



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). For guidance, see the notes written in blue and the separate document "Help with completing a taxonomic proposal"

Please try to keep related proposals within a single document; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

<b>Code assigned:</b>	<b>2011.016aV</b>	(to be completed by ICTV officers)			
<b>Short title:</b> create species <i>Bovine rhinitis A virus</i> within the genus <i>Aphthovirus</i> , family <i>Picornaviridae</i> (e.g. 6 new species in the genus <i>Zetavirus</i> )					
<b>Modules attached</b> (modules 1 and 9 are required)	1 <input checked="" type="checkbox"/> 6 <input type="checkbox"/>	2 <input checked="" type="checkbox"/> 7 <input type="checkbox"/>	3 <input type="checkbox"/> 8 <input type="checkbox"/>	4 <input type="checkbox"/> 9 <input checked="" type="checkbox"/>	5 <input type="checkbox"/>

**Author(s) with e-mail address(es) of the proposer:**

Nick Knowles ([nick.knowles@iah.ac.uk](mailto:nick.knowles@iah.ac.uk)) on behalf of the *Picornaviridae* Study Group.

**List the ICTV study group(s) that have seen this proposal:**

A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (fungal, invertebrate, plant, prokaryote or vertebrate viruses)

*Picornaviridae* Study Group

**ICTV-EC or Study Group comments and response of the proposer:**

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Date first submitted to ICTV:

Date of this revision (if different to above):

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## MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be “unassigned” within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	<b>2011.016aV</b>	(assigned by ICTV officers)
<b>To create one new species within:</b>		
Genus:	<i>Aphthovirus</i>	Fill in all that apply. • If the higher taxon has yet to be created (in a later module, below) write “ <b>(new)</b> ” after its proposed name. • If no genus is specified, enter “ <b>unassigned</b> ” in the genus box.
Subfamily:	<i>n/a</i>	
Family:	<i>Picornaviridae</i>	
Order:	<i>Picornavirales</i>	
<b>And name the new species:</b>		<b>GenBank sequence accession number(s) of reference isolate:</b>
<i>Bovine rhinitis A virus</i>		JN936206

### Reasons to justify the creation and assignment of the new species:

- Explain how the proposed species differ(s) from all existing species.
  - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria.**
  - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 9

The proposed species “Bovine rhinitis A virus” belongs to the genus *Aphthovirus* and consists of two serotypes, bovine rhinitis A virus 1 (BRAV-1) and BRAV-2, formerly known as bovine rhinovirus (BRV) 1 and BRV-3, respectively. The nearly complete genome sequences of three isolates (two BRAV-1 and one BRAV-2) have been determined and the relationship to the aphthoviruses confirmed (Piccone et al., 2009, 2010). Like many picornaviruses it has not been possible to sequence the very 5' end of the genome.

The genome organization is the same as bovine rhinitis B virus (BRBV) and equine rhinitis A virus (ERAV) and lacks the two extra VPg coding regions possessed by foot-and-mouth disease virus (FMDV).

Genome organization of BRAV:

VPg+5'UTR<sup>IRES-II</sup>[L<sup>pro</sup>/1A-1B-1C-1D-2A<sup>np9p</sup>/2B-2C/3A-3B<sup>VPg</sup>-3C<sup>pro</sup>-3D<sup>pol</sup>]3'UTR-poly(A)

BRAV and BRBV do not form a monophyletic group and are distantly related to each other (Figs. 1 and 2). Nucleotide and amino acid distances are consistent with BRAV being a new species in the genus (Tables 1 and 2). Within the genus *Aphthovirus*, BRAV is distinct from the other three species, FMDV, ERAV and BRBV (Figs. 3 and 4).

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

**References:**

Knowles, N.J. (2005). Molecular identification of all three bovine rhinovirus serotypes as members of the genus Aphthovirus. EUROPIC 2005: XIIIth Meeting of the European Study Group on the Molecular Biology of Picornaviruses, Lunteren, The Netherlands, 23-29th May 2005. Abstract A18.

