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

Code[†] 2005.120I.04 To designate the following as species in the genus:

Iflavirus

belonging to the family° : -

Deformed wing virus
Ectropis obliqua virus
Varroa destructor virus-1

[†] Assigned by ICTV officers
° leave blank if inappropriate or in the case of an unassigned genus

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Old Taxonomic Order

Order	-
Family	-
Genus	***Iflavirus***
Type Species	***Infectious flacherie virus***
Species in the Genus	***Perina nuda virus***
	Sacbrood virus

New Taxonomic Order

Order	-
Family	-
Genus	***Iflavirus***
Type Species	***Infectious flacherie virus***
	Infectious flacherie virus (IFV)
Species in the Genus	*Deformed wing virus*
	Deformed wing virus (DWV)
	Kakugo virus (KV)
	Ectropis obliqua virus
	Ectropis obliqua virus (EoV)
	Ectropis oblique picorna-like virus (EoPV)
	Perina nuda virus
	Perina nuda virus (PnV)
	Perina nuda picorna-like virus (PnPV)
	Sacbrood virus
	Sacbrood virus (SBV)
	Varroa destructor virus 1
	Varroa destructor virus 1 (VDV-1)

Species demarcation criteria in the genus

The list of species demarcation criteria is:

- Natural host range: species can be differentiated on the basis of their natural host range
- Sequence identity between the CPs of isolates and strains of a species is above 90%.

Argumentation to justify the designation of new species in the genus

The complete nucleotide sequence of a virus termed Ectropis obliqua picorna-like virus (EoPV) was published in 2004 (Wang *et al*., 2004). Preliminary analysis of this sequence showed it to be arranged in a similar way to that previously described for members of the unaligned genus *Iflavirus*. The primary publication also showed that the virus was quite closely related to the iflavirus, Perina nuda virus (PnV) but only distantly related to the other members of the genus.

The genome of the iflaviruses is arranged with the structural proteins at the 5’ end of the single ORF. Without information on the cleavage between the structural and non-structural proteins it is difficult to know where the structural and non-structural proteins start and stop. However, for the proposes of further analysis of the relationships between EoPV and PnV we looked at the most 5’ 2400 nucleotides of the ORF i.e. corresponding to the first 800 amino acids i.e. the majority of the coat proteins (CPs). Based on the analysis of this region we see sequence identity between the two viruses of 80.3% - which amounts to a 86.0 identity at the amino acid level.

On current species demarcation criteria Ectropis obliqua picorna-like virus should therefore be considered a new species. To avoid future confusion with the picornaviruses *stricto sensu* and following the convention adopted with *Perina nuda virus* (initially termed *Perina nuda* picorna-like virus) the name *Ectropis obliqua virus* is proposed.

The complete genomic sequence for Deformed wing virus (DWV) (AJ489744) appeared on the Genbank website in March 2003. A second independent sequence (AY292384) appeared in June 2003. No specific publications have been associated with the release of either of these sequences, but the Genbank listing shows both sequences to comprise single ORF – with very high homology at the amino acid level.

Subsequent to the release of the DWV sequences the sequence of Kakugo virus (KV) (Fujiyuki *et al*., 2004) and Varroa destructor virus-1 (VDV-1) (Ongus *et al.,* 2004) have been published. The analyses of the genomesin these papers indicate that they viruses have organizations similar to that previously described for members of the unaligned genus *Iflavirus*. Preliminary analysis of the VDV-1 sequence further indicated a close relationship between the sequence of VDV-1, DWV and KV and more distant relationships to the existing members of the genus.

Similar analysis of the structural coding region was undertaken as for PnV/EoV i.e. comparing the 2400 nt at the 5’ end of the coding sequence. This analysis revealed that DWV and KV are 96.8% identical at the nucleotide level – which on current criteria classifies them as strains/isolates of the same species. It is therefore proposed that the species *Deformed wing virus* be created with Kakugo virus listed as an isolate of that species.

In the only published analysis of the relationship of VDV-1 to Deformed wing virus (Ongus *et al.,* 2004) estimates indicate that for the region encoding the structural proteins nucleotide homology between VDV-1 and DWV is around 84%. Reanalysis of the 2400 nt at the 5’ end of the coding sequence give a similar figure of around 82%. Current species demarcation criteria would therefore lead to the conclusion that the species *Varroa destructor virus-1* should be created.

List of created Species in the genus

Deformed wing virus
Ectropis obliqua virus
Varroa destructor virus-1

References

Fujiyuki T., Takeuchi H., Ono M., Sasaki T., Nomoto, A., Kubo, T. (2004) Novel insect picorna-like virus identified in the brains of aggressive worker honeybees, J. Virol. **78**, 1093-1100.

Ongus J.R., Peters D., Bonmatin J.M., Bengsch E., Vlak J.M., van Oers M.M. (2004) Complete sequence of a picorna-like virus of the genus *Iflavirus* replicating in the mite *Varroa destructor*, J Gen Virol. **85**, 3747-3755.

Wang X., Zhang J., Liu J, Fuming Y., Liu C., Hu Y. (2004) Sequence analysis and genomic organization of a new insect picorna-like virus, *Ectropis obliqua* picorna-like virus, isolated from *Ectropis obliqua*, J. Gen. Virol. **85**, 1145-1151.

Wu C.-Y., Lo C.-F., Huang C.-J., Yu,H.-T., 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.

Annexes:

None