FIRST REPORT OF GENOTYPE II FOR THE AFRICAN SWINE FEVER VIRUS OUTBREAK IN BENIN REPUBLIC IN 2023

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1 Introduction

African Swine Fever Virus (ASFV), the causative agent of African Swine Fever (ASF) and the sole member of the Asfarviridae family has been endemic in Benin since its first outbreak in 1997 (Ohouko et al., 2020). Historically, ASFV has been divided into 24 genotypes based on the partial sequencing of the B646L gene, which encodes the major capsid protein P72 (Spinard et al., 2023). Still, recent evidence has shown that strains that are closely related to the genotype I Benin 97/1 strain continue to cause outbreaks in western Africa (Spinard et al., 2024; Goatley et al., 2024). In this study, we discuss two isolates collected in 2023 from swine in southern Benin, which were thought to have perished from ASF.

Summary/Key Points

- ASF endemic in Benin since 1997
- Lack of data to explain the epidemiology
- Xyz
- Xyz

2 Methods/Approach

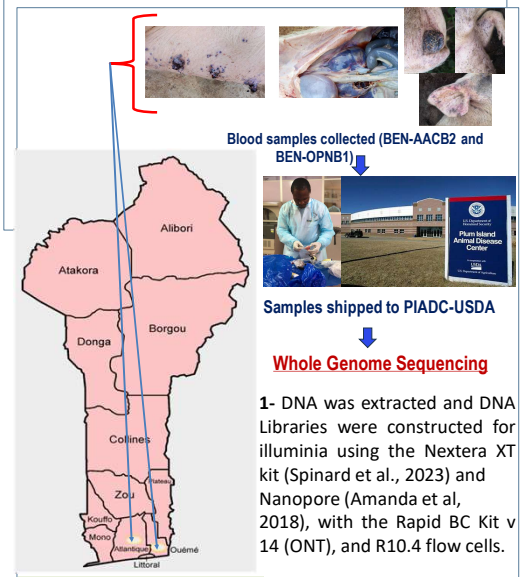

Fig1: Map of the departments of BENIN (in yellow the departments where the outbreaks occurs and samples collected

1- DNA was extracted and DNA Libraries were constructed for illuminia using the Nextera XT kit (Spinard et al., 2023) and Nanopore (Amanda et al, 2018), with the Rapid BC Kit v 14 (ONT), and R10.4 flow cells.

2- Illumina reads were trimmed using fastP (Chen et al., 2001) for adapters, ambiguous nucleotides (max = 2), minimum length (50 nt), quality (min phred score = 20) and nucleotide composition (20 and 5 nts removed from the 5' and 3' ends respectively)

3- To remove non-ASFV reads, reads that mapped to ASFV Georgia 2007/1 (FR682468) (Chapman et al., 2011) using the default parameters of bwa-mem2 (Vasimuddin et al., 2019) were collected. Further, the unmapped reads were collected, mapped to the sus scrofa genome (Warr et al., 2020) using the default parameters of bwa-mem2 except for K = 45, and the reads that did not map were collected

4- De novo assembly was performed using SPAdes (Bankevich et al., 2012) with each sample's minion reads and two sets of illumina paired-reads. Genomes were annotated using the default settings of TheTransporter (Ribeca GitHub). Genotyping and Biotyping were performed (Dinhobl et al., 2023, 2024) .

3 Results (Graphs, Tables, Figures)

Table 1. Summary of Sample and Genome Data

Isolate	Location	Country	Collection Date	Host	Genotype	Historic	Biotype	Genome Size	Genome Coverage (illumina)	GC%
BEN-AACB2	Abomey-Calavi	Benin	9/8/2023	Sus scrofa	2	II	2	180,642	456	38.60
BEN-OPNB1	Porto-Novo	Benin	7/5/2023	Sus scrofa	2	II	2	184,758	728	38.60

Each sample's minion reads and two sets of illumina paired-reads resulting in a 180,642 (BEN-OPNB1) and a 184,758 (BEN-AACB2) nucleotide length contig each with a GC content of 38.6%. Both genomes were Genotype 2 (historic genotype II) and Biotype 2.

The genome sequences for isolates BEN-OPNB1 (and BEN-AACB2 have been deposited in NCBI GenBank under the accession **no. PP552741** and **PP552742** respectively. Raw sequence data can be found in the GenBank SRA under BioProject accession **no. PRJNA1096266**.

4 Discussion

Both genomes (BEN-AACB2 and BEN-OPNB1) exhibited the 14 gene deletion that has been observed in the Georgia variants causing outbreaks in western Africa and analysis of the 3' end of the genome revealed both genomes were more similar to the Ghana 2022 isolates than Nigeria-RV502 as they did not contain the reverse complement of the 5' region.

5 Conclusion

This study present insight on African swine fever dynamic in Benin. It constitutes a guide for the country to establish action plan for better managing the disease for the pork industry protection. To the scientific community, research should focus on developing local vaccine to rapidly tackle the emergence of the strain circulating

6 References & Aknowledgements

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