Piccone, M.E., Kramer, Jr., E.V., Knowles, N.J. and Rieder, A.E. (2009). Sequence analysis of a bovine rhinovirus type 1 strain RS3x. 28th Annual Meeting of the American Society for Virology, The University of British Columbia - Vancouver, BC, 11-15 July 2009. Paper No. 32-8: P. 337.

Piccone, M.E., Wadsworth, J., Kramer, E., Pauszek, S.J., Knowles, N.J. and Rieder, E. (2010). Sequence analysis and molecular features of bovine rhinovirus types 1 and 3 and their taxonomic position in the Aphthovirus genus. EUROPIC 2010: XVI Meeting of the European Study Group on the Molecular Biology of Picornaviruses, St. Andrews, Scotland, 11-16 September 2010.

**Annex:**

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

**Table 1.** Nucleotide and amino acid sequence identities between FMDV strain A24 Cruzeiro and BRBV (BRV-2), BRV types 1 and 3 strains.

Genomic Region	BRV-1 SD-1		BRV-1 RS 3x*		BRV-3 H-1		BRBV (BRV-2) EC 11	
	% ntid	% aa id	% ntid	% aa id	% ntid	% aa id	% ntid	% aa id
5' UTR	72.7†	-	NA	-	56.4‡	-	53.6§	-
Polypeptide	51.7	47.3	51.4	47.6	51.5	47.2	51.7	46.8
LEADER	52.1	44.3	NA	NA	47.8	42.9	46.0	35.5
P1	49.6	44.3	48.5	42.3	49.5	43.5	48.5	43.9
VP4	55.3	52.9	NA	NA	56.1	54.1	56.0	56.0
VP2	51.7	48.1	50.3	46.9	51.9	47.7	49.9	46.1
VP3	52.4	48.4	53.4	48.4	53.3	46.6	51.2	50.7
VP1	41.5	31.1	40.8	30.1	40.0	30.8	41.0	28.6
P2	53.2	47.3	52.2	47.3	51.9	47.0	53.1	47.2
2A	64.8	66.7	61.1	66.7	59.3	66.7	61.1	66.7
2B	43.6	29.9	43.8	29.9	43.0	29.9	43.5	30.5
2C	56.5	53.2	55.1	53.2	55.1	52.9	56.7	53.0
P3	53.6	51.9	53.4	52.2	54.8	52.5	55.2	52.0
3A	32.4	11.1	29.3	13.0	28.8	13.1	27.8	8.7
3B1	37.7	30.4	33.3	30.4	34.8	30.4	46.4	26.1
3B2	47.2	37.5	48.6	37.5	45.8	37.5	51.4	33.3
3B3	50.0	41.7	50.0	41.7	44.4	41.7	55.6	45.8
3C	55.0	54.1	55.0	53.6	56.1	53.6	55.1	51.0
3D	58.6	59.2	58.2	59.9	60.0	60.3	60.9	64.0
3' UTR	45.7	-	40.0	-	45.7	-	28.6	-

\*, based on partial genomic sequences (from VP2 to 3' UTR).

†, based on 171 nt.

‡, based on 558 nt.

§, based on 614 nt.

NA, not available.

**Table 2.** Nucleotide and amino acid sequence identities between BRV-1 strain Sd-1 and BRV-1, BRV-3, BRBV (BRV-2) and ERAV strains.

Genomic Region	BRV-1 RS 3x*		BRV-3 H-1		BRBV (BRV-2) EC 11		ERAV PERV-1	
	% ntid	% aa id	% ntid	% aa id	% ntid	% aa id	% ntid	% aa id
5' UTR	NA	-	92.4†	-	69.5†	-	47.3†	-
Polypeptide	86.3	97.6	81.4	93.1	54.2	52.2	48.0	38.9
LEADER	NA	NA	83.4	92.1	49.7	46.3	46.3	32.2
P1	86.1	98.1	72.9	86.3	50.7	48.3	45.6	35.5
VP4	NA	NA	78.5	94.6	56.8	64.8	50.4	48.8
VP2	87.7	99.5	73.2	86.2	48.7	44.4	47.6	36.5
VP3	86.7	99.1	71.6	85.5	56.6	55.7	49.8	40.6
VP1	83.9	95.7	71.7	84.0	44.5	38.4	37.8	24.9
P2	84.9	98.0	84.6	97.4	58.0	55.5	51.0	45.4
2A	83.3	90.0	86.7	90.0	59.6	73.7	57.4	61.1
2B	84.8	97.6	87.1	98.4	52.4	40.5	43.3	29.9
2C	85.1	98.7	83.5	97.4	60.1	60.5	53.9	50.8
P3	87.3	97.0	87.0	97.4	56.4	55.1	49.6	40.3
3A	85.9	95.4	84.7	95.4	47.7	33.0	32.3	12.8
3B	81.9	95.8	80.6	95.8	54.2	41.7	36.2	17.4
3C	87.4	97.1	86.1	97.6	57.2	59.4	50.7	42.8
3D	87.8	97.4	88.3	97.9	58.3	59.0	51.8	44.6
3' UTR	94.3	-	100.0	-	28.6	-	34.3	-

\*, based on partial genomic sequences (from VP2 to 3' UTR).

†, based on 171 nt.

NA, not available.

