TAXONOMIC PROPOSALS 2000

REOVIRIDAE **PROPOSAL**

2002.V127.02	To remove the species *Kadipiro virus* (KDV) and *Banna virus* (BAV), corresponding to the subgroup B, from the genus *Coltivirus*.
2002.V128.02	To create a new genus to accommodate the two species *Kadipiro virus* (KDV) and *Banna virus* (BAV).
2002.V129.02	To name this newly created genus *Seadornavirus*.
2002.V130.02	To designate *Kadipiro virus* (KDV) as type species of the newly created genus Seadornavirus.
2002.V131.02	To designate the two species *Kadipiro virus* (KDV) and *Banna virus* (BAV) as species members of the genus Seadornavirus.
2002.V132.02	To designate HN59, HN131, HN191, HN295 as isolates of a tentative species of the genus *Seadornavirus*.

1. Proposal

To subdivide the genus *Coltivirus* into two genera. The current Subgroup A viruses (two species: *Colorado tick fever virus* (CTFV) and *Eyach Virus* (EYAV)) will remain in the genus *Coltivirus*. The Subgroup B viruses (two species: *Kadipiro virus* (KDV) and *Banna virus* (BAV)) will be moved to a newly created genus called *Seadornavirus* (sigla from '**S**outh **e**astern **A**sia **do**deca **RNA** **virus**es').

2. Purpose

The complete genomes of KDV and BAV have recently been sequenced (Attoui et al 2000). The sequence of the polymerase protein, which is relatively highly conserved within the members of the *Reoviridae*, was compared to that of CTFV (the *Coltivirus* type species). It was found that the group B viruses contain only approximately 10% amino acid identity with CTFV in the polymerase protein. This low level of sequence homology was also typical when comparisons were made of other proteins from these viruses (see taxonomy report for the *Reoviridae*, Mertens et al 1999).

Comparisons of the polymerase protein from the other genera currently recognised within the family *Reoviridae,* for which the relevant sequences are available (*Othoreovirus*, *Orbivirus*, *Rotavirus*, *Phytoreovirus*, *Oryzavirus* and *Fijivirus*), all showed at least 10% amino acid sequence homology and in some cases as much as 20% sequence homology (*Phytoreovirus* and *Rotavirus,* group A).

The two virus species BAV and KDV share groups of three base pairs, within the conserved terminal regions at either end of the RNA genome segments. These sequences are not found in CTFV. BAV and KDV have been isolated from mosquitoes (*Culex* species), while CTFV was isolated from ticks. The group A coltiviruses have been isolated from North America and Europe while BAV, KDV and related viruses have

only been isolated in Southeast Asia (Indonesia and China). The total genome size of KDV and BAV is 20,682 base pairs. This compares with an estimated genome size for CTFV of 28,530 base pairs. The difference in total size, representing approximately 38% of the entire BAV or KDV genome, is significantly larger than has been observed within any of the other genera of the *Reoviridae*.

BAV and KDV both contain 12 genome segments (like CTFV) however, the data briefly described above indicate that their classification within the genus *Coltivirus* is not valid.

3. Taxonomic situation

List of species in the genus *Coltivirus*

Species in the genus {vector species: host} (serotypes)	sequence accession numbers [ ]	assigned abbreviations ( )
Colorado tick fever virus {Ixodidae ticks : Rodents, Humans } >22 isolates reported: (2 serotypes)		(CTFV)
Colorado tick fever virus	segment 1: [AF134529] segment 9: [AF007172] segment 10:[AF000720] segment 11: [U72694] segment 12: [U5322]	(CTFV)
coltivirus S6-14-03		(CTFV S6-14-03)
Eyach virus {Ixodidae ticks : Possibly Humans } Eyach virus (Germany)		(EYAV) (EYAV-Gr)
Eyach virus (France -577) Eyach virus (France -578)	segment 12: [AF007185]	(EYAV-Fr577) (EYAV-FR578)

List of species in the genus *Seadornavirus*

Species in the genus {vector species: host} (serotypes)	sequence accession numbers [ ]	assigned abbreviations ( )
Kadipiro virus {Culex mosquitoes} Kadipiro virus (Java-7075)	segment 1: [AF133429] segment 2: [AF134509] segment 3: [AF134510] segment 4: [AF134511] segment 5: [AF134512] segment 6: [AF134513] segment 7: [AF052023] segment 8: [AF052022] segment 9: [AF052021] segment 10: [AF052020] segment 11: [AF052019] segment 12: [AF019909]	(KDV) (KDV- Ja7075)
Banna virus {Culex and Anopheles mosquitoes : Humans, other vertebrates} Banna virus (China) Banna virus (Indonesia-6423)	segment 1:[AF134522] segment 2:[AF134523] segment 3:[AF134524] segment 1: [AF133430] segment 2 [AF134514] segment 3: [AF134515] segment 4: [AF134516] segment 5: [AF134517] segment 6: [AF134518] segment 7: [AF052018] segment 7: [AF052018] segment 8: [AF052017] segment 9: [AF052016] segment 10: [AF052015] segment 11: [AF052014] segment 12: [AF019908]	(BAV) (BAV-Ch) (BAV-In6423)

Banna virus (Indonesia-6969) Banna virus (Indonesia-7043)		(BAV-In6969) (BAV-In7043)

Tentative species and unassigned viruses within the genus

Chinese isolates that may belong to the *Banna virus* species based on serological and electrophoretic profile analyses

