

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

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| **Code assigned:** | **2023.005P** |  |
| **Short title:** Create ten (10) new species in the genus *Ilarvirus* (*Martellivirales*: *Bromoviridae*) |
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**Author(s) and email address(es)**

|  |  |
| --- | --- |
|  |  |
| Thompson JR, Canto T, Carr JP, Pallás V, Šafářová, D | jeremy.thompson@mpi.govt.nz; tomas.canto@cib.csic.es; jpc1005@cam.ac.uk; vpallas@ibmcp.upv.es;dana.safarova@upol.cz |

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

|  |
| --- |
|  |

**Corresponding author**

|  |
| --- |
| Thompson JR |

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

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| *Bromoviridae* Study Group |

**ICTV Study Group comments and response of proposer**

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**ICTV Study Group votes on proposal**

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| **Study Group** | **Number of members** |
| **Votes support** | **Votes against** | **No vote** |
| *Bromoviridae* | 5 |  |  |
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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 16, 2023 |
| Date of this revision (if different to above) |  |

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

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| Following the EC request to reconsider the use of acronyms as species epithets, the Study Group confirmed the decision of using the acronyms as species epithets. |

**Part 2:** **NON-TAXONOMIC PROPOSAL**

**Text of proposal**

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

**Name of accompanying Excel module**

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| 2023.005P.Uc.v1.Bromoviridae\_10nsp |

**Abstract**

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| This taxonomic proposal considers the recognition of the following **ten 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% identify for the complete RNA2 2a protein. |

**Text of proposal**

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| **Creation of a first novel species in the genus *Ilarvirus* of the family *Bromoviridae***The full-length genome sequence of a new ilarvirus from kiwifruit (*Actinidia* spp.) from Shaanxi province, China was determined by high-throughput sequencing (Illumina HiSeq X-ten) by Zhao et al (2021). The virus is tentatively named **Actinidia yellowing ringspot virus (AYRSpV)**. Sequences of AYRSpV isolate Meixian were deposited in NCBI in 2021 as accession numbers MN612758, MN612759 and MN612760 for RNA1 (3,357 nt), RNA2 (2,318 nt) and RNA3 (2,229 nt), respectively. The genome organization of AYRSpV is similar to that of members of the genus *Ilarvirus* (Fig. 1). *In silico* translationof open reading frames suggest that the AYRSpV 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 RNA 3 two proteins containing the 5’ putative movement protein (MP) and the 3’ coat protein (CP). Sequence comparisons and phylogenetic analyses of amino acid (aa) sequence alignment of the regions spanning the RNA-directed RNA polymerase motifs I to VII (Koonin 1991) showed AYRSpV grouped into the ilarvirus clade. The aa sequence identity between AYRSpV and its closest known relative sequence American plum line pattern virus is 69.6% for conserved RNA-directed RNA polymerase motifs I to VII and for the whole of the 2a protein 41.9 %. Based on of the existing ICTV species demarcation criteria for ilarviruses of “serology, host range and sequence similarity,” where the latter is not yet officially defined, we suggest a recommended cut-off of 85% could be used even in the absence of more biological data (See identity comparisons Tables S1 (Motifs 1-VII) and S2 (Complete ORF 2a)). We therefore propose to classify this virus as **Actinidia yellowing ringspot virus (AYRSpV),** a member of a novel species named ***Ilarvirus AYRSpV*** 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 apples (*Malus domestica*) from British Columbia, Canada was determined by high-throughput sequencing (Illumina NovaSeq 6000) and PCR by Xiao et al (2022). The virus is tentatively named **Apple Ilarvirus 2 (AIV2).** Sequences of AIV2 isolate BC94 were deposited in NCBI in 2022 as accession numbers ON932434, ON932435 and ON932436 for RNA1 (3,456 nt), RNA2 (2,913 nt) and RNA3 (2,269 nt), respectively. The genome organization of AIV2 is similar to that of members of the genus *Ilarvirus* (subgroup 2) (Fig. 1). *In silico* translationof open reading frames suggest that the AIV2 RNA1 encodes one protein containing the methyltransferase and helicase domains; RNA2 has two ORFs overlapping by 368 nts, coding for protein 2a of 816 aa (92.95 kDa), which has canonical RNA-directed-RNA-polymerase motifs (aa 234–649) and protein 2b of 190 aa (21.73 kDa). Protein 2band RNA 3 two proteins containing the 5’ putative movement protein (MP) and the 3’ coat protein (CP). Sequence comparisons and phylogenetic analyses of aa sequence alignment of the regions spanning the RNA-directed RNA polymerase motifs I to VII (Koonin 1991) showed AIV2 grouped into the ilarvirus clade (subgroup 2). The aa sequence identity between AIV2 and its closest known relative sequence Citrus variegation virus is 90.1 % for conserved RNA-directed RNA polymerase motifs I to VII and for the whole of the 2a protein 65.2 %. Based on of the existing ICTV species demarcation criteria for ilarviruses of “serology, host range and sequence similarity,” where the latter is not yet defined, we suggest a recommended cut-off of 85% could be used even in the absence of more biological data (See identity comparisons Tables S1 (Motifs 1-VII) and S2 (Complete ORF 2a)). We therefore propose to classify this virus as **apple Ilarvirus 2 (AIV2),** a member of a novel species named ***Ilarvirus AIV2*** 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 *Carpotroche brasiliensis* from Brazil was determined by high-throughput sequencing (Illumina MiSeq) by Vieira et al (2022). The virus was tentatively named **Carpotroche-associated ilarvirus (CarIV).** Sequences of CarIV were deposited in NCBI in 2022 as accession numbers OL964100, OL964099 and OL964098 for RNA1 (3,467 nt), RNA2 (2,954 nt) and RNA3 (2,442 nt), respectively. The genome organization of CarIV is similar to that of members of the genus *Ilarvirus* (Fig. 1). *In silico* translationof open reading frames suggest that CarIV 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 RNA 3 two proteins containing the 5’ putative movement protein (MP) and the 3’ coat protein (CP). Sequence comparisons and phylogenetic analyses of aa sequence alignment of the regions spanning the RNA-directed RNA polymerase motifs I to VII (Koonin 1991) showed CarIV grouped into the ilarvirus clade (subgroup 2). The aa sequence identity between CarIV and its closest known relative sequence Rose ilarvirus 2 (also in this in proposal) is 88.3 % for conserved RNA-directed RNA polymerase motifs I to VII and for the whole of the 2a protein 57.5 %. Based on of the existing ICTV species demarcation criteria for ilarviruses of “serology, host range and sequence similarity,” where the latter is not yet defined, we suggest a recommended cut-off of 85% could be used even in the absence of more biological data (See identity comparisons Tables S1 (Motifs 1-VII) and S2 (Complete ORF 2a)). We therefore propose to classify this virus as **Carpotroche-associated ilarvirus 1 (CarIV1),** a member of a novel species named ***Ilarvirus CarIV1*** 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 hydrangea (*Hydrangea macrophylla*) from France was determined by PCR walking and RACE by Parella and Troiano (2022). The virus was tentatively named **hydrangea vein banding virus (HdVBV).