

# Genetic heterogeneity of African swine fever virus within the sylvatic cycle in Central Mozambique

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## Introduction

African swine fever virus (ASFV), the only member of the *Asfarviridae* family, often leads to high mortalities in domestic pigs, resulting in devastating impacts to the pig industry of many countries in sub-Saharan Africa, the Indian Ocean and more recently, in eastern Europe.

The natural reservoirs of ASF in Africa are the argasid ticks of the genus *Ornithodoros* and wild suids, primarily warthogs (*Phacochoerus africanus*) and bushpigs (*Potamochoerus larvatus*), in which infection is inapparent.

The disease hampers food security and impacts on the well-being of small scale farmers and the development of pig farming in Mozambique. The Sofala Province in Central Mozambique is particularly prone to frequent outbreaks.

Previous studies indicated the frequent occurrence of ASF outbreaks in areas adjacent to the Gorongosa National Park (GNP) in Sofala Province. However, the possible source of those outbreaks has never been investigated.

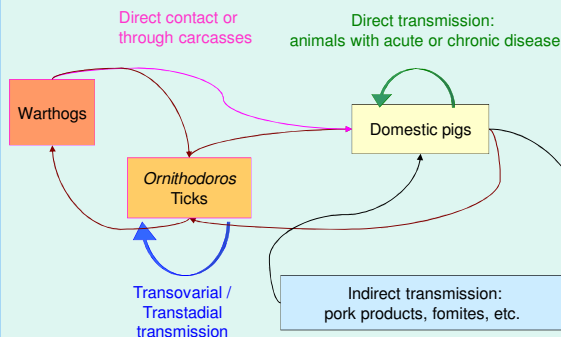


Figure 1: Potential transmission pathways of ASF in Mozambique

## Objectives

- ❖ To identify the presence of soft ticks at the wildlife/livestock interface of the GNP
- ❖ To determine the prevalence of ASFV in these vectors
- ❖ To characterize the genetic diversity of ASFV found in soft ticks and compare to isolates found elsewhere in Africa and beyond

## Materials and Methods



Figure 2: Study areas in Mozambique



Figure 3: Soft tick sampling in the warthog burrow

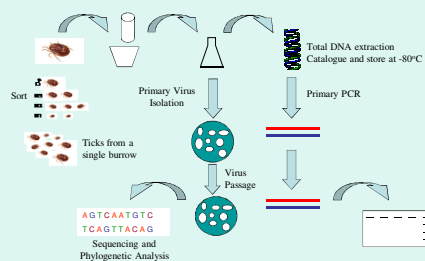


Figure 4: ASFV detection in soft ticks

These viruses were genotyped using a combination of partial gene sequencing (*p72*, *p30* and *p54*) and phylogenetic comparisons and analysis of the central variable region (CVR) of the B602L gene.

## Acknowledgements

The project was supported by The Wellcome Trust (Project number 210183, 183 AHDW03/04). We thank the GNP authorities for permission and relevant information, the field staff at the Agricultural District Directorate in Gorongosa and The Carbon Sequestration Project in Nhamitla at GNP for their support during the field work. The following people were involved in the laboratory analysis: Ricardo Gomes Souto from the Faculty of Veterinary Medicine, Eduardo Mondlane University, Mozambique; Dr. Rahana Dwarika and Ms. Nontobeko Ntshali of the TADP; OVI, Ms Heloise Heyne was responsible for the soft tick identification. Dr Penrith reviewed the manuscript. Dr Carlos Lopes Pereira for helping with the warthog sampling and Dr. Elisabeth Specht, the former head of Regional Veterinary Laboratory provided unflinching support.

## Results

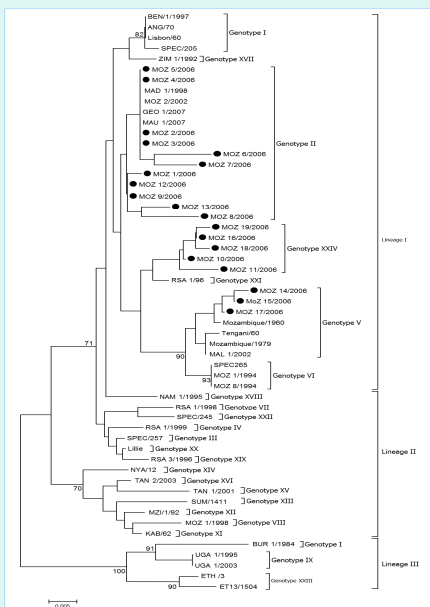


Figure 5: Evolutionary relationships of taxa for *p72* gene

**Tabela 1:** Central variable regions (CVR) of the 9RL ORF tetrameric amino acid repeat alignment from the isolates collected in the Gorongosa National Park (GNP) and buffer zone