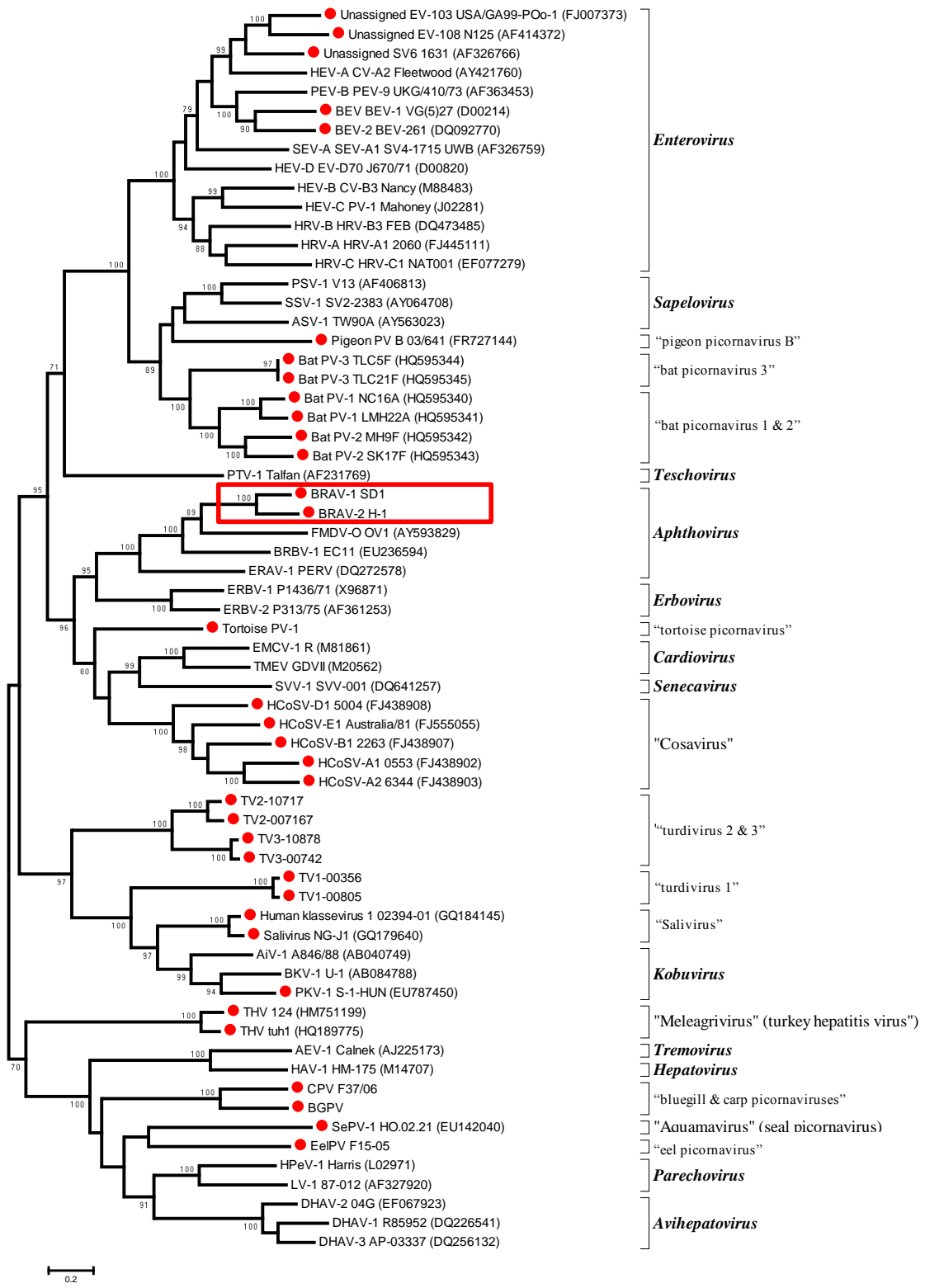


Figure 1. Phylogenetic tree of the P1 capsids of picornaviruses (amino acid Tamura-Nei model, maximum likelihood, 1000 bootstrap replicates using MEGA 5). The species proposed is highlighted in a red box. Red dots mostly indicate new picornaviruses.

