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Genomic analysis of Sardinian 26544/OG10 isolate of African swine fever virus

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Abstract

Comparative genomic analysis aims to underscore genetic assortment diversification in distinct viral isolates, to identify deletions and to carry out evolutionary studies. We sequenced the first complete genome of an ASFV p72 genotype I strain isolated from domestic pigs in Sardinia (Italy) using Next-Generation Sequence (NGS) technology. The genome is 182,906 bp long, contains 164 ORFs and has a 99.20% nucleotide identity to the L60 strain. Comparison analysis against the 16 ASFV genomes available in the database showed that 136 ORFs are present in nine ASFV isolates annotated to date. The most divergent ORFs codify for uncharacterized proteins such as X69R and DP96R, which have 51.3% and 70.4% nucleotide identity to the other isolates. A comparison between the Sardinian isolate and the avirulent isolates OURT 88/3, NHV, BA71V was also carried out. Major variations were found within the multigene families (MGFs) located in the left and right genome regions.

Keywords: African swine fever virus, Whole genome sequence, Next generation sequencing, B407L, Multigene family

1. Introduction

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