Key: B = CADT; N = NVDT/NVGT; D = CASM; A = CAST; L = CTST; H = NEDT; P = NADT; S = SAST; O = NASI; F = NAST; Q = NADI; V = NANT; M = NANI; T = NVNT; C = GAST; K = CANT

Isolate	Place/country of origin	Species of origin	<i>p72</i> Genotype	CVR tetrameric amino acid sequences *	N° of repeats	CVR subgroups
Moz 2/2006	Gorongosa Park	Ticks	II	INDNDNDNAL	10	XXIII
Moz 3/2006	Gorongosa Park	Ticks	II			
Moz 4/2006	Gorongosa Park	Ticks	II			
Moz 5/2006	Gorongosa Park	Ticks	II			
Moz 7/2006	Gorongosa Park	Ticks	II			
Moz 8/2006	Gorongosa Park	Ticks	II			
Moz 9/2006	Gorongosa Park	Ticks	II			
Moz 12/2006	Gorongosa Park	Ticks	II			
Moz 13/2006	Gorongosa Park	Ticks	II			
MAD1/98	Madagascar	Domestic pig	II			
MAU/2007/1	Mauritius	Domestic pig	II			
MOZ/2002	Mozambique	Domestic pig	II			
Tengani/00	Tengani/Malawi	Warthog	V	ABABNBABHAL	11	XXI
Moz 12/2006	Gorongosa Park	Ticks	II	APSPFOPNALNFOFNOPNALNFOFNQVMY	31	XXIIa
Moz 15/2006	Gorongosa Park	Ticks	V			
Moz 14/2006	Gorongosa Park	Ticks	V	ABHABNBABHAL	12	XXIb
Moz 17/2006	Gorongosa Park	Ticks	V			
Moz/1979	Beira/Mozambique	Domestic pig	V			
Moz/1960	Beira/Mozambique	Domestic pig	V	ABNSAANAABNBABNBABHAL	22	XXIc
Moz 12/2006	Gorongosa Park	Ticks	XXIV	BNABRBNVA	7	XXIIIb
Moz 16/2006	Gorongosa Park	Ticks	XXIV	ABHABNBABHAL	12	XXIIIb
Moz 18/2006	Gorongosa District	Ticks	XXIV	ABHABNBABHAL	12	XXIIIb

## Results

A total of 1658 soft ticks were recovered from warthog burrows and pig pens at the wildlife-livestock interface of the GNP.

Viral DNA was confirmed in 19% of *Ornithodoros porcinus porcinus* and 15% of *O. p. domesticus*. Live virus was obtained in approximately 50% of the PCR-positive samples with 19 haemadsorbing virus isolates recovered.

Phylogenetic analysis based on the *p72* showed isolates clustering in genotype II (homologous to contemporary isolates from southern Africa, the Indian Ocean and Eastern Europe), genotype V (similar to previous isolates from Mozambique and Malawi) and within a new, previously unidentified genotype, designated genotype XXIV.

The isolates classified within genotypes II and XXIV clustered into three major sub-types based on their *p30* and *p54* sequences.

Based on analysis of the CVR gene, the viruses were classified into eight subgroups.

## Conclusion

The results suggest that soft ticks found in natural and domestic habitats at the GNP interface act as a permanent source of different strains of ASFV for domestic pigs.

The high infestation rates and genetic diversity of viruses found in those ticks were pronounced and included previously identified genotypes (II, V) and but also a newly identified genotype (XXIV).

This highlights the epidemiological importance of the sylvatic cycle in harboring and disseminating new and existing virus strains in the Mozambican pig value chain.

The recent recurrent emergence of genotype II ASF outbreaks outside the African continent is concerning.

The isolates in this study were genetically linked to viruses currently circulating in eastern Europe, Russia and China. This highlights the importance and the need to further investigate the characteristics, distribution and diversity of the ASFV maintained within wild hosts in East and southern Africa and the transmission patterns and pathways.

## References

- Bastos, et al., 2004: Veterinary Microbiology, 103, 169-182.
- Boshoff, et al., 2007: Veterinary Microbiology, 121, 45-55.
- Nix et al., 2006: Archives of Virology, 151, 2475-2494.