** Sequences of HdVBV (isolate Fitolab) were deposited in NCBI in 2022 as accession numbers OK666835, OK666836 and OK666837.1 for RNA1 (3,422 nt), RNA2 (2,905 nt) and RNA3 (2,299 nt), respectively. The genome organization of HdVBV is similar to that of members of the genus *Ilarvirus* (Fig. 1). *In silico* translationof open reading frames suggest that the HdVBV RNA1 encodes one protein containing the methyltransferase and helicase domains; RNA2 two proteins, one protein containing the RNA-directed RNA polymerase domain (2a) and the other (2b) shares 54-85% identity with its orthologous in subgroup 2; and RNA 3 two proteins containing the 5’ putative movement protein (MP) and the 3’ coat protein (CP). Sequence comparisons and phylogenetic analyses of aa sequence alignment of the regions spanning the RNA-directed RNA polymerase motifs I to VII (Koonin 1991) showed HdVBV grouped into the ilarvirus clade (subgroup 2). The aa sequence identity between SIlV1 and its closest known relative sequence asparagus virus 2 (AV2) and Citrus variegation virus is 96.7 % for conserved RNA-directed RNA polymerase motifs I to VII and for the whole of the 2a protein 90%. Based on of the existing ICTV species demarcation criteria for ilarviruses of “serology, host range and sequence similarity,” where the latter is not yet defined, we suggest a recommended cut-off of 85% could be used even in the absence of more biological data (See identity comparisons Tables S1 (Motifs 1-VII) and S2 (Complete ORF 2a)). In the case of HdVBV, serological differences between it and AV2 and indications of recombination in RNA3 with shifting phylogenetic affinities of the predicted (3a) MP and (3b) CP suggest speciation. We therefore propose to classify this virus as **hydrangea vein banding virus (HdVBV)** as a member of a novel species named ***Ilarvirus HdVBV*** in the genus *Ilarvirus* of the family *Bromoviridae* (Table 1).**Creation of a fifth novel species in the genus *Ilarvirus* of the family *Bromoviridae*.** The full-length genome sequence of a new ilarvirus from sweet cherry (*Prunus avium*) from Greece was determined by high-throughput sequencing (Illumina Hi-seq 4000 platform) by Orfanidou et al (2021). The virus was tentatively named **Prunus virus I (PrVI).** Sequences of PrVI (isolate c18) were deposited in NCBI in 2021 as accession numbers MW579753, MW579754 and MW579755 for RNA1 (3,474 nt), RNA2 (2,911 nt) and RNA3 (2,231nt), respectively. The genome organization of CarIV is similar to that of members of the genus *Ilarvirus* (Fig. 1). *In silico* translationof open reading frames suggest that the PrVI RNA1 encodes one protein containing the methyltransferase and helicase domains; RNA2 two proteins, one protein containing the RNA-directed RNA polymerase domain (2a) and the other (2b) suggested to have gene silencing activity; and RNA 3 two proteins containing the 5’ putative movement protein (MP) and the 3’ coat protein (CP). Sequence comparisons and phylogenetic analyses of aa sequence alignment of the regions spanning the RNA-directed RNA polymerase motifs I to VII (Koonin 1991) showed PrVI grouped into the ilarvirus clade (subgroup 1). The aa sequence identity between PrVI and its closest known relative sequence Strawberry necrotic shock virus is 89.2 % for conserved RNA-directed RNA polymerase motifs I to VII and for the whole of the 2a protein 72.2 %. Based on of the existing ICTV species demarcation criteria for ilarviruses of “serology, host range and sequence similarity,” where the latter is not yet defined, we suggest a recommended cut-off of 85% could be used even in the absence of more biological data (See identity comparisons Tables S1 (Motifs 1-VII) and S2 (Complete ORF 2a)). We therefore propose to classify this virus as **Prunus virus 1 (PrV1),** a member of a novel species named ***Ilarvirus PrV1*** in the genus *Ilarvirus* of the family *Bromoviridae* (Table 1).**Creation of a sixth novel species in the genus *Ilarvirus* of the family *Bromoviridae*.** The full-length genome sequence of a new ilarvirus from rose from the United Kingdom was determined by high-throughput sequencing (Oxford Nanopore Technologies MinION Flongle) by Vazquez-Iglesias et al (2021). The virus is tentatively named **rosa ilarvirus-1 (RIV-1).