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 sarcid 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 Gorongoza National Park (GNP) in Sofala Province. However, the possible source of those outbreaks has never been investigated.

Materials and Methods

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 D. 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 undefined 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.

Results

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

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References

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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 infection rates and genetic diversity of viruses found in those ticks were pronounced and included previously identified genotypes (II, V) and 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 virus 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.