FAO World Reference Laboratory for Foot-and-Mouth Disease (WRLFMD)

Genotyping Report

Report Date: 19/07/2026

Batch number: WRLFMD/2026/000010

Date received: 13/05/2026

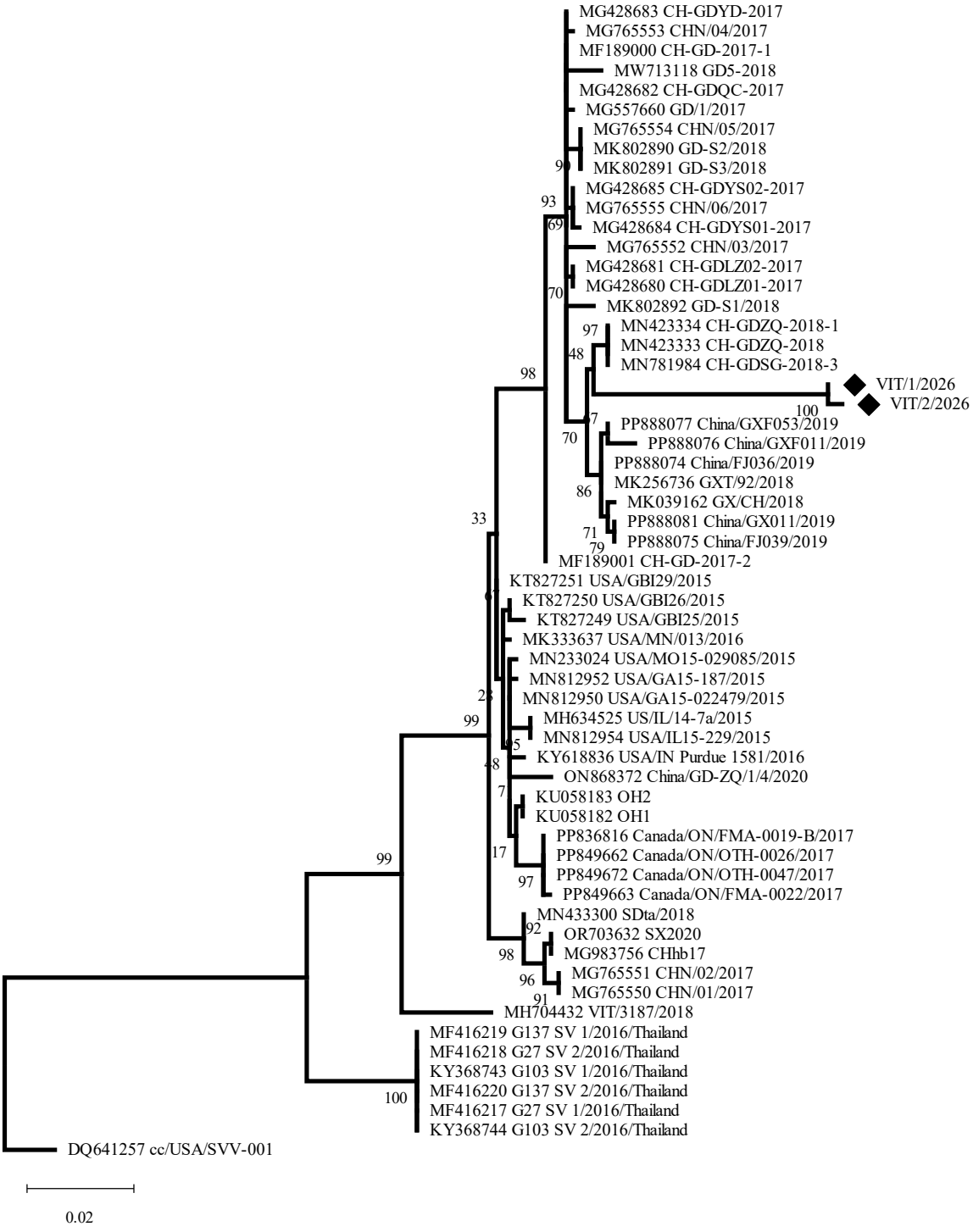
Virus species: *Senecavirus valles*
Virus common name: Seneca Valley virus (SVV)
Country: Vietnam
Period: 2026
No. of samples: 2
Sequences: VP1 (792 nt)

Sample information:

WRLFMD Ref. No.	Sender Ref.	Date collected	Species	Location
VIT/1/2026	26-H149	21/03/2026	pig	My Loi, Dong Thap Province
VIT/2/2026	26-H038	04/04/2026	pig	My Loi, Dong Thap Province

Top 10 closet matches using NCBI BLAST (percent nucleotide identity)

Virus name	Accession	VIT/1/2026	VIT/2/2026
CH-GDZQ-2018-1	MN423334.1	95.83	95.58
CH-GDLZ02-2017	MG428681.1	95.83	95.58
CH-GDSG-2018-3	MN781984.1	95.83	95.58
CH-GDLZ01-2017	MG428680.1	95.83	95.58
CH-GDZQ-2018	MN423333.1	95.83	95.58
CH-GD-S2/2018	MK802890.1	95.71	95.45
CH-GD-S3/2018	MK802891.1	95.71	95.45
China/FJ036/2019	PP888074.1	95.71	95.45
CH-GDQC-2017	MG428682.1	95.71	95.45
CHN/05/2017	MG765554.1	95.71	95.45



Evolutionary analysis by the Maximum Likelihood method

The phylogeny was inferred using the Maximum Likelihood method and Kimura (1980) 2-parameter model [1] of nucleotide substitutions and the tree with the highest log likelihood (-2,278.68) is shown. The percentage of replicate trees in which the associated taxa clustered together (1,000 replicates) is shown next to the branches [2]. The initial tree for the heuristic search was selected by choosing the tree with the superior log-likelihood between a Neighbor-Joining (NJ) tree [3] and a Maximum Parsimony (MP) tree. The NJ tree was generated using a

matrix of pairwise distances computed using the Kimura (1980) 2-parameter model [1]. The MP tree had the shortest length among 10 MP tree searches, each performed with a randomly generated starting tree. The rate model allowed for 61.97% of sites to be evolutionarily invariable (*I*). The analytical procedure encompassed 59 coding nucleotide sequences using 1st, 2nd, 3rd, and non-coding positions with 792 positions in the final dataset. Evolutionary analyses were conducted in MEGA12 [4] utilizing up to 4 parallel computing threads.

1. Kimura M. (**1980**). A simple method for estimating evolutionary rate of base substitutions through comparative studies of nucleotide sequences. *Journal of Molecular Evolution* **16**:111-120.

2. Felsenstein J. (**1985**). Confidence limits on phylogenies: An approach using the bootstrap. *Evolution* **39**:783-791.

3. Saitou N. and Nei M. (**1987**). The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution* **4**:406-425.

4. Kumar S., Stecher G., Suleski M., Sanderford M., Sharma S., and Tamura K. (**2024**). Molecular Evolutionary Genetics Analysis Version 12 for adaptive and green computing. *Molecular Biology and Evolution* **41**:1-9.