# Advances in molecular epidemiology of the African swine fever virus in Rwanda and Tanzania

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## 1 Introduction

African swine fever (ASF)

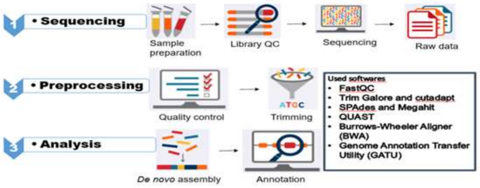
- ❑ Increased ASF outbreaks in eastern and southern Africa
- ❑ No ASF virus (ASFV) from Rwanda has been genetically characterized, and few complete genomes of ASFV from Tanzania have been described
- ❑ This study reports, for the first time, the ASFV genotypes causing outbreaks in Rwanda and the complete genome sequences of ASFV from Tanzania.

## 2 Methods

- Samples collection

- DNA extraction and ASFV confirmation using real time and conventional PCR

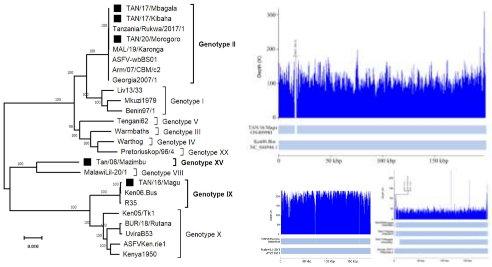
- Next-generation sequencing (NGS)



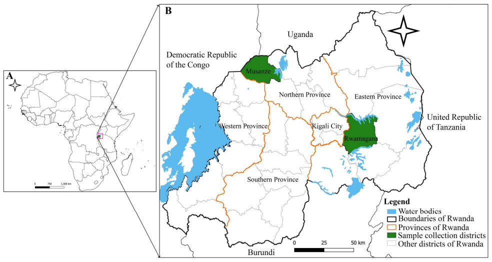
Used softwares
- FastQC
- Trim Galore and cutadapt
- SPAdes and Megahit
- QUAST
- Burrows-Wheeler Aligner (BWA)
- Genome Annotation Transfer Utility (GATU)

- Bioinformatics and phylogeographic analysis

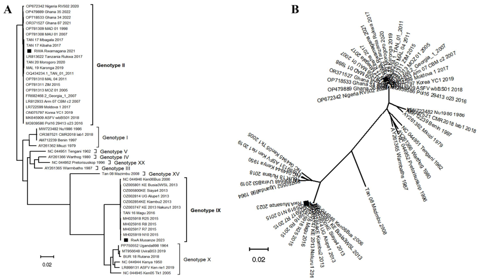
## 3 Results



- First complete genome sequence of ASFV genotype XV
- In addition, the first Tanzanian complete genome of ASFV genotype IX and three ASFV strains belonging to genotype II collected during ASF outbreaks in domestic pigs in Tanzania were determined in this study



- Samples were collected in two districts of Rwanda during ASF outbreaks



- Complete genome analysis of the ASFV genotypes II and IX responsible for the 2021 and 2023 outbreaks in Rwanda

## 4 Discussion

- The ASFV genotype II strains circulating in Tanzania and Rwanda are closely related to isolates previously reported elsewhere in the world
- Phylodynamic analysis indicated that the ASFV responsible for the 2021 outbreak in the eastern Rwanda was closely related to isolates previously described in Africa, Europe and Asia
- The ASFV genotype IX responsible for the 2023 outbreak in northern Rwanda clustered closely with isolates previously reported from neighboring countries
- The first complete genome of ASFV genotype XV was generated in this study adding more value to further comparative genomic studies.

## 5 Conclusion

- The extension of the geographical range of genotype II in eastern Africa is of concern
- The ongoing spread of ASFV genotype IX across Africa poses a risk of spreading beyond the continent and potentially impacting the domestic pig industry globally
- Phylogeographic and phylogenetic analyses revealed potential inter-countries viral spread events in eastern Africa
- The results of this study provide insights into the genomic structure of ASFV circulating in Rwanda and Tanzania and can be used to monitor changes within the ASFV genome and improve our understanding of ASF transmission dynamics for improved prevention and control.

## 6 References

- Hakizimana, J.N., et al., 2025. Complete genome analysis of the African swine fever virus genotypes II and IX responsible for the 2021 and 2023 outbreaks in Rwanda. Front. Vet. Sci. 12. https://doi.org/10.3389/fvets.2025.1532683
- Hakizimana, J.N., et al., 2023. Complete genome analysis of African swine fever virus genotypes II, IX and XV from domestic pigs in Tanzania. Sci Rep, vol. 13, Mar. 2023, https://doi.org/10.1038/s41598-023-32625-1.

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