

The International Committee on Taxonomy of Viruses

Taxonomy Proposal Form, 2024

**Part 1a: Details of taxonomy proposals**

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| **Title:**  | Create four (4) new species in the genus *Ilarvirus* (*Martellivirales*: *Bromoviridae*) |
| **Code assigned:**  | 2024.011P.A.v1.Bromoviridae\_4nsp |

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**Part 1b: Taxonomy Proposal Submission**

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| **ICTV Subcommittee:**  |
| Animal DNA Viruses and Retroviruses |  | Bacterial viruses |  |
| Animal minus-strand and dsRNA viruses |  | Fungal and protist viruses |  |
| Animal positive-strand RNA viruses |  | Plant viruses | **X** |
| Archaeal viruses |  | General - |  |

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| **List the ICTV Study Group(s) that have seen or have been involved in creating this proposal:**  |
| *Bromoviridae* SG |

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| **Optional – complete only if formally voted on by an ICTV Study Group:**  |
| **Study Group** | **Number of members** |
| **Votes in support** | **Votes against** | **No vote** |
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| **Submission date:** |  10/06/2024 |

**Part 1c: Feedback from ICTV Executive Committee (EC) meeting**

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| **Executive Committee Meeting Decision code:** | **X** |
| A – Accept |  |
| Ac – Accept subject to revision by relevant subcommittee chair. No further vote required | **X** |
| U – Accept without revision but with re-evaluation and email vote by the EC |  |
| Uc – Accept subject to revision and re-evaluation and email vote by the EC |  |
| Ud – Deferred to the next EC meeting, with an invitation to revise based on EC comments |  |
| J – Reject |  |
| W – Withdrawn |  |

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| **Comments from the Executive Committee:** |
| The EC invited the Study Group to reconsider species names and replace the use of abbreviations as epithet. Moreover, the SG is kindly asked to formalize demarcation criteria in the chapter. |

**Part 1d: Revised Taxonomy Proposal Submission**

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| **Response of proposer:**  |
| The SG has already considered the nomenclature options as requested in 2022 and 2023 based on the naming options provided by the President and EC. The vote from the SG was a clear majority in favor of Genus+acronym on the grounds it was more practical than the other options. The species demarcation criterion of <85% amino acid identity for the whole 2a protein is being formalized in the X Report chapter. |

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| **Revision date:** |  07/10/2024 |

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

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| **Name of accompanying Excel module:**  |
| 2024.011P.A.v1.Bromoviridae\_4nsp.xlsx |

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| **Taxonomic changes proposed:**  |
| Establish new taxon | **X** | Split taxon |  |
| Abolish taxon |  | Merge taxon |  |
| Move taxon |  | Promote taxon |  |
| Rename taxon |  | Demote taxon |  |
| Move and rename |  |

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| **Is any taxon name used here derived from that of a living person:**  |  **N** |
| **Taxon name** | **Person from whom the name is derived** | **Attached X** |
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| **Abstract of Taxonomy Proposal:**  |
| This taxonomic proposal considers the recognition of the following **four new virus species** (Table 1) based on species demarcation criteria in the family *Bromoviridae* genus *Ilarvirus* of “serology, host range and sequence similarity”. In the absence of biological information, we propose to include a refinement of the “sequence similarity” criterion to require less than 85% identity for the complete RNA2 2a protein. |

