This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

Code(s) assigned:	***2008.123-126V***	(to be completed by ICTV officers)

Short title: create genus Nebovirus (type species Newbury-1 virus) in the family Caliciviridae
(e.g. 6 new species in the genus *Zetavirus*; re-classification of the family *Zetaviridae* etc.)

Modules attached
(please check all that apply):

1 ☐ **2** ☐ **3** ☐ **4** ☐ **5** ☐
6 ☐ **7** ☐

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

Marion Koopmans

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

Study group *Caliciviridae*, with input from Dr. Linda Saif and Dr Janice Bridger JBridger@RVC.AC.UK, saif.2@osu.edu; with confirmation of the final genus name from the new SG Chairman, Ian Clarke (inc@soton.ac.uk).

MODULE 4: <u>**NEW GENUS**</u>

(if more than one genus is to be created, please complete additional copies of this section)

Code	***2008.123V***	(assigned by ICTV officers)

To create a new genus assigned as follows:

Subfamily:	
Family:	***Caliciviridae***
Order:	

Fill in all that apply. Ideally, a genus should be placed within a higher taxon, but if not put “unassigned” here.

Code	***2008.124V***	(assigned by ICTV officers)

To name the new genus: ***Nebovirus***

Code	***2008.125V***	(assigned by ICTV officers)

To assign the following as species in the new genus:

Newbury-1 virus

comprising the following enteropathic bovine calicivirus isolates:

Newbury-1 virus, Bo/BV/Newbury-1/1976/UK (DQ013304)(Oliver et al., 2006),
BEC-NB, Bo/BV/BEC-NB/1980/US ((NC_004064)(Smiley et al, 2002)]

Code	***2008.126V***	(assigned by ICTV officers)

To designate the following as the type species in the new genus:
Newbury-1 virus

Argument to justify the creation of a new genus

Viruses detected in calf feces in the UK and in the US have been characterized as caliciviruses. In the UK, the Newbury 1 virus was originally identified in a stool sample taken in 1976 from a calf with diarrhea by its calicivirus-like appearance in the electron microscope (Woode and Bridger, 1978). Subsequent studies, showed that Newbury 1 was pathogenic for calves and serologically unrelated to other caliciviruses, including the bovine norovirus Newbury2, (Bridger et al, 1984; Oliver et al., 2007), had a particle diameter of 36.6nm, a buoyant density of 1.34 g cm $^{-3}$ and possessed a single major polypeptide (Dastjerdi et al., 2000). Nebraska virus was originally detected by electron microscopy of feces from a diarrheic calf in Nebraska, US, in 1980. The first full genome characterization was published in 2002 showing that the Nebraska strain genomic organization is similar to that of viruses in the genera *Sapovirus* and *Lagovirus*, but by phylogenetic analysis based on the major capsid protein sequence, it separates as a new branch within *Caliciviridae*, sharing only 14.7-26.7% amino acid identities with the other four genera within the *Caliciviridae*. Likewise analysis of the other major viral proteins reveals low percent identities (Annex) (Smiley et al., 2002). The full genome sequence of Newbury 1 virus was published in 2006, showing high sequence homology across the genome between Newbury-1 and Nebraska virus (Oliver et al, 2006). Further strains identified in 2000, one from the US and nine from the UK, all clustered with the Nebraska and Newbury1 viruses based on partial genome sequence analysis. Phylogenetic clustering based on full genome sequences sets Newbury1 and the Nebraska viruses apart on a separate branch at similar distances as viruses belonging to the other genera within the family (Farkas et al., 2008).

Origin of the new genus name: Several names have been proposed and used in the literature, referring to the bovine enteric caliciviruses, Newbury1 and BEC-NB / Nebraska. The names of the other genera in the genus refer to historic type strains (Noro, Sapo), symptoms (Vesi), or host (lago), and therefore do not offer an unambiguous framework. The name chosen, Nebovirus (which could represent both Newbury1 and Nebraska) was thought preferable to Becovirus, since there are other bovine enteric caliciviruses.