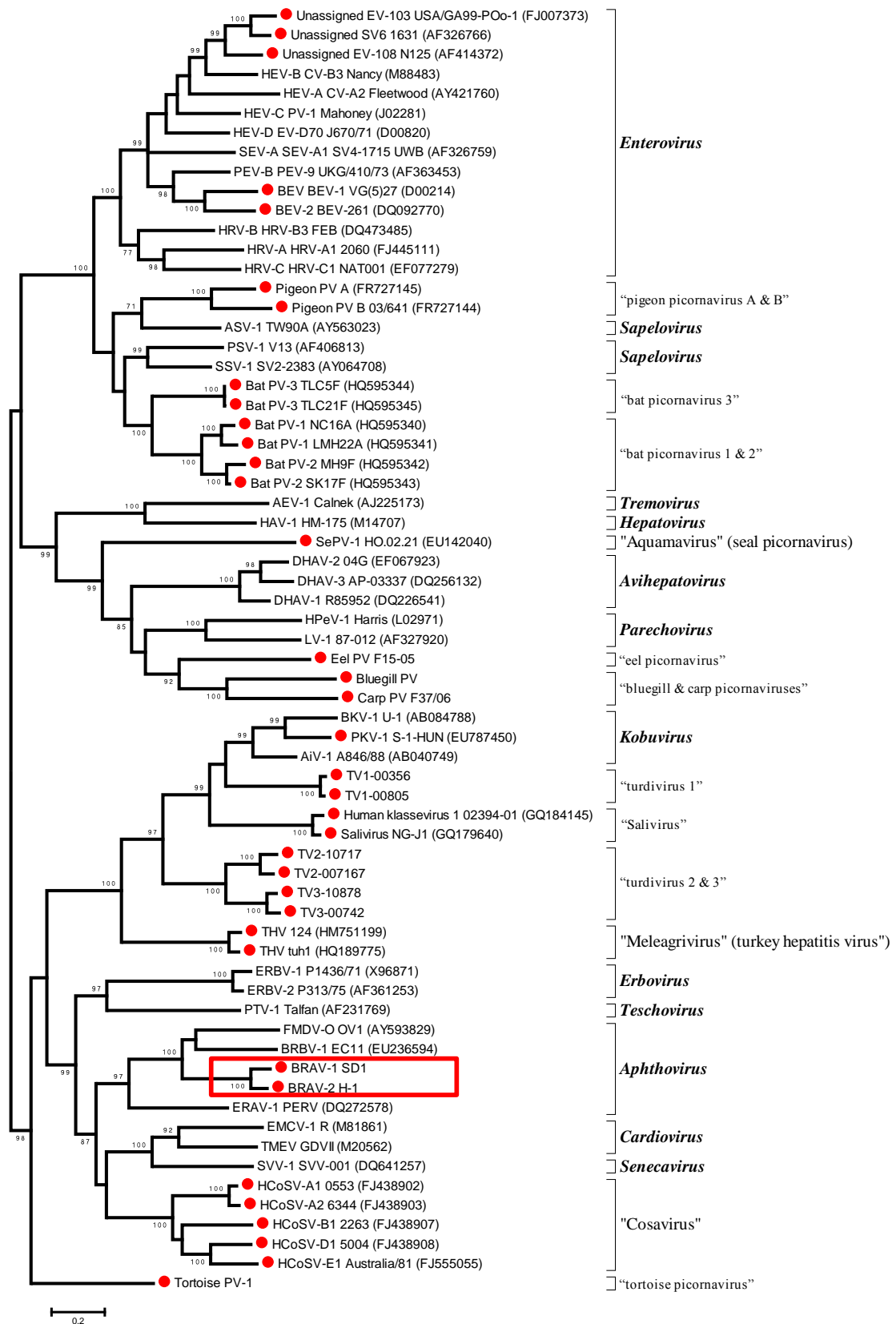


Figure 2. Phylogenetic tree of the 3CD polypeptides of picornaviruses (amino acid Tamura-Nei model, maximum likelihood, 1000 bootstrap replicates using MEGA 5). The species proposed is highlighted in a red box. Red dots mostly indicate new picornaviruses.