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| **Text of Taxonomy proposal:**  |
| **Creation of a first novel species in the genus *Ilarvirus* of the family *Bromoviridae*.** The full-length genome sequence of a new ilarvirus from apples (*Malus domestica*) from Apple Research Station, NARO, Japan was determined by high-throughput sequencing (Illumina HiSeq 2000) and RACE-PCR by Noda et al (2017). The virus is tentatively named **apple necrotic mosaic virus (ApNMV).** Sequences of ApNMV isolate P129 were deposited in NCBI in 2016 as accession numbers LC108993, LC108994 and LC108995 for RNA1 (3,378 nt), RNA2 (2,767 nt) and RNA3 (1,956 nt), respectively. The genome organization of ApNMV is similar to that of members of the genus *Ilarvirus* (subgroup 2) (Fig. 1). *In silico* translationof open reading frames suggest that ApNMV RNA1 encodes one protein containing the methyltransferase and helicase domains (1a); RNA2 codes for two proteins, one containing the RNA-directed RNA polymerase domain (2a) and one encoding a putative gene silencing suppressor (2b); and RNA3 encodes two proteins, the 5’ putative movement protein (MP) and the 3’ coat protein (CP). Sequence comparisons and phylogenetic analyses of aa sequences amino acid alignment of regions spanning the RNA-directed RNA polymerase motifs I to VII (Koonin 1991) showed ApNMV grouped into the ilarvirus clade 3/4. The aa sequence identity between ApNMV and its closest known relative sequence Prunus necrotic ringspot virus is 92% for conserved RNA-directed RNA polymerase motifs I to VII and 60% for the whole of the 2a protein. Based on a recommended cut-off of 85% for the whole 2a protein, as proposed last year in the absence of more biological data, we therefore propose to classify this virus as **apple necrotic mosaic virus (ApNMV),** a member of a novel species named ***Ilarvirus ApNMV*** in the genus *Ilarvirus* of the family *Bromoviridae* (Table 1).**Creation of a second novel species in the genus *Ilarvirus* of the family *Bromoviridae***The full-length genome sequence of a new ilarvirus from babaco (*Vasconcellea x heilbornii*) from Azuay province in Ecuador was determined by high-throughput sequencing (Illumina HiSeq 4000 platform) by Reyes-Proaño et al 2023) combined with Sanger sequencing of RACE clones. The virus is tentatively named **babaco ilarvirus 1 (BabIV1)**. Sequences of BabIV1 isolate Paute were deposited in NCBI in 2023 as accession numbers OQ256238, OQ256239 and OQ256240 for RNA1 (3,299 nt), RNA2 (2,675 nt) and RNA3 (1,802 nt), respectively. The genome organization of BabIV1 is similar to that of members of the genus *Ilarvirus* (Fig. 1). *In silico* translationof open reading frames suggests that the BabIV1 RNA1 encodes one protein containing the methyltransferase and helicase domains (1a); RNA2 two proteins, one containing the RNA-directed RNA polymerase domain (2a) and one encoding a putative gene silencing suppressor (2b); and RNA3 encodes two proteins, the 5’ putative movement protein (MP) and the 3’ coat protein (CP). Sequence comparisons and phylogenetic analyses of aa sequences amino acid alignment of regions spanning the RNA-directed RNA polymerase motifs I to VII (Koonin 1991) showed BabIV1 grouped into the ilarvirus clade 3/4. The aa sequence identity between BabIV1 and its closest known relative sequence apple necrotic mosaic virus (ApNMV) (also in this proposal) is 90% for conserved RNA-directed RNA polymerase motifs I to VII and 55.1% for the whole of the 2a protein. Based on a recommended cut-off of 85% for the whole 2a protein, as proposed last year in the absence of more biological data, we therefore propose to classify this virus as **babaco ilarvirus 1** **(BabVI1),** a member of a novel species named ***Ilarvirus BabVI1*** in the genus *Ilarvirus* of the family *Bromoviridae* (Table 1).**Creation of a third novel species in the genus *Ilarvirus* of the family *Bromoviridae*.** The full-length genome sequence of a new ilarvirus from pooled tomato (*Solanum lycopersicum*) samples from Slovenia was determined by high-throughput sequencing (Illumina HiSeq 2500) by Rivarez et al (2023). The virus was tentatively named **tomato ilarvirus 1 (TIV1).** Sequences of TIV1 isolate MIR20AT were deposited in NCBI in 2022 as accession numbers OL472057, OL472058 and OL472059 for RNA1 (3,392 nt), RNA2 (2,866 nt) and RNA3 (2,181 nt), respectively. The genome organization of TIV1 is similar to that of members of the genus *Ilarvirus* (Fig. 1). *In silico* translationof open reading frames suggests that TIV1 RNA1 encodes one protein containing the methyltransferase and helicase domains; RNA2 two proteins, one (2a) containing the RNA-directed RNA polymerase domain, and second (2b) putative gene silencing suppressor; and RNA3 encodes two proteins, the 5’ putative movement protein (MP) and the 3’ coat protein (CP). Sequence comparisons and phylogenetic analyses of aa sequences amino acid alignment of regions spanning the RNA-directed RNA polymerase motifs I to VII (Koonin 1991) showed TIV1 grouped into the ilarvirus clade 2. The aa sequence identity between TIV1 and its closest known relative sequence rose ilarvirus 2 is 89% for conserved RNA-directed RNA polymerase motifs I to VII and 58.5% for the whole 2a protein of asparagus virus 2. Based on a recommended cut-off of 85% for the whole 2a protein, as proposed last year in the absence of more biological data, we therefore propose to classify this virus as **tomato ilarvirus 1 (TIV1),** a member of a novel species named ***Ilarvirus TIV1*** in the genus *Ilarvirus* of the family *Bromoviridae* (Table 1).**Creation of a fourth novel species in the genus *Ilarvirus* of the family *Bromoviridae*.** The full-length genome sequence of a new ilarvirus from tomato (*Solanum lycopersicum*) from Indiana, USA was determined by Illumina NextSeq and RACE by Bratsch et al (2019). The virus was tentatively named **tomato necrotic spot virus (ToNSV).** Sequences of ToNSV (isolate Indiana) were deposited in NCBI in 2018 as accession numbers MH780154, MH780155 and MH780156 for RNA1 (3,519 nt), RNA2 (2,903 nt) and RNA3 (2,290 nt), respectively. The genome organization of ToNSV is similar to that of members of the genus *Ilarvirus* (Fig. 1). *In silico* translationof open reading frames suggest that TIV1 RNA1 encodes one protein containing the methyltransferase and helicase domains; RNA2 two proteins, one (2a) containing the RNA-directed RNA polymerase domain, and second (2b) putative gene silencing suppressor; and RNA3 encodes two proteins, the 5’ putative movement protein (MP) and the 3’ coat protein (CP). Sequence comparisons and phylogenetic analyses of aa sequences amino acid alignment of regions spanning the RNA-directed RNA polymerase motifs I to VII (Koonin 1991) showed TIV1 grouped into the ilarvirus clade 1. The aa sequence identity between TIV1 and its closest known relative sequence babaco ilarvirus 1 (BabIV1) (also in this proposal) is 90% for conserved RNA-directed RNA polymerase motifs I to VII and 60% for the whole of the 2a protein to prunus necrotic ringspot virus. Based on a recommended cut-off of 85% for the whole 2a protein, as proposed last year in the absence of more biological data, we therefore propose to classify this virus as **tomato necrotic spot virus (ToNSV)** as a member of a novel species named ***Ilarvirus ToNSV*** in the genus *Ilarvirus* of the family *Bromoviridae* (Table 1). |

