ABSTRACT
These findings suggest that a common pattern of structure and function is shared among viral transmembrane fusion proteins from different virus families, which could lead to the development of'superfluid' viruses or superfamily members.

INTRODUCTION
For the last two decades, the field of virology has been developing models that enable us to understand the evolution of viral and host proteins by observing the sequence of their proteins. These models attempt to account for the presence of a common ancestor between viruses and their hosts. This common ancestor may have emerged from a common ancestor, or it may have arisen as a minor difference between the two viruses. However, the origins of viruses and their hosts are constantly changing, and the origin of the common ancestor is always unknown.

In this article, we discuss a potential evolutionary scenario that could explain the divergence of Arenavirus and Filovirus glycoproteins from a common RNA virus ancestor. The authors discuss the evolutionary implications of this scenario in relation to the A number of laboratories have found that the transmembrane (TM) proteins of several RNA viruses contain shared structural and functional elements that are essential for virus entry, such as a hydrophobic region designated as "fusion peptide" and fibrous structure defined by two antiparallel alpha helices. These principles can also be used to describe other viral infections, including Ebola and Rous sarcoma viruses, where there is significant sequence identity within some isolated viruses or even within broader family structures like the Retroviridae. However, A general model of the Arenavirus glycoproteins has been proposed, which is based on the detailed study of LCMV and influenza viruses. The GP-C precursor is proteolytically cleaved to form gp-1 and PG-2, with CGPM being one of them. Here, we present a detailed model of GP-2 for Lassa fever virus, an Arenavirus associated with multiple epidemics of hemorrhagic fever with high mortality rates in West Africa, as well as for the related lymphocytic choriomeningitis virus (LCMV) which has been associated to sporadic outbreaks human disease in Europe and North America; this model shows that several different regions of the TM superfamily of Organismoviruses share specific sequence and structural motifs, showing that these regions are directly correlate relationships with E

CONCLUSION
Remarkable conclusions Due to the similarities in their agents, it is probable that they both derive from a common viral ancestor, as evidenced by the type of each Arenavirus found in large areas and the stability of isolates within confined areas over time. This suggests that the conservation of such peptide sequences could be significant in the biology of these agents. Modeling studies conducted in the late 1980s have identified several common and homologous sequence motifs for infection that were not previously recognized in sequence homology studies. These models may now offer a universally applicable approach to antiviral inhibition of virus entry into host cells, which is applicable to various virus families.