the 13 states studied, 12 had genotype I and II co-circulating, while only one state had genotype I alone circulating.

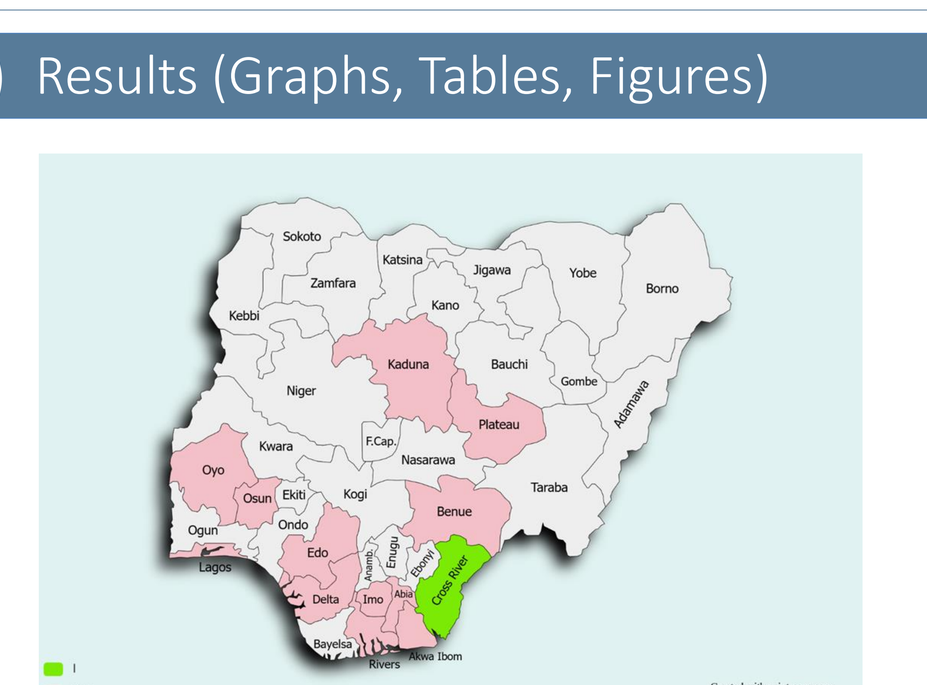
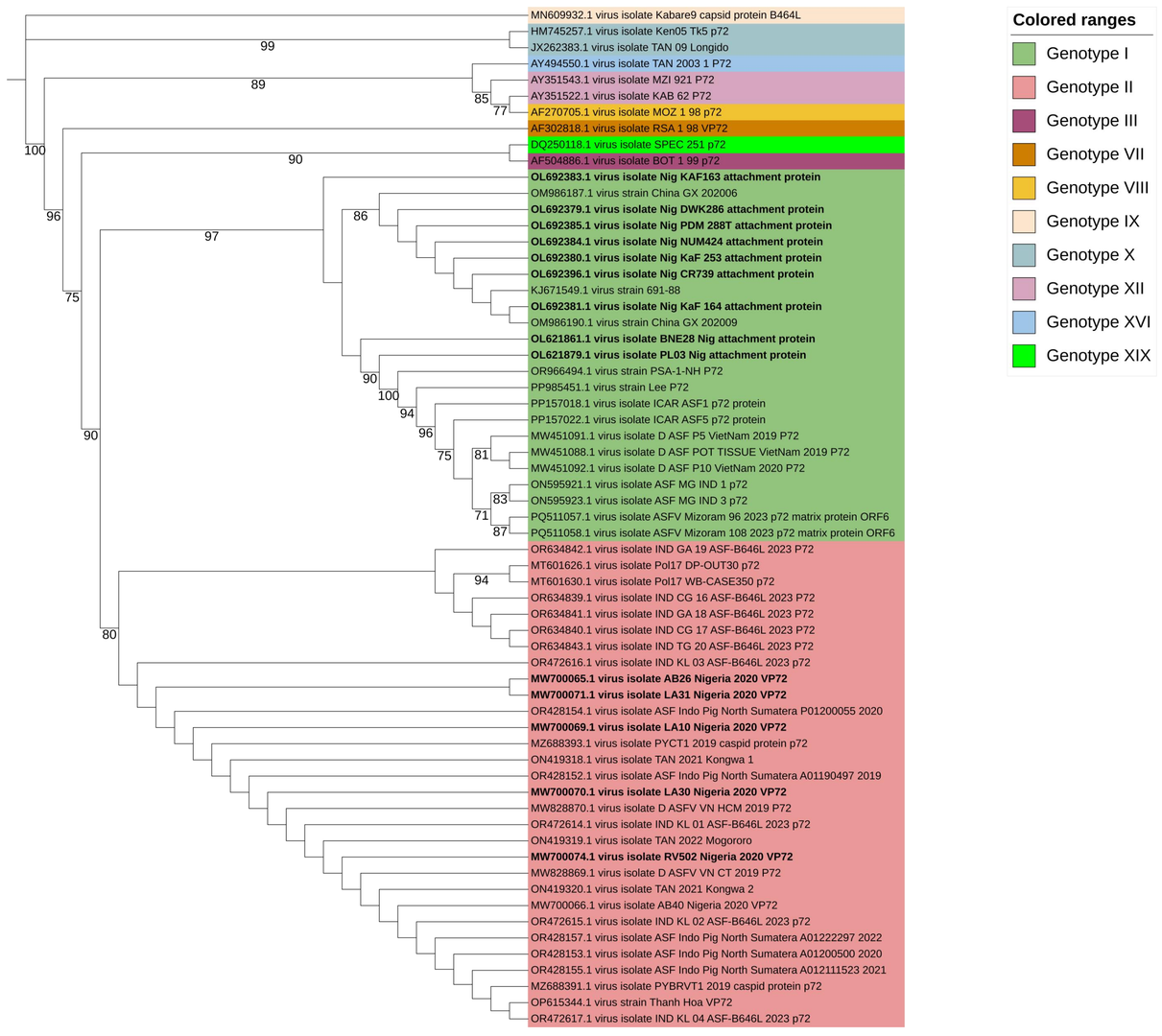