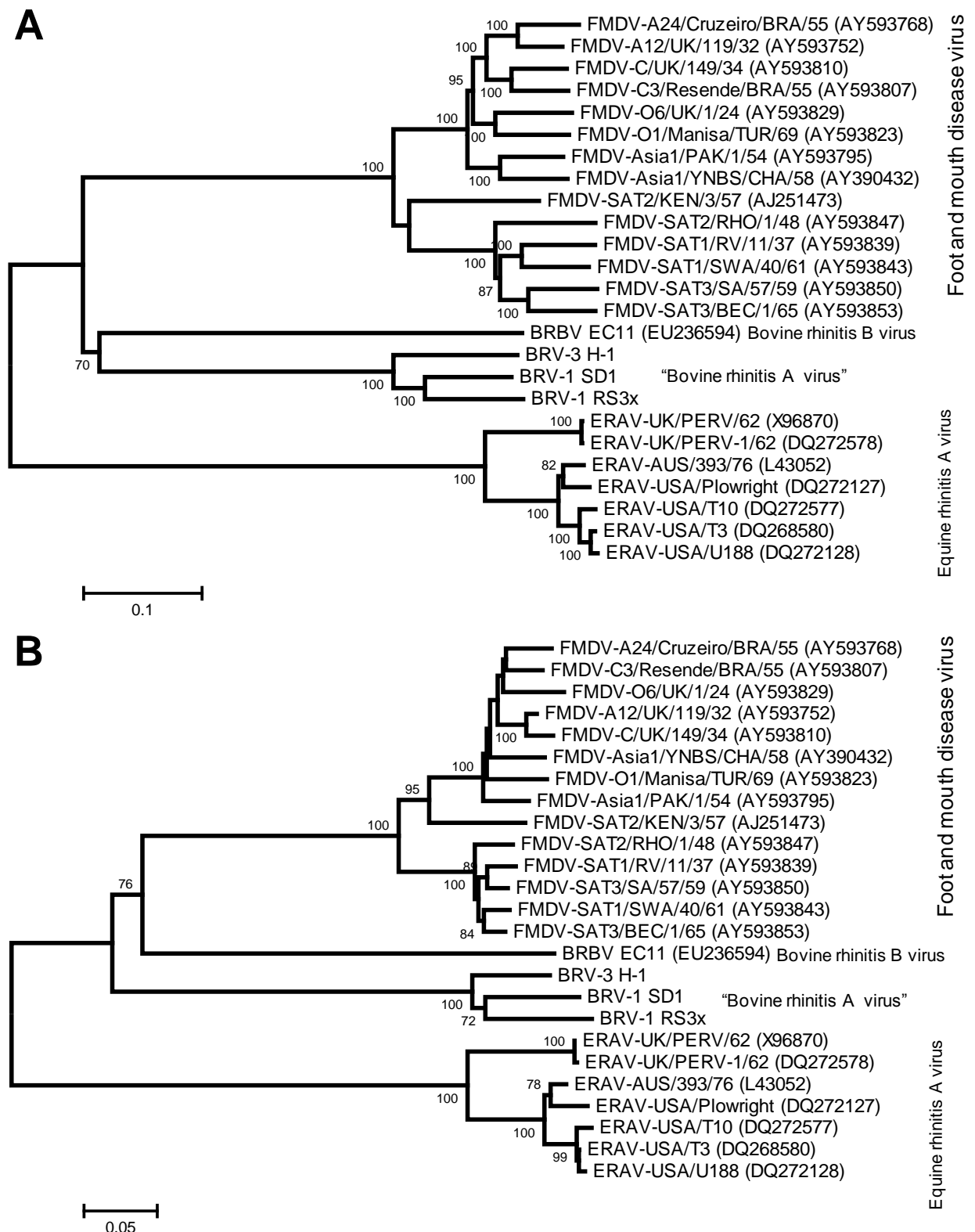
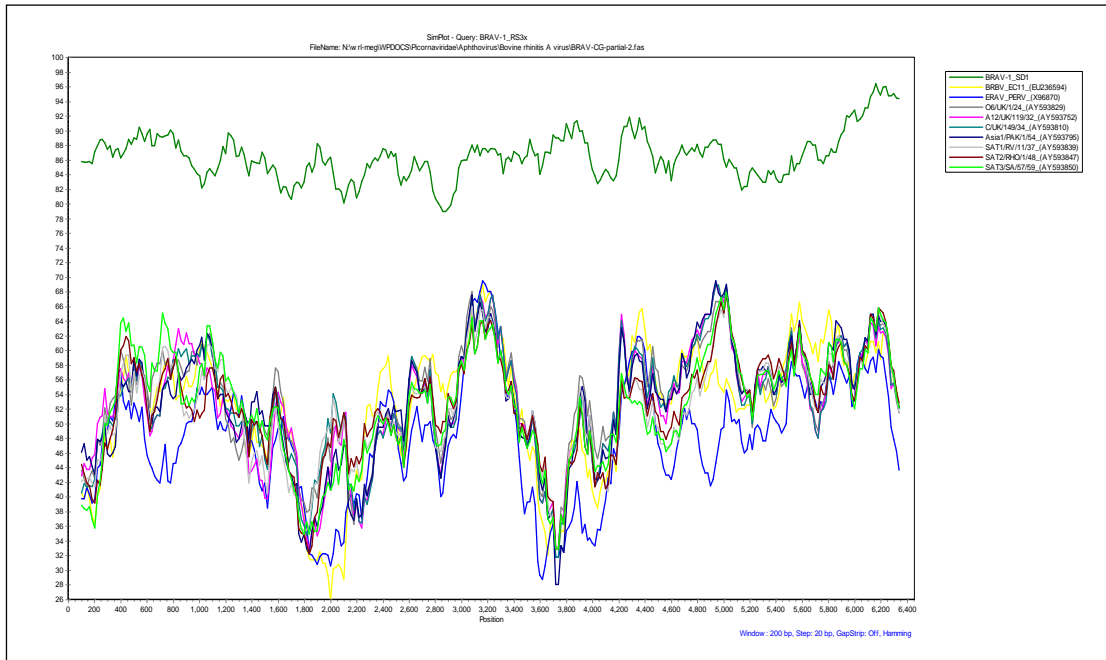