Argument to justify the choice of type species:
This was the first strain that was identified and described

Species demarcation criteria in the genus:

Species demarcation criteria in the genus:

At present there is insufficient data to define demarcation criteria.

References:

Woode G and Bridger J. Isolation of small viruses resembling astroviruses and caliciviruses from acute enteritis of calves. Journal of Medical Microbiology 1978;11: 441-452

Bridger JC, Hall GA, Brown JF. Characterization of a calici-like virus (Newbury agent) found in association with astrovirus in bovine diarrhea. Infect Immun. 1984 Jan;43(1):133-8.

Dastjerdi A.M, Snodgrass D R, Bridger, J C. Characterisation of the bovine enteric calici-like virus, Newbury agent 1. FEMS Microbiology Letters 2000, 192 125-131.

Smiley JR, Hoet AE, Tråvén M, Tsunemitsu H, Saif LJ. Reverse transcription-PCR assays for detection of bovine enteric caliciviruses (BEC) and analysis of the genetic relationships among BEC and human caliciviruses. J Clin Microbiol. 2003 Jul;41(7):3089-99.

Smiley JR, Chang KO, Hayes J, Vinjé J, Saif LJ. Characterization of an enteropathogenic bovine calicivirus representing a potentially new calicivirus genus. J Virol. 2002 Oct;76(20):10089-98.

Oliver SL, Asobayire E, Dastjerdi AM, Bridger JC. Genomic characterization of the unclassified bovine enteric virus Newbury agent-1 (Newbury1) endorses a new genus in the family Caliciviridae. Virology. 2006 Jun 20;350(1):240-50. Epub 2006 Mar 30.

Oliver S L, Asobayire E, Charpilienne A, Cohen J Bridger, JC. 2007. Complete genomic characterisation and antigenic relatedness of genogroup III, genogroup 2 bovine noroviruses. 2007 Arch Virol 152, 257-272.

Farkas et al. Characterization of a rhesus monkey calicivirus representing a new Genus of *Caliciviridae.* J. Virol 2008;82:5408-5416 that provide the support for above proposal.

Annexes:

1. Data from Smiley JR, Chang KO, Hayes J, Vinjé J, Saif LJ. Characterization of an enteropathogenic bovine calicivirus representing a potentially new calicivirus genus. J Virol. 2002 Oct;76(20):10089-98.
2. Data from Oliver SL, Asobayire E, Dastjerdi AM, Bridger JC. Genomic characterization of the unclassified bovine enteric virus Newbury agent-1 (Newbury1) endorses a new genus in the family Caliciviridae. Virology. 2006 Jun 20;350(1):240-50. Epub 2006 Mar 30.
3. *Data from* Farkas et al. Characterization of a rhesus monkey calicivirus representing a new Genus of *Caliciviridae.* J. Virol 2008;82:5408-5416 that provide the support for above proposal.

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From: Smiley JR, Chang KO, Hayes J, Vinjé J, Saif LJ. Characterization of an enteropathogenic bovine calicivirus representing a potentially new calicivirus genus. J Virol. 2002 Oct;76(20):10089-98.

