

## Taxonomic Proposals from the ICTV *Dicistroviridae* Study Group

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- 2002.I095.04: To create a new floating genus closely related to the family *Dicistroviridae*
- 2002.I096.04: To name this new genus *Iflavirus*
- 2002.I097.04: To assign the species *Infectious flacherie virus* (IFV) as type species for the *Iflavirus* genus
- 2002.I098.04: To assign *Sacbrood virus* (SBV) and *Perina nuda virus* (PnV) as species in the genus *Iflavirus*

### 1.1 Purpose

Since the preparation of the VIIIth Report the complete genome sequence of sacbrood virus (SBV) and *Perina nuda* picorna-like virus (PnPV) have been published (Ghosh *et al.*, 1999; Wu *et al.*, 2002). The sequence data have shown that the genome of these viruses encode a single polyprotein, with the sequences encoding the structural proteins located at the 5' end of the genome and those encoding the non-structural proteins located at the 3' end of the genome. This genomic organisation is identical to that of another insect virus namely, Infectious flacherie virus (Isawa *et al.*, 1998) (IFV) of silkworms, which along with SBV were classified as unclassified viruses in the VIIIth Report

The sequence and biophysical analyses of IFV, SBV and PnPV have shown that these viruses share the following characteristics:

- icosahedral/spherical particles (about 30nm in diameter)
- positive sense ssRNA of around 10kb, polyadenylated at the 3' end
- genome comprised of a single ORF encoding the non-structural proteins towards the 3' of the genome and the structural proteins encoded towards the 5' end of the genome.
- 3 major capsid proteins of between 25 and 35 kDa. IFV and PnPV also contain a smaller capsid protein of around 8kDa. When present the smaller capsid protein is encoded between the first and second coat-proteins in the capsid-coding region of the polyprotein (coat proteins designated in the order CP1, CP2, CP3 in the NH<sub>2</sub>-COOH direction).
- The deduced amino acid sequences of the non-structural proteins contain core motifs for the RNA helicase, cysteine protease and the RNA polymerase.

The above characteristics are very similar to those of the picornaviruses – particularly in the arrangement of the genome. The absence of two distinct ORFs in the genome clearly separates the the IFV/PnPV/SBV group from the dicistroviruses. However, the genomic location of the VP4 coding sequence is a feature shared with the dicistroviruses and clearly separates the IFV/PnPV/SBV group from the picornaviruses. In many respects, the IFV/PnPV/SBV appear to be a sister group to both the picornaviruses and the dicistroviruses.

However, phenetic analyses of the conserved helicase and RdRp domains of viruses in the putative “Picorna-like virus superfamily” (i.e. picornaviruses, dicistroviruses, comoviruses, sequiviruses and IFV/PnPV/SBV) (Leat *et al.*, 2000; Wu *et al.*, 2002) show that:

- IFV, PnPV and SBV are distantly related to each other but form a monophyletic lineage

- IFV, PnPV and SBV are no more closely related to the picornaviruses than to any other picorna-like virus family

The available data and analyses therefore indicate the well characterised viruses, IFV, PnPV and SBV, are a natural lineage and clearly distinct from any other picorna-like virus family. It therefore proposed that these viruses be assigned to a new unaligned genus named *Iflavirus*. Infectious flacherie virus is to be assigned as the type virus for this genus.

**NOTE:** Although this proposal has originated from the “Cricket paralysis-like virus” Working Group we wish to stress that the proposed Genus *Iflavirus* should not be considered as part of the newly established *Dicistroviridae*.

## 1.2 Taxonomic Implications

In the VIIIth report of the ICTV, Infectious flacherie virus (IFV) and Sacbrood virus were listed as Unassigned Viruses (Invertebrate Viruses). *Perina nuda* picorna-like virus (PnPV) had not been fully described at the time the VIIIth report was published. As a result of this proposal these viruses would become members of the new provisional genus *Iflavirus*. This genus would not be placed within any existing family.

*Infectious flacherie virus* would be assigned as the type virus for the genus

The recognised members of the genus will comprise the species as shown below:

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>Infectious flacherie virus</i>	[AB000906]	(IFV)
<i>Perina nuda picorna-like virus</i>	[AF323747]	(PnPV)
<i>Sacbrood virus</i>	[AF092924]	(SBV)

There will be no tentative members of the genus

## 1.3 Derivation of Names

The name *Iflavirus* is a sigla from the type virus of the genus **Infectious flacherie virus**.

