

Template for Taxonomic Proposal to the ICTV Executive Committee Creating Species in an existing genus

Code[†] **FT2003.102I.01** To designate the following viruses as species in the genus:

Betatetravirus

belonging to the family[°] : ***Tetraviridae***

Antheraea eucalypti virus (AeV)

[†] Assigned by ICTV officers

[°] leave blank if inappropriate or in the case of an unassigned genus

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Chair *Tetraviridae* SG

New Taxonomic Order

Family

Tetraviridae

Genus

Betatetravirus

Type Species

Species in the Genus

Thosea asigna virus (TaV)

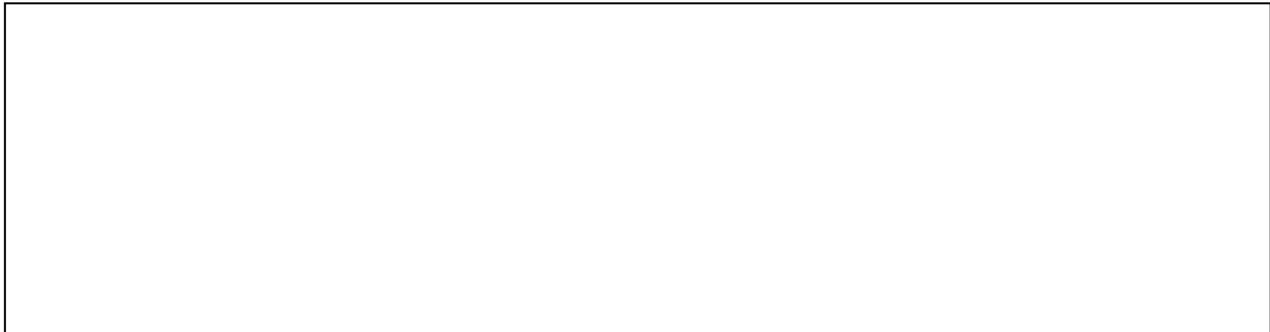
Dasychira pudibunda virus (DpV)

Tentative Species in the Genus

Unassigned Species in the family

Argumentation to justify the designation of new species in the genus

Species demarcation criteria in the genus



Argumentation to justify the designation of new species in the genus

AeV was the first tetravirus described (Grace and Mercer, 1968) and was listed as a member of the genus until the VIth report. In the VIIth report, it was revised to be listed as an alternative name for N β V, the type member. Although the reasons for this are unclear, it appears to have been because of their immunological relationship and because N β V is able to infect *A. helena*, a relative of *A. eucalypti*. Neither of these grounds represents a compelling argument that these viruses are identical, and so it is proposed to restore AeV as a distinct member of the genus, until its complete nucleotide sequence is available to allow a definitive analysis of their relationship.

The complete genome sequence of EeV has been determined since the preparation of the VIIIth report (Zeddarn *et al.*, in preparation; see Gorbalenya *et al.*, 2002). The biophysical and genome organisation and sequence characteristics of the virus show it to be very closely related to SaV/TaV. In particular, EeV shows the following characteristics:

positive sense ssRNA of 5698 nts (vs 5715 for SaV/TaV)

icosahedral/spherical particles (about 40nm in diameter)

major capsid protein of 60 kDa and a smaller capsid protein of <10kDa produced by processing of the larger capsid precursor.

genome very similar (68% nucleotide sequence identity) to that of SaV/TaV, comprised of two distinct ORFs that overlap by approximately 500 bases, organised with the ORF encoding the non-structural proteins towards the 5' end of the genome (ORF 1) and the structural proteins encoded by the ORF at the 3' end of the genome (ORF2).

The deduced amino acid sequences of ORF1 is closely related to the predicted SaV/TaV replicase (68% amino acid sequence identity) and contains core motifs for the RNA polymerase in the most conserved regions; as for the SaV/TaV replicase and in contrast to the HaSV and N β V replicases, no RNA helicase or methyltransferase motifs were identified.

Coding sequence for the capsid proteins is a close homolog (84% amino acid sequence identity) of, and is predicted to have a similar expression strategy to, the capsid gene of SaV/TaV.

List of created Species in the genus

The recognised members of the *Betatetravirus* genus will comprise the species as shown below. *Nudaurelia β virus* remains the type member. Official virus species names are in italics. Tentative virus species names, alternative names(), strains, or serotypes are not italicized. Virus names, genome sequence accession numbers [], and assigned abbreviations () are:

<i>Dasychira pudibunda virus</i>			(DpV)
	(<i>Calliteara pudibunda virus</i>)		(CpV)
<i>Darna trima virus</i>			(DtV)
<i>Euprosterina elaeasa virus</i>		[AF461742]	(EeV)
<i>Nudaurelia capensis β virus</i>		[AF102884]	(NβV)
<i>Antheraea eucalypti virus</i>			(AeV)
<i>Philosamia cynthia x ricini virus</i>			(PxV)
<i>Providence virus</i>		[AF548354]	(PrV)
<i>Pseudoplusia includens virus</i>			(PiV)
<i>Thosea asigna virus</i>		[AF82930]	(TaV)
	(<i>Setothosea asigna virus</i>)		(SaV)
<i>Trichoplusia ni virus</i>			(TnV)

References

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Annexes: