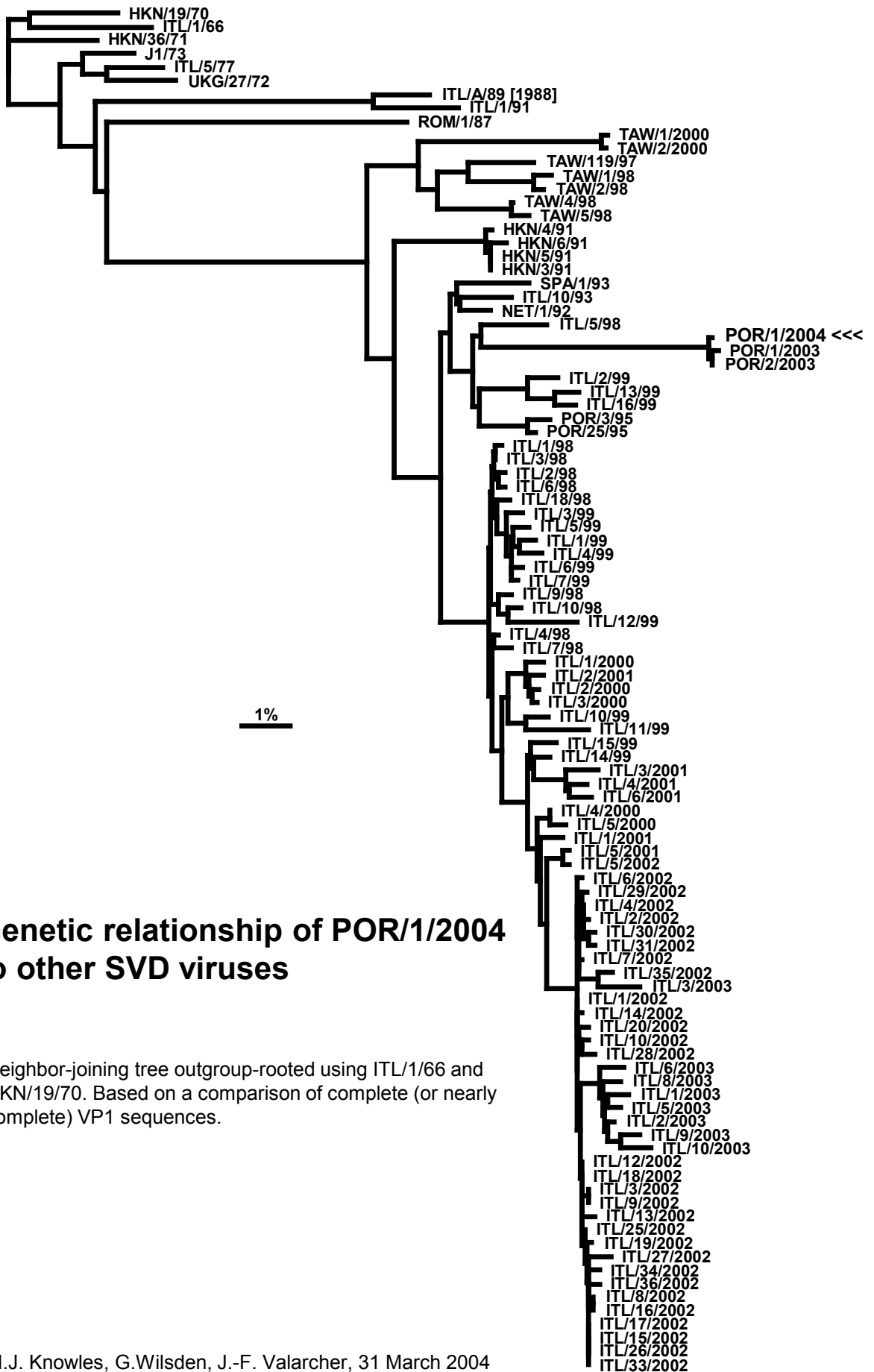


**Report from the Molecular Epidemiology Section of the Dept. of Exotic Disease Control to  
the Head of the World Reference Laboratory for FMD (Non-QAU Form)**

Serotype: SVDV	Report date: 24/03/2004						
WRL Ref No: POR/1/2004	Reported by: N.J. Knowles						
Date collected: 09/01/2004	Checked by: J.-F. Valarcher						
Date received: 13/02/2004							
Species: Porcine	Topotype:						
Material used: 10% epith. susp.	Genotype/strain:						
Region sequenced: VP1	Sequence filename: POR04-01.SEQ						
RT-PCR primers: SKH2163F/NK44	Date sequence last updated: 21/03/2004						
No. of Nt determined: 849	Total no. of comparisons: 271						
No. of ambiguities: 0							
Gene length: 849							
Comments:							
<b>Ten Most Closely Related Viruses</b>							
Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	POR/2/2003	POR03-02	849	847	0	99.76	0.24
2	POR/1/2003	POR03-01	849	847	0	99.76	0.24
3	ITL/2/92	ITL92-02	214	204	0	95.33	4.67
4	NET/2/94	NET94-02	310	295	0	95.16	4.84
5	NET/3/94	NET94-03	283	268	0	94.70	5.30
6	NET/1/94	NET94-01	572	541	3	94.58	5.42
7	POR/3/95	POR95-03	849	798	0	93.99	6.01
8	ITL/5/97	ITL97-05	297	279	0	93.94	6.06
9	ITL/5/98	ITL98-05	849	797	0	93.88	6.12
10	POR/25/95	POR95-25	849	797	0	93.88	6.12
<b>Relationships to Reference Virus Strains</b>							
Pos.	Virus name	Filename	No. nt compared	No. nt matched	No. of ambiguities	% Identity	% Difference
1	NET/1/92	NET92-01	849	791	0	93.17	6.83
2	HKN/4/91	HKN91-04	849	776	0	91.40	8.60
3	TAW/119/97	TAW97119	849	764	0	89.99	10.01
4	HKN/18/87	HKN87-18	830	714	0	86.02	13.98
5	HKN/36/71	HKN71-36	816	701	2	85.91	14.09
6	HKN/3/81 (1980)	HKN81-03	812	694	8	85.47	14.53
7	ITL/1/66	ITL66-01	825	705	5	85.45	14.55
8	UKG/27/72	UKG72-27	849	725	0	85.39	14.61
9	ROM/1/87	ROM87A01	849	698	0	82.21	17.79
10	ITL/A/89 (1988)	ITL89-0A	820	672	7	81.95	18.05
nt, nucleotides							
*, not a WRLFMD reference number							

cc. Head of Experimental Epidemiology Group  
cc. Head of Vesicular Diseases Group



## Genetic relationship of POR/1/2004 to other SVD viruses

Neighbor-joining tree outgroup-rooted using ITL/1/66 and HKN/19/70. Based on a comparison of complete (or nearly complete) VP1 sequences.