## 1.4 References

- Ghosh, R., Ball, B.V., Willcocks, M.M. and Carter, M.J. (1999) The nucleotide sequence of sacbrood virus of the honey bee: an insect picorna-like virus. *J. Gen. Virol.* **80**, 1541-9.
- Isawa,H., Asano,S., Sahara,K., Iizuka,T. and Bando,H. (1998) Analysis of the genetic information of an insect picorna-like virus, infectious flacherie of silkworm: evidence for evolutionary relationships among insect, mammalian and plant picorna(-like) viruses. *Arch. Virol.*, **143**, 127-143.
- Wu,C.-Y., Lo,C.-F., Huang,C.-J., Yu,H.-T. and Wang,C.-H. (2002) The complete genome sequence of *Perina nuda* picorna-like virus, an insect-infecting RNA virus with a genome organization similar to that of the mammalian picornaviruses. *Virology*, **294**, 312-323.

### Genbank Accessions

- IFV: AB000906
- PnPV: AF277675
- SBV: AF092924

## 2002.I099.04: To recognise *Taura syndrome virus* (TSV) as a species in the genus *Cripavirus*

### 2.1 Purpose

Since the revision of the family for the Houston meeting earlier this year, the full genomic sequence of Taura syndrome virus (TSV) has been published (Mari et al., 2002). Taura syndrome virus was first isolated from *Penaeus vannamei* (rustaea, Decapoda), and as such represents the first dicistro-like virus isolated from organisms other than an insect. The known properties of this virus are very similar to those of the viruses currently recognised as comprising the *Dicistroviridae*. In particular TSV shows the following characteristics of the *Dicistroviridae*:

- positive sense ssRNA of around 10kb, polyadenylated at the 3' end,
- no sub-genomic RNAs produced
- icosahedral/spherical particles (about 30nm in diameter)
- 3 major capsid proteins of between 25 and 40 kDa .
- a genome comprising two distinct ORFs separated by an untranslated region of approximately 190 bases genome organised with the ORF encoding the non-structural proteins towards the 5' of the genome (ORF 1) and the structural proteins encoded by the ORF at the 3' end of the genome (ORF2).
- coding sequence for the capsid proteins (from 5' to 3') are organised VP2, VP3 and VP1. The terminology for these proteins is derived by homology with the structural proteins of picornaviruses and as exemplified by *Cricket paralysis virus* – for which the 3D structure is known.
- the deduced amino acid sequences of ORF1 contain core motifs for the RNA helicase, cysteine protease and the RNA polymerase.

The major characteristic of the *Dicistroviridae* not shown by TSV is the apparent absence of the small capsid protein (using the structural analogy outlined above, termed VP4). However, this feature is polythetic in the dicistroviruses and also absent from two other members of the family i.e. *Rhopalosiphum padi virus* (RhPV) and *Triatoma virus* (TrV). In the case of TSV, the lack of cleavage of a VP4 capsid protein from its precursor (usually termed VP0 = VP4 + VP2) manifests as a larger VP2 protein. Phenetic analyses from the putative RdRp sequences of the non-structural protein and of VP3 indicate that while TSV clusters with the dicistroviruses it is the most divergent dicistrovirus isolated to date.

### 2.2 Taxonomic Implications

The recognised members of the Genus will now comprise the species as shown below:

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>Cricket paralysis virus</i>	[AF218039]	(CrPV)
<i>Acute bee paralysis virus</i>	[AF150629]	(ABPV)
<i>Black queen cell virus</i>	[AF183905]	(BQCV)
<i>Drosophila C virus</i>	[AF014388]	(DCV)
<i>Himetobi P virus</i>	[AB017037]	(HiPV)
<i>Plautia stali intestine virus</i>	[AB006531]	(PSIV)
<i>Rhopalosiphum paid virus</i>	[AF022937]	(RhPV)
<i>Taura syndrome virus</i>	[AF277675]	(TSV)
<i>Triatoma virus</i>	[AF178440]	(TrV)

### **2.3 Derivation of proposed names**

Names and abbreviations follow those widely recognised and in current use with workers in the field.

### **2.4 References**

Mari,J., Poulos,B.T., Lightner,D.V. and Bonami,J.-R. (2002) Shrimp Taura syndrome virus: genomic characterization and similarity with members of the genus *Cricket paralysis-like viruses*. J. Gen. Virol. **83**, 915-926.