Figure 2: Using the EP402R gene that encodes the CD2v protein, our study reported serogroup 4 and 8 co-circulating in the country



B646L (p72) gene phylogeny

4 Discussion

This study reveals the epidemiological evolvement of African swine fever virus (ASFV) in Nigeria, which is marked by the co-circulation of both genotypes I and II in most of the states sampled. The detection of the two genotypes within the same geographic location indicates that Nigeria currently experience the circulation of the two genotypes, which may be a result of either repeated virus introduction or the sustained transmission of the two genotypes over time.

Historically, Genotype I has been consistently reported as the only genotype circulating in West Africa is associated with the long-time endemic form of ASF in West Africa, appears to be well establish study regions, especially Nigeria, also Genotype II has happened to been linked to the more recent global outbreaks including Asia and Europe is now increasingly being detected in Nigeria from 2020 to date. The co-circulation of the two genotypes in same areas raises a question about the viral competition, pathogenicity and transmission dynamics.

In addition to the co-circulation, the detection of serogroups 2 and 8 indicates antigenic diversity, particularly related to the CD2v protein, which plays a vital role in immune response and host interaction. The existence of multiple genotypes and serogroups could complicate control and diagnostics measures, particularly vaccine development which often relies on a stable antigenic target

5 Conclusion

The co-circulation of AFSV, both Genotypes I and II and also the presence of serogroups 2 and 8 across pig-producing states in Nigeria explain the virus's ongoing evolution and diversification. This genetic variability is a clear indication that the virus is no longer a static genetic entity but has a shifting epidemiological threat that requires a quick, dynamic and informed response. The findings in this report focus on emphasising the urgent need for continuous molecular surveillance, not only to monitor the spread pattern and emergence of new genotypes and serogroups, but also to guide targeted control strategies

6 References & Aknowledgements

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