



Variants Evolution of African Swine Flu Virus

Giuseppe Mancía*

Department of Pathology, University of London, UK

INTRODUCTION

The large and intricate DNA virus known as African Swine Flu Virus (ASFV) is found in soft ticks and indigenous suids in sub-Saharan Africa. It has spread to swine populations in Europe and Asia. This virus, which causes African swine flu, a severe hemorrhagic disease with extremely high mortality rates in domestic and wild pigs, has exhibited remarkable genetic stability for more than a decade. As a result, few resources have been allocated to whole-genome genomic surveillance, and studies of virus evolution and molecular epidemiology have frequently failed to provide a genetic basis for tracing outbreaks. ASFV unexpectedly diverged into five distinct lineages during its recent invasion of Germany in 2020, each with at least 10 distinct variants characterized by novel high-impact mutations. Noticeably, all of the new variants share a frame shift mutation at the 3' end of the DNA polymerase PolX gene O174L, pointing to a possible mutation gene as the cause. Despite the fact that increased mutation rates were supported by epidemiological modeling, it is still unknown how quickly viruses could evolve under these conditions.

DESCRIPTION

In addition, we were able to locate regional clusters for the first time using a specialized Sanger sequencing strategy. In conclusion, our findings suggest that this brand-new factor has the potential to have a significant impact on the course of the ASFV pandemic, though the outcome is still unknown. As a result, our work emphasizes the significance of whole-genome genomic surveillance of ASFV. It is now common knowledge that most vi-

rus populations are made up of multiple genetic variants rather than a single clonal virus. The virus-specific mutation rate is what drives the emergence of these virus variants. This rate is influenced by a number of factors, such as the mode of replication, the fidelity of polymerases, the availability of repair mechanisms, and selection. The emergence of new virus variants demonstrates that these two factors, taken together, are responsible for the rate of evolution (evolutionary rate). While the recent SARS-CoV2 pandemic demonstrated how quickly some viruses evolve and produce new variants, other viruses exhibit a high degree of genetic stability and evolve very slowly.

The virus was transferred to Eurasia in 2007 and has since spread to domestic and wild pig populations there. Despite the fact that domestic pigs and Eurasian wild boar are extremely susceptible to the virus, African warthogs remain largely symptomless following infection. Amoeba-associated viruses with some degree of similarity to *Iridoviruses* and *poxviruses* have been found to be distantly related, but there are currently no viruses that are closely related. Because it is the only known member of its family *Asfarviridae* and the genus *Asfivirus*, ASFV is still considered a mystery in modern virology.

CONCLUSION

As a result, it was only recently included in the *Nucleocytoviricota* phylum. The emergence of distinct ASFV variants that point to a higher level of ASFV sequence variability in strains discovered at the German-Polish border is described here. As a possible cause, we identified a frame shift mutation in the O174L/PolX gene that affects the enzyme's 5' binding pocket.

Received:	02-January-2023	Manuscript No:	IPJIDT-23-15747
Editor assigned:	04-January-2023	PreQC No:	IPJIDT-23-15747 (PQ)
Reviewed:	18-January-2023	QC No:	IPJIDT-23-15747
Revised:	23-January-2023	Manuscript No:	IPJIDT-23-15747 (R)
Published:	30-January-2023	DOI:	10.36648/2472-1093-9.1.03

Corresponding author Giuseppe Mancía, Department of Pathology, University of London, UK, E-mail: GiuseppeMancia445@yahoo.com

Citation Giuseppe M (2023) Variants Evolution of African Swine Flu Virus. J Infect Dis Treat. 9:03.

Copyright © 2023 Giuseppe M. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.