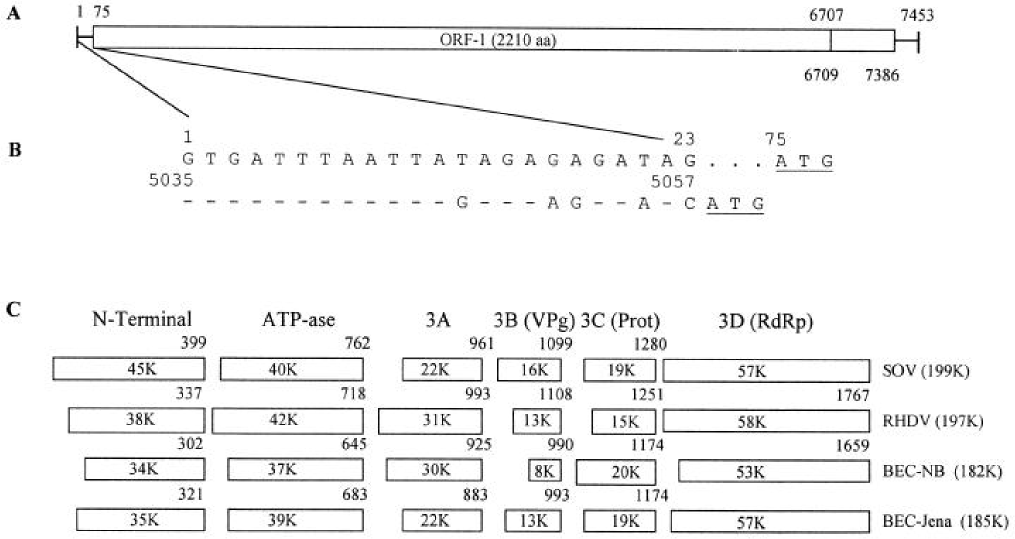

FIG. 1. Genome organization, 5′ UTR and subgenomic conserved sequences, and predicted ORF-1 NS proteins of the BEC-NB strain. (A) ORFs and UTR sequences in the complete 7,453-bp genome. (B) Locations and sequence conservation of the 5′ UTR (nucleotides 1 to 23) and subgenomic (nucleotides 5035 to 5057) sequence segments in BEC-NB. Only differences are indicated. (C) Predicted ORF-1 NS proteins of BEC-NB and the NLV BEC-Jena based on sequence comparison with maps of characterized cleavage products of a lagovirus, RHDV, and a human NLV, SOV. The calculated protein molecular weights are shown, and the COOH-terminal amino acid residue in the predicted virus ORF-1 sequence is shown above each box.

From: Smiley JR, Chang KO, Hayes J, Vinjé J, Saif LJ. Characterization of an enteropathogenic bovine calicivirus representing a potentially new calicivirus genus. J Virol. 2002 Oct;76(20):10089-98.

Percent amino acid identity of BEC-NB virus with other caliciviruses in regions aligned for phylogenetic comparison[a]

Genus	**Virus**[b]	**% Identity**					
		ORF-1 NS	**2C helicase**	**3C protease**	**RdRp**	**VP1**	**VP2**[c]
SLV	Manchester	21.1	37.4	35.4	33.0	21.0	16.9
	PEC	21.7	40.0	30.7	34.8	19.9	13.9
NLV	Jena	15.0	31.2	14.2	29.8	14.7	17.0
	Norwalk	14.7	31.2	17.5	30.7	15.7	15.5
	SOV	13.8	31.9	16.2	29.8	15.4	16.1
	Hawaii	14.3	29.4	14.9	27.5	14.6	12.9
	Lordsdale	14.1	29.4	14.2	28.4	14.8	17.3
Vesivirus	VESV-A48	21.5	40.6	30.4	32.5	17.8	16.2
	SMSV-1	22.3	41.9	30.4	33.0	17.8	16.2
	PAN-1	22.0	40.6	32.0	32.1	17.8	15.3
	WCV	22.3	41.2	30.4	33.0	18.2	15.3
	FCV-F4	21.8	40.6	25.0	34.8	17.8	16.8
	FCV-F9	22.6	40.6	24.2	34.8	18.0	15.0
Lagovirus	EBHSV	21.9	37.8	24.0	41.0	26.6	20.0
	RHDV	21.6	36.5	22.4	40.5	26.7	21.2

[a] See Table 1 and footnotes for descriptions of aligned regions.

[b] EBHSV, European brown have syndrome virus; VESV, vesicular exanthema of swine virus; SMSV, San Miguel sea lion virus; WCV, walrus calicivirus.

[c] Sequence identities calculated for complete VP2 ORF alignment.

J Virol. 2002 October; 76(20): 10089–10098.
doi: 10.1128/JVI.76.20.10089-10098.2002.

Data from: Oliver SL, Asobayire E, Dastjerdi AM, Bridger JC. Genomic characterization of the unclassified bovine enteric virus Newbury agent-1 (Newbury1) endorses a new genus in the family Caliciviridae. Virology. 2006 Jun 20;350(1):240-50. Epub 2006 Mar 30.