HN59,   HN131,   HN191,   HN295

PHYLOGENETIC TREES

Figure 1: Phylogenetic tree of the amino acid sequences of the polymerase protein of some representative members of the different genera of the family *Reoviridae*.
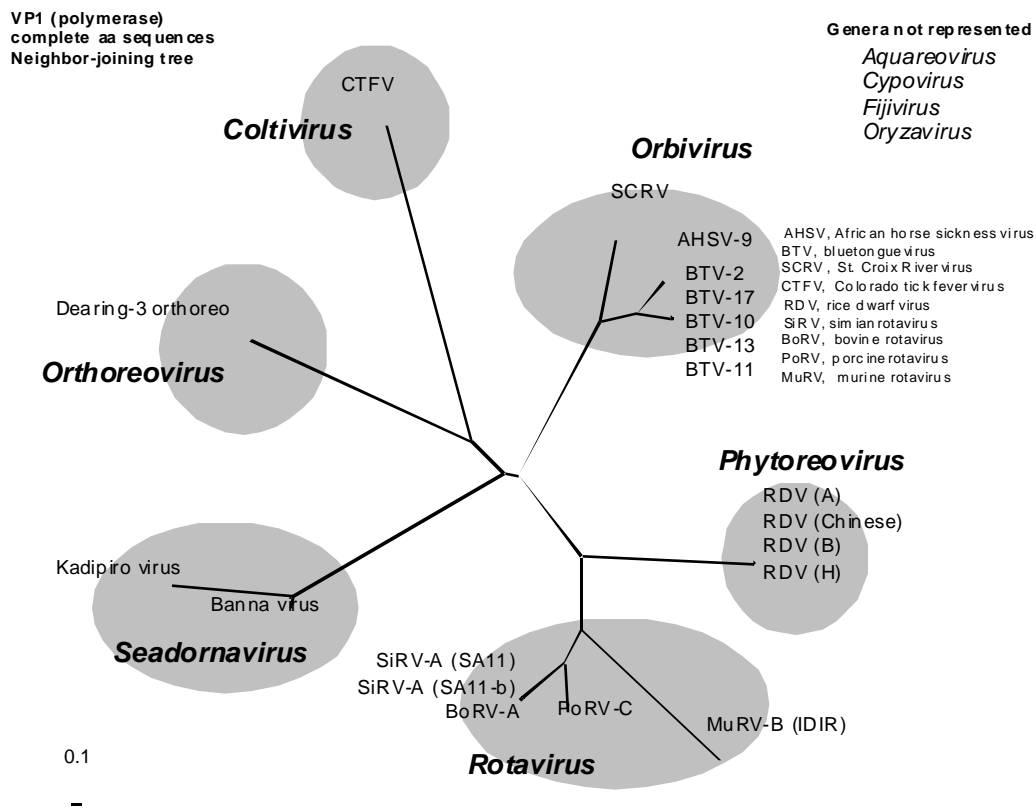
VP1 (polymerase)
complete aa sequences
Neighbor-joining tree

Genera not represented
Aquareovirus
Cypovirus
Fijivirus
Oryzavirus

CTFV

Coltivirus

Orbivirus

SCRV

AHSV-9
BTV-2
BTV-17
BTV-10
BTV-13
BTV-11

AHSV, African horse sickness virus
BTV, bluetongue virus
SCRV, St. Croix River virus
CTFV, Colorado tick fever virus
RDV, rice dwarf virus
SiRV, simian rotavirus
BoRV, bovine rotavirus
PoRV, porcine rotavirus
MuRV, murine rotavirus

Dearing-3 orthoreo

Orthoreovirus

Phytoreovirus

RDV (A)
RDV (Chinese)
RDV (B)
RDV (H)

Kadipiro virus
Banna virus

Seadornavirus

SiRV-A (SA11)
SiRV-A (SA11-b)
BoRV-A
PoRV-C
MuRV-B (IDIR)

0.1

Rotavirus

Figure 1: Phylogenetic tree for the *Reoviridae* RNA polymerase. Amino acid sequences derived from the nucleotide sequence of the relevant genome segment (segment 1 in each case, except for

genome segment 4 of rice ragged stunt virus - *Oryzavirus)*, were aligned by using the CLUSTALW 1.60 program (Higgins & Sharp, 1989). The Neighbour-joining tree was prepared using Clustal X (Thompson et al., 1997), allowing for multiple substitutions and ignoring gaps and drawn with TreeView 1.5 (Page, 1996). Strains of viruses and their sequences used: *Orthoreovirus* - Mammalian orthoreovirus subgroup 1, serotype Dearing 3 (MRV-3) M24734; Orbivirus - African horse sickness virus serotype 9 (AHSV-9) U94887; bluetongue virus, serotype 2 (BTV-2) L20508; bluetongue virus, serotype 10 (BTV-10) X12819; bluetongue virus, serotype 11 (BTV-11) L20445; bluetongue virus, serotype 13 (BTV-13) L20446; bluetongue virus, serotype 17 (BTV-17) L20447. *Rotavirus* - bovine rotavirus, Group A (A-BoRV) J04346; simian rotavirus, Group A (SA11 A-SiRV) AF015955; murine rotavirus IDIR, Group B (B-MuRV) M97203; porcine rotavirus, Group C (C-PoRV) M74216; *Fijivirus*- Nilaparvata lugens reovirus Izumo strain (NLRV) D49693; Phytoreovirus - rice dwarf virus, Chinese strain (RDV) U73201; rice dwarf virus, strain H (RDV) D10222; rice dwarf virus (RDV) D90198; *Oryzavirus* - rice ragged stunt virus, Thai strain (RRSV) U66714. *Coltivirus* - Colorado tick fever virus (CTFV): [AF134529] . *Seadornavirus* – Banna Virus (BAV-In6423) [AF133430] and Kadipiro virus (KDV- Ja7075) [AF133429]. No polymerase sequences have either been identified or are currently available for any cypoviruses, aquareoviruses or any of the unclassified viruses of invertebrates.