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- a, unknown number of outbreaks-
 - b, not confirmed by laboratory investigations
 - c, one clinical outbreak and one farm where SVDV was isolated from healthy pigs
 - d, all from clinically normal pigs
 - e, 100-200 outbreaks ?
 - f, vesicular disease in pigs on a few farms, SVD suspected but no virus isolated (origin: pig meat from China)
 - g, dates and numbers of outbreaks not known
 - h, no clinical disease, diagnosis based on serology
 - i, virus isolated from one farm, however, approx. four more farms were sero-positive
 - j, sequence analysis suggested that the virus isolated was a laboratory contaminant
 - k, all were sub-clinical infections

SUPPLEMENTARY TABLE S2

GARD analyses

GARD Analysis #	Genome Region	Alignment # seq/51 length	Analysis Converged	Breakpoint positions
1	Full	51/51 7412	NO	566, 3602***, 5206***
2	5'UTR-1B	51/51 1733	YES	566, 932***
3	1B-1D (external capsid)	51/51 2346	YES	1778***
4	1C-2D	51/51 2310	YES	2495*
5	1D-3C	51/51 2583	YES	3088***
6	2B-3C	51/51 2166	YES	4583***
7	3A-3D	51/51 2268	YES	-
8	3D-3'UTR	51/51 1496	YES	-
9	Full	26/51 7412	NO	566, 818, 1295**, 1727***, 3587***, 5216
10	Full	25/51 7412	YES	1295, 3184***
11	Full	23/51 7412	NO	566, 818, 1094***, 1658, 3689**
12	Full	15/51 7412	YES	572, 815, 1082***, 1883, 2271, 3839***, 5206
13	Full	51/51 7412	NO	566, 3482***, 5141***
14	5'UTR- 3'UTR (trimmed)	15/51 7335	NO	574, 819, 1146***, 1878***, 3645, 3873, 5207, 5391
15	5'UTR (trimmed)- 3'UTR (trimmed)	15/51 6938	YES	2702, 3529*, 3716***, 4946

Analysis #1 is the basic SVDV alignment (BSA). Analysis #10 has the complementary taxa to analysis #9. Analyses 11 and 12 are reduced sets of analysis 9. Analysis 13 only differs from #1 by trimmings in the 5'UTR and 3'UTR. No * means that there was no support from the Kishino-Hasegawa test, one, two and three stars mean support at $p = 0.10$, $p = 0.05$ and $p = 0.01$, respectively.

SUPPLEMENTARY TABLE S3

Historical occurrence of foot-and-mouth disease in 4 European countries

Reproduced from G. N.Mowat. Epidemiology of foot-and-mouth disease in Europe. *Rev. sci. tech. Off. Int. Epiz.*, 1986, 5 (2), 271-277.

	Belgium	France	Netherlands	United Kingdom
1957	328	99424	40	184
1958	588	14127	11	116
1959	57	6188	6	45
1960	180	7382	3	298
1961	121	2626	179	103
1962	6	199	5470	5
1963	67	28	2103	0
1964	2	56	146	0
1965	112	10	1426	1
1966	323	59	2194	34
1967	22	17	196	2210
1968	1	40	0	187
1969	3	35	0	0
1970	2	4	0	0
1971	1	8	21	0
1972	0	2	7	0
1973	0	1	0	0
1974	60	89	3	1
1975	21	2	2	0
1976	1	0	0	0
1977	0	0	1	0
1978	0	1	0	0
1979	0	21	0	0
1980	0	0	0	0
1981	0	18	0	2
1982	0	0	0	0
1983	0	0	4	0
1984	0	0	2	0
1985	0	0	0	0

SUPPLEMENTARY TABLE S4

Existing full or near-full genome sequenced SVDV isolates
included in the basic SVDV alignment

Accession#	Isolate ref.	Origin	Date collected
KF963276	HKN/8/73	Tong Yan San Tsuen, Ping Shan, Y.L., Hong Kong	30. Mar. 1973
KF963277	HKN/18/74	Lo Shu Leng, Ta Kwu Ling, N.T., Hong Kong	11. Sep. 1974
KF963278	HKN/25/75	Shueng Tsuen, Pat Heung, Y.L., N.T., Hong Kong	1. Mar. 1975
KF963274	HKN/1/77	Pak Sah, Sap Pat Hueng, Y.L., Hong Kong	10. Mar. 1976
KF963275	HKN/5/77	Ping Che, Ta Kwu Ling, N.T., Hong Kong	7. May 1976
AY429470	HK'70	Hong Kong	
X54521	UKG/27/72	United Kingdom	11. Dec. 1972
D16364	J1'73	Japan	Nov.-Dec. 1973
D00435	H3'76	Japan	1976
AF268065	NET/1/92	Netherlands	1992
EU151450	ITL/1/92	Italy	1. Jun. 1992
EU151454	ITL/2/92	Italy	2. Sep. 1992
EU151451	ITL/6/92	Italy	16. Jun. 1992
EU151452	ITL/8/92	Italy	14. Aug. 1992
EU151448	ITL/18/92	Italy	5. Nov. 1992
EU151455	ITL/19/92	Italy	16. Nov. 1992
EU151456	ITL/1/97	Italy	30. Jan. 1997
EU151457	ITL/2/97	Italy	3. Feb. 1997
EU151449	ITL/3/97	Italy	7. Feb. 1997
EU151458	ITL/10/98	Italy	2. Nov. 1998
EU151459	ITL/1/99	Italy	11. Jan. 1999
EU151460	ITL/3/99	Italy	25. Jan. 1999
EU151461	ITL/5/99	Italy	4. Feb. 1999
EU151453	ITL/7/99	Italy	5. Feb. 1999

SUPPLEMENTARY TABLE S5

Analyses run in GARLI

Alignment	#Taxa	Length	Model
5'UTR	189	741	SYM [012345] eq. freq. + I + 4G
1A (VP4)	180	207	TIM2 [010232] + I + 4G
1B (VP2)	124	767	TIM2 [010232] + I + 4G
1C (VP3)	98	714	TIM2 [010232] eq. freq. + 4G
1D (VP1)	427	850	GTR + 4G
2A	197	450	TIM2 [010232] eq. freq. + I + 4G
2C	307	987	GTR + I + 4G
3C (Protease)	218	549	GTR + I + 4G
3D (Polymerase)	489	1386	GTR + I + 4G

SUPPLEMENTARY TABLE S6

Parameter priors used in BEAST analyses

Parameter	Prior	Bound
CP1+2.kappa	LogNormal [1, 1.25], initial = 2	[0, inf.]
CP3.kappa	LogNormal [1, 1.25], initial = 2	[0, inf.]
CP1+2.mu	LogNormal [0, 1], initial = 1	[0, inf.]
CP3.mu	LogNormal [0, 1], initial = 1	[0, inf.]
frequencies	Uniform [0, 1], initial = 0.25	[0, 1]
CP1+2.alpha	Exponential [0.5], initial = 0.5	[0, inf.]
CP3.alpha	Exponential [0.5], initial = 0.5	[0, inf.]
clock.rate	Gamma [0.001, 1000], initial = 1	[0, inf.]
uced.mean	Gamma [0.001, 1000], initial = 1	[0, inf.]
ucl.d.mean	Gamma [0.001, 1000], initial = 1	[0, inf.]
ucl.d.stdev	Exponential [0.333333], initial = 0.3333...	[0, inf.]
treeModel.rootHeight	Using Tree Prior in [40.167123, inf.]	←
constant.popSize	Gamma [0.001, 1000], initial = 10	[0, inf.]
exponential.popSize	Gamma [0.001, 1000], initial = 10	[0, inf.]
logistic.popSize	Gamma [0.001, 1000], initial = 10	[0, inf.]
skyline.popSize	Exponential [1000], initial = 100	[0, inf.]
exponential.growthRate	Laplace [0, 0.023026], initial = 0.4	[-inf., inf.]
logistic.growthRate	Laplace [0, 0.017269], initial = 1	[-inf., inf.]
logistic.t50	Gamma [0.001, 1000], initial = 1	[0, inf.]
meanRate	Indirectly Specified Through Other Parameters	n/a
covariance	Indirectly Specified Through Other Parameters	n/a
coefficientOfVariation	Indirectly Specified Through Other Parameters	n/a
origin	Exponential [100], initial = 440	[0, inf.]
R0	LogNormal [1, 1], initial = 5	[0, inf.]
recoveryRate	Gamma [1, 1], initial = 0.05	[0, inf.]
samplingProbability	Beta [1, 1], initial = 0.05	[0, 1]