** Sequences of RIV-1 were deposited in NCBI in 2021 as accession numbers MT017861, MT017862 and MT017863 for RNA1 (3,346 nt), RNA2 (3,063 nt) and RNA3 (2,329 nt), respectively. The genome organization of RIV-1 is similar to that of members of the genus *Ilarvirus* (Fig. 1). *In silico* translationof open reading frames suggest that the RIV-1 RNA1 encodes one protein containing the methyltransferase and helicase domains; RNA2 two proteins, one protein containing the RNA-directed RNA polymerase domain (2a) and the other (2b) potentially involved in RNA silencing suppression; and RNA 3 two proteins containing the 5’ putative movement protein (MP) and the 3’ coat protein (CP). Sequence comparisons and phylogenetic analyses of aa sequence alignment of the regions spanning the RNA-directed RNA polymerase motifs I to VII (Koonin 1991) showed RIV-1 grouped into the ilarvirus clade (subgroup 2). The aa sequence identity between RIV-1 and its closest known relative sequence citrus leaf rugose virus and tentative species rose ilarvirus 2 is 97.2% for conserved RNA-directed RNA polymerase motifs I to VII and tomato necrotic streak virus for the whole of the 2a protein 77.5%. Based on of the existing ICTV species demarcation criteria for ilarviruses of “serology, host range and sequence similarity,” where the latter is not yet defined, we suggest a recommended cut-off of 85% could be used even in the absence of more biological data (See identity comparisons Tables S1 (Motifs 1-VII) and S2 (Complete ORF 2a)). We therefore propose to classify this virus as **rose ilarvirus 1 (RIV1),** a member of a novel species named ***Ilarvirus RIV1*** in the genus *Ilarvirus* of the family *Bromoviridae* (Table 1).**Creation of a seventh novel species in the genus *Ilarvirus* of the family *Bromoviridae*.** The full-length genome sequence of a new ilarvirus from rose from Taiwan was determined by high-throughput sequencing (Illumina NovaSeq 6000) by Chen et al (2022). The virus is tentatively named **rose ilarvirus 2 (RIV-2).** Sequences of RIV-2 were deposited in NCBI in 2022 as accession numbers ON843765, ON843766 and ON843767 for RNA1 (3,408 nt), RNA2 (3,022 nt) and RNA3 (2,377 nt), respectively. The genome organization of RIV-2 (isolate TW) is similar to that of members of the genus *Ilarvirus* (Fig. 1). *In silico* translationof open reading frames suggest that the RIV-1 RNA1 encodes one protein containing the methyltransferase and helicase domains; RNA2 two protein, one protein containing the RNA-directed RNA polymerase domain (2a) and the other (2b) potentially involved in RNA silencing suppression; and RNA 3 two proteins containing the 5’ putative movement protein (MP) and the 3’ coat protein (CP). Sequence comparisons and phylogenetic analyses of aa sequence alignment of the regions spanning the RNA-directed RNA polymerase motifs I to VII (Koonin 1991) showed RIV-2 grouped into the ilarvirus clade (subgroup 2). The aa sequence identity between RIV-2 and its closest known relative sequence tentative species rose ilarvirus 1 is 97.2% for conserved RNA-directed RNA polymerase motifs I to VII and tomato necrotic streak virus for the whole of the 2a protein 78.7%. Based on of the existing ICTV species demarcation criteria for ilarviruses of “serology, host range and sequence similarity,” where the latter is not yet defined, we suggest a recommended cut-off of 85% could be used even in the absence of more biological data (See identity comparisons Tables S1 (Motifs 1-VII) and S2 (Complete ORF 2a)). We therefore propose to classify this virus as **rose ilarvirus 2 (RIV2),** a member of a novel species named ***Ilarvirus RIV2*** in the genus *Ilarvirus* of the family *Bromoviridae* (Table 1).**Creation of an eighth novel species in the genus *Ilarvirus* of the family *Bromoviridae*.** The full-length genome sequence of a new ilarvirus from soybean (*Glycine max*) from USA was determined by high-throughput sequencing (Illumina HiSeq 3000) by Elmore et al (2022). The virus was tentatively named **soybean ilarvirus 1 (SIlV1).** Sequences of SIlV1 (isolate IA-2016) were deposited in NCBI in 2022 as accession numbers OL539723, OL539724 and OL539725 for RNA1 (3,466 nt), RNA2 (2,955 nt) and RNA3 (2,327nt), respectively. The genome organization of SIlV1 is similar to that of members of the genus *Ilarvirus* (Fig. 1). *In silico* translationof open reading frames suggest that the SIlV1 RNA1 encodes one protein containing the methyltransferase and helicase domains; RNA2 two proteins, one protein containing the RNA-directed RNA polymerase domain (2a) and the overlapping ORF2b (201aa); and RNA 3 two proteins containing the 5’ putative movement protein (MP) and the 3’ coat protein (CP). Sequence comparisons and phylogenetic analyses of aa sequence alignment of the of regions spanning the RNA-directed RNA polymerase motifs I to VII (Koonin 1991) showed CarIV1 grouped into the ilarvirus clade (subgroup 1). The aa sequence identity between SIlV1 and its closest known relative sequence Parietaria mottle virus is 89.7 % for conserved RNA-directed RNA polymerase motifs I to VII and for the whole of the 2a protein 70.7 %. Based on of the existing ICTV species demarcation criteria for ilarviruses of “serology, host range and sequence similarity,” where the latter is not yet defined, we suggest a recommended cut-off of 85% could be used even in the absence of more biological data (See identity comparisons Tables S1 (Motifs 1-VII) and S2 (Complete ORF 2a)). We therefore propose to classify this virus as **soybean ilarvirus 1 (SoIV1)** as a member of a novel species named ***Ilarvirus SoIV1*** in the genus *Ilarvirus* of the family *Bromoviridae* (Table 1).