

The first complete genome analysis of an African swine fever virus in the Mekong delta revealing a novel variant of the genotype 2

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Abstract

The objective of this study is to report the complete genome sequence of a field African swine fever virus (ASFV) causing a fatal outbreak in domestic pigs in the Mekong delta, namely ASF/VN/CanTho-OM/2021 (GenBank accession number: ON402789). The complete genome sequencing detected an 18-bp nucleotide deletion in the EP402R gene (encoding for serotype-specific proteins CD2v) of ASF/VN/CanTho-OM/2021 which is determined to belong to the genotype 2 and serotype 8. This mutation pattern was confirmed as unique in the GenBank; thus, ASF/VN/CanTho-OM/2021 can be considered as a novel variant with potential change of sero-characteristics within the genotype 2. Additional unique mutation of 78-bp nucleotide insertion was also observed in the B475L gene. Besides, four copies of tandem repeats sequences were found in the intergenic gene (IGR) located between I73R and I329L that is previously assigned as the IGR III variant. This study is the first to report the complete genome of ASFV in the Mekong delta and highlights the necessity for strengthening of molecular surveillance in order to provide further knowledge on evolution and incursion of ASFV in the Mekong delta and Vietnam.

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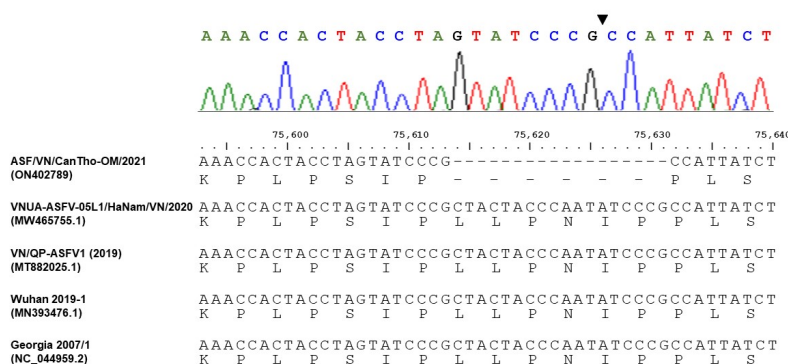


Fig. 1B.
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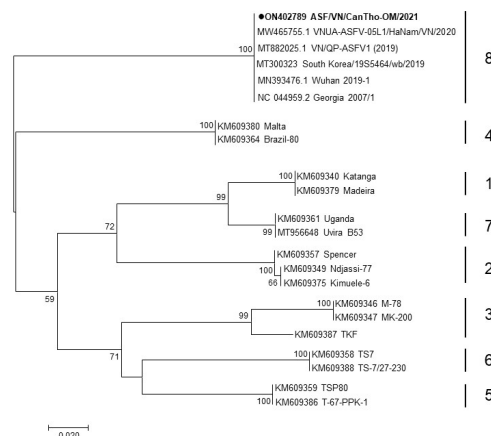


Fig. 1A.
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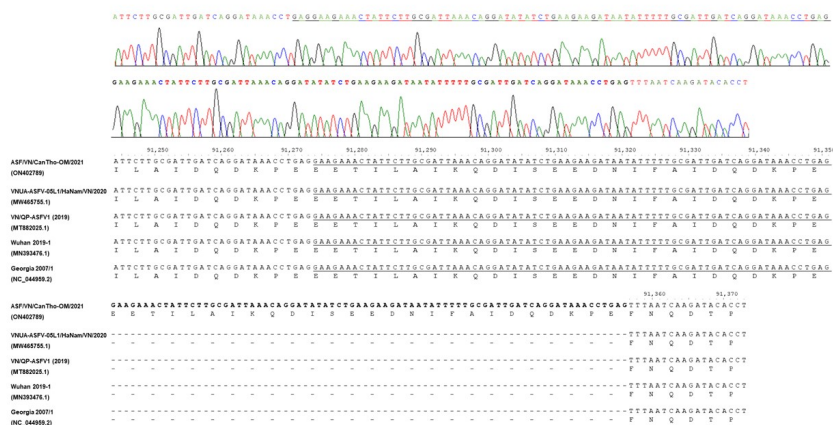


Fig. 2.
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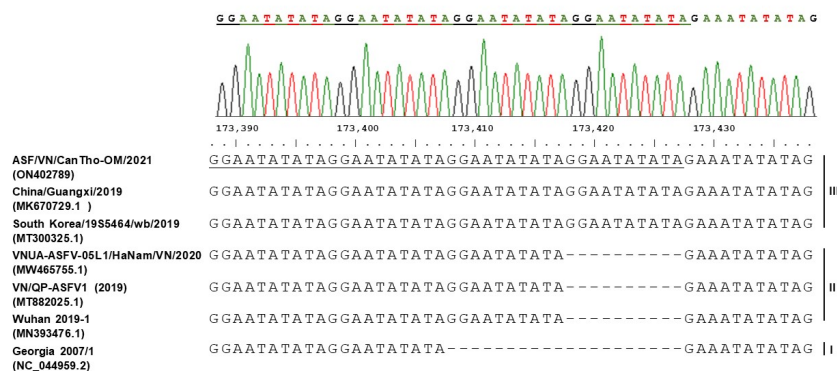


Fig. 3.
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