

**Part 1:** **TITLE, AUTHORS, APPROVALS, etc**

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| **Code assigned:** | **2021.003S** |  |
| **Short title:** Abolish one species and rename one species in the genus *Iflavirus* (*Picornavirales*: *Iflaviridae*) | | |
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**Author(s) and email address(es)**

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| Chen YP, Valles SM, Jan E, Firth A, de Miranda J, Ryabov E, Schroeder D, Echeverría MG, Zheng HQ | [judy.chen@usda.gov](mailto:judy.chen@usda.gov);  [steven.valles@usda.gov](mailto:steven.valles@usda.gov);  [ej@mail.ubc.ca](mailto:ej@mail.ubc.ca);  aef24@cam.ac.uk;  [joachim.de.miranda@slu.se](mailto:joachim.de.miranda@slu.se); [eugene.ryabov@gmail.com](mailto:eugene.ryabov@gmail.com);  [dcschroe@umn.edu](mailto:dcschroe@umn.edu);  [gecheverria@fcv.unlp.edu.ar](mailto:gecheverria@fcv.unlp.edu.ar);  hqzheng@zju.edu.cn |

**Author(s) institutional address(es) (optional)**

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| USDA-ARS Bee Research Laboratory, Beltsville, MD, USA [YPC]  USDA-ARS Imported Fire Ant and Household Insects Research, Gainesville, FL, USA [SMV]  Department of Biochemistry and Molecular Biology, University of British Columbia, Vancouver, BC, Canada [EJ]  Department of Pathology, Division of Virology, University of Cambridge, Cambridge CB2 0QQ, UK [AF]  Department of Ecology, Swedish University of Agricultural Sciences, Uppsala, Sweden [JM]  USDA-ARS Bee Research Laboratory, Beltsville, MD, USA [ER]  Virology Department, Faculty of Veterinary Sciences, University of La Plata, Argentina [MGE]  Department of Veterinary Population Medicine, University of Minnesota, USA [DS]  College of Animal Sciences, Zhejiang University, Hangzhou, China [HQZ] |

**Corresponding author**

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| Chen, Yan Ping (Judy), judy.chen@usda.gov |

**List the ICTV Study Group(s) that have seen this proposal**

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| Dicistroviridae/Iflaviridae Study Group |

**ICTV study group comments and response of proposer**

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**Authority to use the name of a living person**

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| **Is any taxon name used here derived from that of a living person (Y/N)** | N |

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| **Taxon name** | **Person from whom the name is derived** | **Permission attached (Y/N)** |
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**Submission dates**

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| Date first submitted to SC Chair | June 2, 2021 |
| Date of this revision (if different to above) | September 17, 2021 |

**ICTV-EC comments and response of the proposer**

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| Many thanks for submitting the three taxonomy proposals for species designation in the *Iflavivirdae*. This was reviewed at the ICTV Executive Committee meeting yesterday as it was given a designation of Ac. This means that it is accepted pending minor changes as listed below:   1. The changes in the three proposals were coded on the same spreadsheet but actually three separate spreadsheets are required, one for each proposal. So can these be separated? 2. There is a formal check done of the spreadsheet and I attach the errors detected. Can you take a look at these and correct where indicated. You don’t need to include taxonomy above the level of order so you can remove some of the errors by just deleting the higher ranks. 3. The proposed names were not in a binomial format. There is now a two year remaining period for species names to be re-formatted, and the general advice would be to ensure that any new names are compliant. However, you may want to think about the best way to do this and you might keep the proposed species names as they are pending a comprehensive renaming at a later date. 4. As an advisory note, sequences used in trees produced to support proposals are best labelled with nucleotide accession numbers rather than the derived protein accession number or virus names (although a combined label with nucleotide accession numbers and virus names is ideal). However there is no need to change this in the current proposals.   Response   1. The spreadsheets have now been split so there is one for each proposal 2. The spreadsheets have been checked and passed without errors 3. We will review species names for the whole virus family and may be in a position to rename them all in binomial format for the next round of taxonomy proposals 4. Noted |

**Part 3:** **TAXONOMIC PROPOSAL**

**Name of accompanying Excel module**

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| 2021.003S.R.Iflavirus\_abo1sp\_ren1sp.xlsx |

