

Spatiotemporal distribution of endemic classical swine fever virus in Cuba and molecular characterization of a low virulence strain

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In Cuba, Classical Swine Fever (CSF) has become an endemic disease since 1993 with several outbreaks each year, despite vaccination and control programs that are implemented. Its presentation forms are diversified. From chronic and acute form to subclinical, depending on the virulence of the strain, and the immunological condition and age of the pigs. Characterizing the disease, as well as assessing the field situation would enable to implement measures of effective control to eradicate it. For this study, information provided by Laboratorio Nacional de Diagnóstico Veterinario (National Vet Diagnostic Lab) about 846 CSF confirmed focus at national level between 2010 and 2016 and clinical signs reported were used. The probabilistic space-temporal permutation model (SaTScan 9.4) proved that high and low rates grouping prevail in the West and East, respectively. Some works were made to assess the positive selection pressure on E2 partial gene of CSF viruses from infected animals with non-acute haemorrhagic form of the disease to get insights into the mechanisms governing virulence and the driving forces of classical swine fever virus evolution in swine population under regular vaccination programs. It was found that G761R mutation was caused by positive selective pressure that seemed to be an important factor in the virulence of the virus inducing variation on the clinical manifestations of the disease in the field. Nevertheless, a pathogenicity study of isolated with the same mutation (Pinar de Rio, Holguín y Santiago de Cuba) showed different clinic performances. This study shows that Pinar del Rio strain, is clearly low virulent during the endemic phase. Next, we analysed the complete nucleotide sequence of the Pinar del Rio virus isolated. More importantly, a novel unique poly-uridine tract was found in the 3'UTR of the Pinar del Rio virus, which was not found in the parental Margarita virus. Some studies on the late finding are carried out at present. These data provide novel insights into viral molecular features associated with adaptation of CSFV for persistence in the field.