**Creation of a ninth novel species in the genus *Ilarvirus* of the family *Bromoviridae*.** The full-length genome sequence of a new ilarvirus from water chestnut from China was determined by high-throughput sequencing (Illumina NovaSeq 6000) by Lv et al (2021). The virus is tentatively named **water chestnut virus A (WCVA).** Sequences of WCVA were deposited in NCBI in 2021 as accession numbers MZ170696, MZ170697 and MZ170698 for RNA1 (3,578 nt), RNA2 (2,873 nt) and RNA3 (2,073 nt), respectively. The genome organization of WCVA (isolate Guangxi) is similar to that of members of the genus *Ilarvirus* (Fig. 1). *In silico* translationof open reading frames suggest that the WCVA RNA1 encodes one protein containing the methyltransferase and helicase domains; RNA2 one protein containing the RNA-dependent RNA polymerase domain; and RNA 3 two proteins containing the 5’ putative movement protein (MP) and the 3’ coat protein (CP). Sequence comparisons and phylogenetic analyses of aa sequence alignment of the regions spanning the RNA-directed RNA polymerase motifs I to VII (Koonin 1991) showed CarIV1 grouped into the ilarvirus clade (subgroup 4). The aa sequence identity between WCVA and its closest known relative sequence Prune dwarf virus is 78.3 % for conserved RNA-directed RNA polymerase motifs I to VII and Fragaria chiloensis latent virus for the whole of the 2a protein 47.6 %. Based on of the existing ICTV species demarcation criteria for ilarviruses of “serology, host range and sequence similarity,” where the latter is not yet defined, we suggest a recommended cut-off of 85% could be used even in the absence of more biological data (See identity comparisons Tables S1 (Motifs 1-VII) and S2 (Complete ORF 2a)). We therefore propose to classify this virus as **water chestnut virus A (WCVA)**, a member of a novel species named ***Ilarvirus WCVA*** in the genus *Ilarvirus* of the family *Bromoviridae* (Table 1).**Creation of a tenth novel species in the genus *Ilarvirus* of the family *Bromoviridae*.** The full-length genome sequence of a new ilarvirus from pooled ***Physalis* sp.** gathered at the immediate surroundings of tomato farms in Slovenia was determined by high-throughput sequencing (HiSeq 2500) by Rivarez et al (2023). The virus is tentatively named **Solanum nigrum ilarvirus 1 (SnIV1).** Sequences of SIlV1 (isolate JUR20SW1) were deposited in NCBI in 2022 as accession numbers OL472060, OL472061 and OL472062 for RNA1 (3,445 nt), RNA2 (2,842 nt) and RNA3 (2,272 nt), respectively. The genome organization of SnIV1 is similar to that of members of the genus *Ilarvirus* (Fig. 1). *In silico* translationof open reading frames suggest that the SnIV1 RNA1 encodes one protein containing the methyltransferase and helicase domains; RNA2 two proteins, one protein containing the RNA-directed RNA polymerase domain (2a) and the other (2b) potentially involved in RNA silencing suppression; and RNA 3 two proteins containing the 5’ putative movement protein (MP) and the 3’ coat protein (CP). Sequence comparisons and phylogenetic analyses of aa sequence alignment of the of regions spanning the RNA-directed RNA polymerase motifs I to VII (Koonin 1991) showed SnIV1 grouped into the ilarvirus clade (subgroup 1). Closely related exemplars of this virus have previously been found *S. lycopersicum* and *S. nigrum* plants in France (Ma et al., 2020), in a pooled sample consisting of various legume species (Trifolium sp. and Vicia sp.), in Germany (Gaafar et al., 2020), and on grapevine leaves infected by *Plasmopara viticola* (Chiapello et al 2019), the fungus *Erysiphe necator* (unpublished), and lastly in pepper (*Capsicum annuum*) (Orfanidou et al 2022). This latter study was the first to demonstrate Koch’s postulates for the virus. Which complete genome should serve as the reference is open to debate. The *Physalis* sp. isolate used here is judged to be the first quality complete sequence submitted to GenBank that was characterized as plant-infecting. The aa sequence identity between SnlV1 and its closest known relative sequence Parietaria mottle virus is 86.4 % for conserved RNA-directed RNA polymerase motifs I to VII and for the whole of the 2a protein 70.5 %. Based on of the existing ICTV species demarcation criteria for ilarviruses of “serology, host range and sequence similarity,” where the latter is not yet defined, we suggest a recommended cut-off of 85% could be used even in the absence of more biological data (See identity comparisons Tables S1 (Motifs 1-VII) and S2 (Complete ORF 2a)). We therefore propose to classify this virus as **Solanum nigrum ilarvirus 1 (SnIV1)** as a member of a novel species named ***Ilarvirus SnIV1*** in the genus *Ilarvirus* of the family *Bromoviridae* (Table 1). |