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| **References:**  |
| Bratsch SA, Grinstead S, Creswell TC, Ruhl GE, Mollov D. Characterization of Tomato necrotic spot virus, a subgroup 1 ilarvirus causing necrotic foliar, stem, and fruit symptoms in tomatoes in the United States. Plant disease. 2019 Jun 16;103(6):1391-6. Noda H, Yamagishi N, Yaegashi H, Xing F, Xie J, Li S, Zhou T, Ito T, Yoshikawa N. Apple necrotic mosaic virus, a novel ilarvirus from mosaic-diseased apple trees in Japan and China. Journal of General Plant Pathology. 2017 Mar;83:83-90.Koonin EV. The phylogeny of RNA-dependent RNA polymerases of positive-strand RNA viruses. J Gen Virol. 1991 Sep;72 ( Pt 9):2197-206. doi: 10.1099/0022-1317-72-9-2197. PMID: 1895057.Reyes-Proaño EG, Cañada-Bautista MG, Cornejo-Franco JF, Alvarez-Quinto RA, Mollov D, Sanchez-Timm E, Quito-Avila DF. The Virome of Babaco (Vasconcellea× heilbornii) Expands to Include New Members of the Rhabdoviridae and Bromoviridae. Viruses. 2023 Jun 16;15(6):1380.Rivarez MPS, Pecman A, Bačnik K, Maksimović O, Vučurović A, Seljak G, Mehle N, Gutiérrez-Aguirre I, Ravnikar M, Kutnjak D. In-depth study of tomato and weed viromes reveals undiscovered plant virus diversity in an agroecosystem. Microbiome. 2023 Mar 28;11(1):60. doi: 10.1186/s40168-023-01500-6. PMID: 36973750; PMCID: PMC10042675.   |

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| **Tables, Figures:**  |

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**Table 1:** List of newly proposed virus species in the family *Bromoviridae* with their names, genus and NCBI accession numbers (\*) for each RNA.

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| Virus Name | Virus Species | Genus | RNA1\* | RNA2\* | RNA3\* |
|  Apple necrotic mosaic virus | *Ilarvirus ApNMV* | *Ilarvirus* | NC\_040469  | NC\_040471  | NC\_040470  |
|  Babaco ilarvirus 1 | *Ilarvirus BabIV1* | *Ilarvirus* | OQ256238 | OQ256239  | OQ256240 |
|  Tomato ilarvirus 1  | *Ilarvirus TIV1* | *Ilarvirus* | OL472057  | OL472058  | OL472059  |
|  Tomato necrotic spot virus | *Ilarvirus ToNSV* | *Ilarvirus* | MH780154  | MH780155  | MH780156  |

**Figure 1.** Schematic genome organization for members of the family *Bromoviridae*: (a) genera *Alfamovirus*, *Bromovirus*, *Ilavirus* subgroups 3 and 4 and *Oleavirus*. (b) genus *Anulavirus*. (c) genera *Cucumovirus* and *Ilarvirus* subgroups 1 and 2. The 3′-termini form either tRNA-like (b) or complex structures (a, c) are shown as black or grey square boxes, respectively.



**Figure 2.** Neighbor-joining phylogenetic tree generated from an alignment of the *RdRp* gene (motifs I-VII) (Koonin 1991). Viruses described in this proposal are highlighted in brown. Bar = genetic distance. Numbers at nodes = bootstrap values. 