**Abstract**

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| *Varroa destructor* virus 1 (VDV1), a member of the species *Varroa destructor virus 1* was first isolated from *Varroa destructor*, an external parasitic mite of honey bees. Growing evidence shows that VDV1 is capable of causing infection in honeybees. Further, there is a high level of amino acid identity between the capsid protein of VDV1 and deformed wing virus (DWV), a member of the viral species *Deformed wing virus* in the genus *Iflavirus*, family *Iflaviridae* that had been circulating in honeybee populations long before the *V. destructor* invasion. These findings clearly indicate that VDV1 and DWV are two isolates of the same virus species on the basis of established criteria. Therefore, we are proposing 1) to remove *Varroa destructor virus 1* from the species list of the *Iflavirus* genus, *Iflaviridae* family. |

**Text of proposal**

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| |  | | --- | | Species demarcation criteria have already been established for the members of the genus Iflavirus: 1) natural host range: species can be differentiated on the basis of their natural host range; and 2) sequence identity between the capsid proteins (CPs) of isolates and strains of a species is above 90%.  Characterization of *Varroa destructor* virus 1 (VDV1) and its complete sequence (exemplar GenBank accession: AY251269) were published by Ongus et al., (2004). The virus was first isolated from *Varroa destructor,* an external parasitic mite that attacks honey bees *Apis mellifera* and *Apis cerana*. A proposal to create the species *Varroa destructor* virus *1* as well as *Deformed wing virus* (exemplars GenBank accessions AY292384 and AJ489744) (Lanzi et al., 2006), which had been circulating in *A.mellifera* populations long before the *Varroa* invasion as two independent species in the genus *Iflavirus*, family *Iflaviridae* was submitted in 2005 with code 2005.120I.04.  Over the past decade, accumulated scientific evidence clearly showed that VDV1 is capable of causing infection in honey bees and therefore many scientific publications has referred VDV1 as DWV Type B. The alignment of capsid proteins present in the N-terminal region of the polyprotein revealed that sequences of VDV1 and DWV share 97% amino acid identity. Phylogenetic analyses of the amino acid sequences of the polyprotein of iflaviruses revealed that VDV1, DWV and DWV Type C which is a DWV variant more recently found in honey bees in the UK (exemplar EBI accession CEND01000001 (Mordecai et al., 2016), form a monophyletic clade separated from other Iflaviruses (Figure 1). High amino acid identity between capsid proteins of DWV, VDV1 and DWV Type C (at least 90%) and the same principal host species (*Apis mellifera*) clearly indicate that these isolates belong to the same virus species on the basis of established criteria. Therefore we are proposing 1) to remove *Varroa destructor virus 1* from the species list of the *Iflavirus* genus, *Iflaviridae* family. | |

**Supporting evidence**

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**Figure 1.** Phylogenetic tree of iflaviruses. The phylogenetic analysis was conducted in MEGA 7 based on the amino acid sequences of the polyprotein. The tree was constructed by the maximum likelihood method. The tree is drawn to scale, with branch lengths measured using the same units as those of the evolutionary distances that are used to infer the phylogenetic tree. The scale bar shows the number of substitutions per base. The reliability of the tree topology was determined by the bootstrap analysis (1,000 replicates). The clade containing three types of deformed wing virus is encircled. The bootstrap values that were greater than 60% were given at the nodes. The names and accession numbers of the *Iflavirus* taxon are shown.

**References**

Lanzi G, de Miranda JR, Boniotti MB, Cameron CE, Lavazza A, Capucci L, Camazine SM, Rossi C. 2006. Molecular and biological characterization of deformed wing virus of honeybees (Apis mellifera L.). J Virol. 80(10):4998-5009. PMID: 16641291 PMCID: PMC1472076 DOI: 10.1128/JVI.80.10.4998-5009

Mordecai GJ, Wilfert L, Martin SJ, Jones IM, Schroeder DC. 2016. Diversity in a honey bee pathogen: First report of a third master variant of the Deformed Wing Virus quasispecies. ISME J., 10, 1264–1273. PMID: 26574686 PMCID: PMC5029213 DOI: 10.1038/ismej.2015.178.

Ongus JR, Peters D, Bonmatin JM, Bengsch E, Vlak JM, van Oers, MM. 2004. Complete sequence of a picorna-like virus of the genus Iflavirus replicating in the mite *Varroa destructor*. J. Gen. Virol. 85:3747–3755. PMID: 15557248 DOI: 10.1099/vir.0.80470-0.