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**Supporting evidence**

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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Virus Name | Virus Species | Genus | RNA1\* | RNA2 | RNA3 |
| Actinidia yellowing ringspot virus | *Ilarvirus AYRSpV* | *Ilarvirus* | MN612758  | MN612759  | MN612760  |
| Apple ilarvirus 2  | *Ilarvirus AIV2* | *Ilarvirus* | ON932434  | ON932435  | ON932436  |
| Carpotroche-associated ilarvirus | *Ilarvirus CarIV1* | *Ilarvirus* | OL964100  | OL964099  | OL964098  |
| Hydrangea vein banding virus | *Ilarvirus HdVBV* | *Ilarvirus* | OK666835  | OK666836  | OK666837  |
| Prunus virus I | *Ilarvirus PrV1* | *Ilarvirus* | MW579753  | MW579754  | MW579755  |
| Rosa ilarvirus-1 | *Ilarvirus RIV1* | *Ilarvirus* | MT017861  | MT017862  | MT017863  |
| Rose ilarvirus-2  | *Ilarvirus RIV2* | *Ilarvirus* | ON843765  | ON843766  | ON843767  |
| Solanum nigrum ilarvirus 1 | *Ilarvirus SnIV1* | *Ilarvirus* | OL472060  | OL472061  | OL472062  |
| Soybean ilarvirus 1  | *Ilarvirus SolV1* | *Ilarvirus* | OL539723  | OL539724  | OL539725  |
| Water chestnut virus A | *Ilarvirus WCVA* | *Ilarvirus* | MZ170696  | MZ170697  | MZ170698  |

**Figure 1.** Schematic genome organization for members of the family *Bromoviridae*: (a) genera *Alfamovirus*, *Bromovirus*, *Ilarvirus* 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) 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 in red. Bar = genetic distance. Numbers at nodes = bootstrap values.



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