

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

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| **Code assigned:** | **2021.002S** |  |
| **Short title:** Create one new species in the genus *Iflavirus* (*Picornavirales*: *Iflaviridae*) | | |
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**Author(s) and email address(es)**

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**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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| 2021.002S.R.Iflavirus\_1nsp.xlsx |

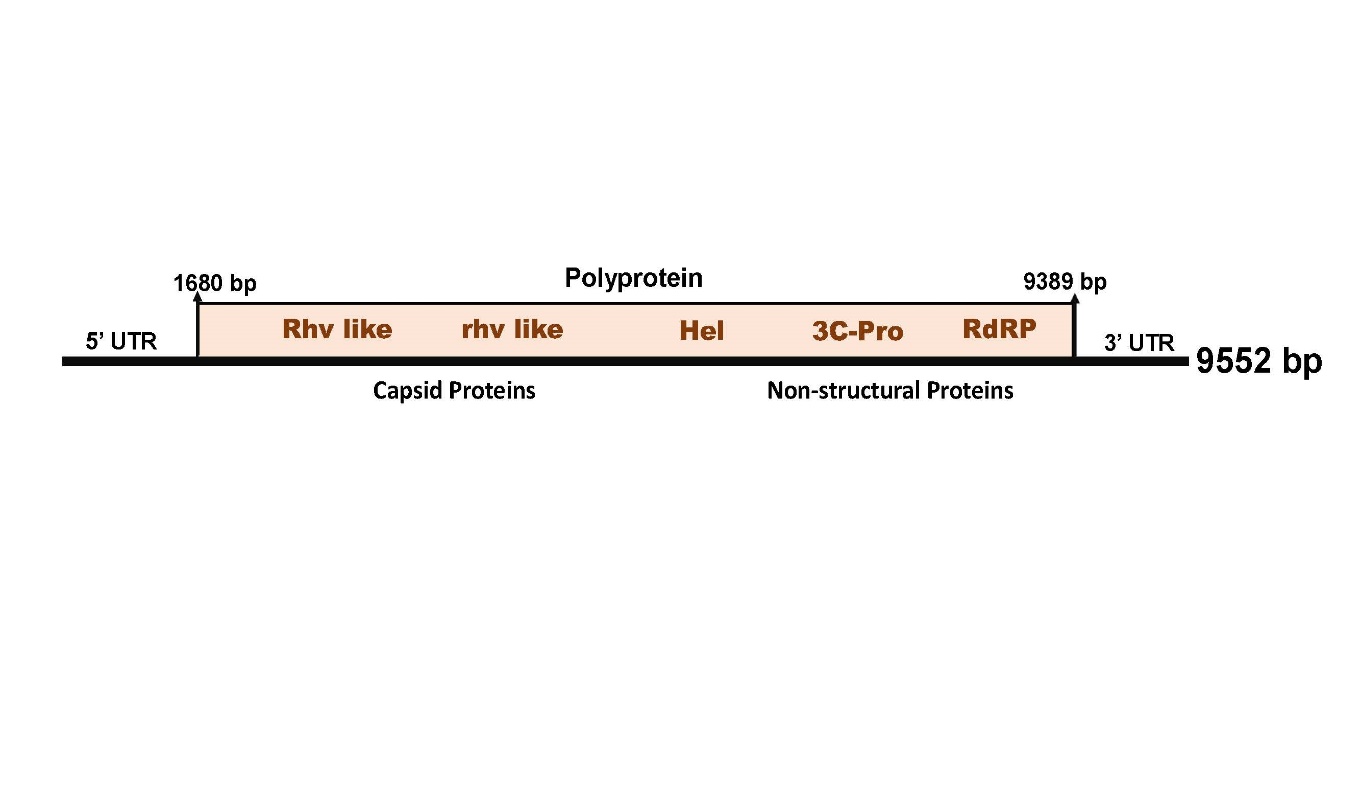
**Abstract**

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| The complete genome sequence of newly identified virus exclusively from the parasitic mite *Varroa destructor* shows the genomic organization features that fulfill the *Iflavirus* genus inclusion criteria: sharing 34.14% sequence homology with *Lymantria dispar* iflavirus 1, the closest species in the genus *Iflavirus*, family *Iflaviridae*. We propose to assign the virus, Varroa destructor virus 2 (VDV2) as a member of a new species, *Varroa destructor iflavirus 1* (VDI1) to reflect its status as the first iflavirus to be exclusively isolated from *V. destructor*. |

**Text of proposal**

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| |  | | --- | | **Reasons to justify the creation and assignment of the new species:**  Species demarcation criteria for the members of the genus *Iflavirus*   * 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%.   ----------------------------------------------------------------------------------------------------------  The genome sequence of Varroa destructor virus 2 (VDV2), that we propose to assign to species *Varroa destructor iflavirus 1* was originally found in the transcriptome data of the ectoparasitic mite, *Varroa destructor* (Levin et al., 2016), that lives in and feeds on the honey bees *Apis cerana* and *Apis mellifera*. Further PCR amplification of cDNA generated by reverse transcription of RNA extracted from virome preparation and 3'-RACE analyses of cDNA led to a complete viral genome assembly. The complete genome sequence of VDV2 (GenBank Accession# KX578271.1) shows the following features that fulfill the *Iflavirus* genus inclusion criteria:  Genome: Positive-sense, single stranded RNA genome which is approximately 9552 nt long and contains a single open reading frame (ORF). The ORF encodes a polyprotein of 2570 amino acid residues flanked by approximately 1679 nt of 5’-UTR and 163 nt of 3’-UTR. The N-terminal portion of the polyprotein shows two conserved functional motifs, rhinovirus-like (rhv) motifs belonging to the picornavirus capsid protein-like domain. The C-terminal portion of the polyprotein exhibits non-structural proteins in the order: helicase, 3C-like cysteine protease, and RNA-dependent RNA polymerase (Figure 1).  Phylogeny: Phylogenetic analysis with the amino acid sequences of the polyprotein of iflaviruses reveals that VDV2 forms a clade or monophyletic group (Figure 2). A BLASTP search for conserved domains of capsid proteins revealed that *Lymantria dispar iflavirus* 1 is the top hit among iflavirusesand shares 34.14% sequence homology with VDV2, justifying the classification of VDV2 as a novel species in the genus *Iflavirus*, family *Iflaviridae*.  Natural host range: VDV2 is associated exclusively with *V. destructor* and is absent in honey bees *A. mellifera* and *A. cerana* (Chen et al., 2021; Levin et al., 2016)  VDV2 (Levin et al., 2016)) is now being proposed as a new species *Varroa destructor* iflavirus 1 (VDI1) to emphasize that it is the first iflavirus exclusively isolated from *Varroa destructor*. | |

**Supporting evidence**.



**Figure. 1**: Genome organization of VDV-2.

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**Figure 2.** 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 bootstrap values that were greater than 60% were given at the nodes. The names and accession numbers of the iflavirus taxa are shown. The position of VDV-2 is marked by a red star.

**References**

Chen G, Wang S, Jia S, Feng Y, Hu F, Chen Y, Zheng HA. 2021. New Strain of Virus Discovered in China specific to the parasitic mite *Varroa destructor* poses a potential threat to honey bees. Viruses. 13: 679. Doi: 10.3390/v13040679.

Levin S, Sela N, Chejanovsky N. 2016. Two novel viruses associated with the *Apis mellifera* pathogenic mite *Varroa destructor*. Sci. Rep. 6: 37710, doi:10.1038/srep37710.