



Complete Genome Sequence of O/VN1/2014, a Foot-and-Mouth Disease Virus of Serotype O Isolated in Vietnam in 2014

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ABSTRACT In this article, we report the complete genome sequence of foot-and-mouth disease virus (FMDV) strain O/VN1/2014 isolated in Vietnam (Lao Cai) in 2014. The virus belongs to serotype O, topotype South East Asia (SEA), and genotype Mya-98 (O/SEA/Mya-98). It is the latest complete genome information for the genotype O/SEA/Mya-98 in Vietnam since 2009.

Foot-and-mouth disease viruses (FMDVs) are highly contagious in cloven-hoofed animals, such as cattle and pig, and are classified under seven serotypes (O, A, Asia1, C, SAT1, SAT2, and SAT2). FMDVs are prevalent in most Southeast Asian countries, including Vietnam (1, 2). Serotype O and A of FMDV have most commonly been occurring endemically, and the O/SEA/Mya-98 genotype was one of the indigenous genotypes and has shown a high incidence rate in Vietnam (3, 4).

In this study, we isolated the FMDV strain O/VN1/2014 from an epithelial sample of a pig with clinical symptoms of FMDV in northern Vietnam (Lao Cai Province) in October 2014. The virus was cultured until passage 2 in the cell line ZZR-127, originated from a fetal goat tongue epithelium (5). Viral RNA was extracted with an RNeasy mini kit (Qiagen), and the full genome was amplified by PCR using a Qiagen one-step reverse transcriptase PCR (RT-PCR) kit and 19 overlapping pairs of FMDV-specific primers, based on the sequence of O/SKR/JC/2014 (GenBank accession no. [MG257782](https://doi.org/10.1128/MRA.01343-18)). The PCR products were subjected to direct sequencing using a ABI 3730XL instrument with a BigDye Terminator v3.1 cycle sequencing kit. The sequences of the PCR products were assembled by Clustal W multiple alignment with default parameters using the software BioEdit (version 7.2.5.). A single open reading frame (ORF; protein-coding region) was predicted by comparing the sequence of O/SKR/JC/2014 with the FMDV reference sequence (GenBank accession no. [MG257782](https://doi.org/10.1128/MRA.01343-18)). The sequence homology was determined by BLAST via the NCBI website.

The complete genome of O/VN1/2014 was 8,131 nucleotides (nt) in length, including a 5' untranslated region (UTR) of 1,011 nt with a poly(C) of 19 nt and a 3' UTR of 121 nt with a poly(A) tail of 26 nt. A single ORF of 6,999 nt was predicted to encode a polyprotein of 2,332 amino acids (aa) containing of four structural (VP4, VP2, VP3, and VP1) and eight nonstructural proteins (L, 2A, 2B, 2C, 3A, 3B, 3C, and 3D). O/VN1/2014 belongs to the topotype SEA and genotype Mya-98 of FMDV serotype O (O/SEA/Mya-98). The virus is most closely related to a Korean FMDV isolate, O/SKR/JC/2014 in the public database, with a 97.3% nt identity and no indels at the ORF (6,810/6,999 nt). But, it is less related to a Vietnam FMDV isolate, O/VN/QB88/2009 (GenBank accession no. [GU582115](https://doi.org/10.1128/MRA.01343-18); only with ORF), with a 90.1% nt identity at the ORF (6,306/6,999 nt).

Our findings confirmed that at least two genetically different O/SEA/Mya-98 genotypes, one closely related to the Korean FMDV strain from 2014, have been circulating

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in Vietnam. The complete genome sequence of O/VN1/2014 could provide the valuable information for further study of the genetic diversity and the antigenic relationship of FMDVs in the Asian region, with the ultimate aim to control and prevent FMDV.

Data availability. The complete genomic sequence of O/VN1/2014 has been deposited in GenBank under the accession no. [MH845413](https://doi.org/10.1016/j.vetmic.2010.06.030).

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