Figure 3. Neighbor-joining phylogenetic tree based on the partial genomic sequence (from VP2 to 3'UTR) and complete 3D polymerase coding sequence (panels A and panel B respectively) showing the relationships between the bovine rhinovirus types 1-3 and other members of the Aphthovirus genus. Numbers at nodes indicate bootstrap percentages obtained using 1000 replicates. The bar indicates genetic distance. The GenBank accession numbers corresponding to the viruses are indicated in parenthesis.

A.



B.

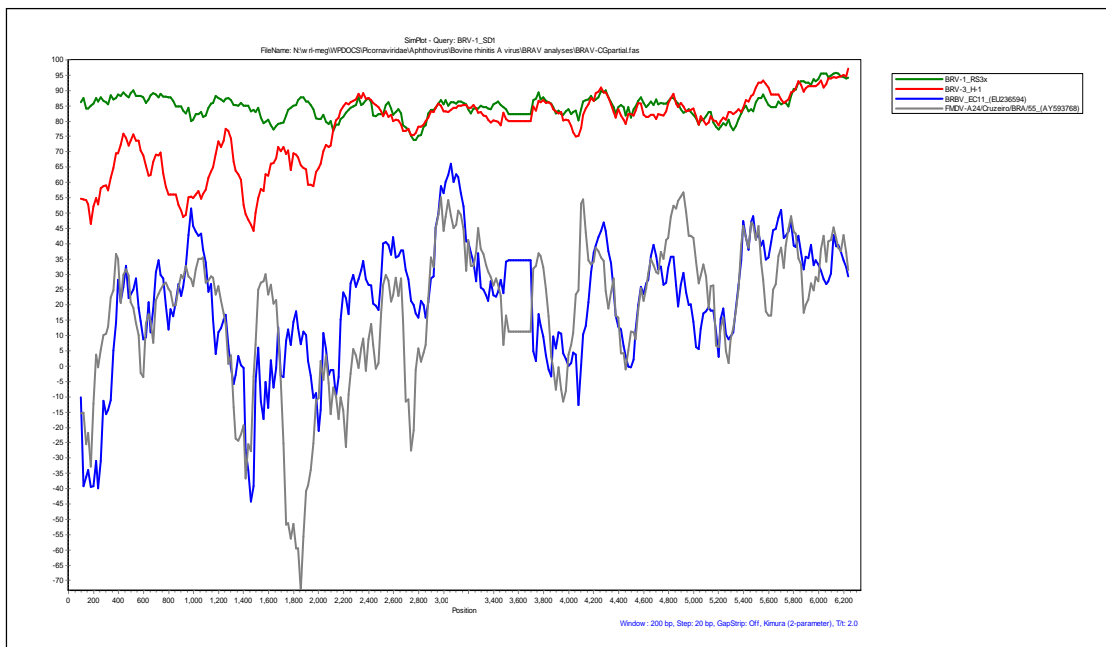


Figure 4. SlimPlot analysis of BRV type 1. (A) The partial genomic sequence (from VP2 to 3'UTR) of BRV-1 RS3x was chosen as query and BRV-1 Sd-1, BRV-2 EC11, ERAV and selected FMDV strains as references. (B) SimPlot comparison of BRV-1 Sd-1 to BRV-1 RS3x, BRV-3 H-1, BRV-2 EC11 and FMDV A24 Cruzeiro. The nucleotide sequences were analyzed in a window of 200 nt and steps of 20 nt between points. GenBank accession numbers are indicated in parenthesis.