Table 1.
Bo/Newbury1/1976/UK compared to representative viruses for the 4 genera in the family *Caliciviridae*

Genus	**Virus**	**Genome length (nt)**	**Length of the 5′ UTR (nt)**	**Length of the 3′ UTR (nt)**	**Number of ORFs**	**ORF overlap (nt)**		**Length of ORF (nt[a] [translated aa])**		
						1–2	**2–3**	**ORF1**	**ORF2**	**ORF3**
Nebovirus (proposed)	Newbury1	7454	75	67	2	1[b]	NA	6633 [2210][c]	678 [225][d]	NA
	NB	7453	74	67	2	1[b]	NA	6633 [2210][c]	678 [225][d]	NA
Lagovirus	RHDV-FRG	7437	9	59	2	8	NA	7035 [2344][c]	354 [117][d]	NA
	EBHSV-GD	7442	8	92	2	20	NA	7005 [2334][c]	345 [114][d]	NA
Sapovirus	Manchester	7431	12	82	2 (3)[e]	4	NA	6843 [2280][c]	498 [165][d]	NA
	Dresden	7429	12	80	2 (3)[e]	4	NA	6843 [2280][c]	498 [165][d]	NA
	Cowden	7320	9	55	2	4	NA	6765 [2254][c]	495 [164][d]	NA
Vesivirus	VESV-48	8284	19	179	3	5[b]	4	5646 [1881][f]	2106 [701][g]	333 [110][d]
	SMSV-1	8284	19	182	3	5[b]	4	5640 [1879][f]	2109 [702][g]	333 [110][d]
	FCV-CFI/68	7677	19	43	3	2[b]	4	5289 [1762][f]	2007 [668][g]	330 [109][d]
	FCV-Urbana	7683	19	46	3	2[b]	4	5292 [1763][f]	2007 [668][g]	321 [106][d]
	CCV	8513	11	235	3	2[b]	4	5790 [1929][f]	2076 [691][g]	402 [133][d]
Norovirus	Norwalk	7654	4	66	3	17	1	5370 [1789][f]	1593 [530][h]	639 [212][d]
	Southampton	7708	4	78	3	17	1	5367 [1788][f]	1641 [546][h]	636 [211][d]
	SMV	7537	4	45	3	20	1	5100 [1699][f]	1629 [542][h]	780 [259][d]
	Lordsdale	7555	4	45	3	20	1	5100 [1699][f]	1620 [539][h]	807 [268][d]
	Newbury2	7311	21	43	3	14	209 (11)[i]	5055 [1684][f]	1569 [522][h]	849 [282][d]
	Jena	7338	21	67	3	14	11	5043 [1680][f]	1560 [519][h]	672 [223][d]

See Materials and methods for references and accession numbers. NB: Nebraska virus; RHDV: Rabbit Hemorrhagic Disease Virus; EBHSV: European Brown Hare Syndrome Virus; VESV: Vesicular Exanthema of Swine Virus; SMSV: San Miguel Sea Lion Virus; FCV: Feline Calicivirus; CCV: Canine Calicivirus; SMV: Snow Mountain Virus. nt—nucleotides; UTR—Untranslated Region; ORF—Open Reading Frame; aa—amino acids.[a]

termination codon.

[b] ORF1 and 2 do not overlap but are separated by the number of nucleotides shown.

Data from Farkas et al. Characterization of a rhesus monkey calicivirus representing a new Genus of *Caliciviridae.* J. Virol 2008;82:5408-5416 that provide the support for above proposal.

FIG. 3. Unrooted phylogenetic trees based on amino acid sequence alignments of CV NTPase (A), polymerase (B), and VP1 (C). Trees were constructed by the neighbor-joining clustering method of MEGA 3.1, with Poisson distance calculations. The scale bars represent the phylogenetic distances expressed as units of amino acid substitutions per site. The confidence values of the internal nodes were obtained by performing 1,025 bootstrap analyses. Trees constructed for the NS polyprotein and protease exhibited similar topologies (data not shown). BEC: bovine enteropathogenic calicivirus (for “Becovirus”, read “Nebovirus”, the name currently proposed for the genus incorporating Newbury-1 virus).