This form should be used for all taxonomic proposals. Please complete all those modules that are applicable.

For guidance, see the notes written in blue and the separate document “Help with completing a taxonomic proposal”

Please try to keep related proposals within a single document.

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

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Code assigned:** | ***2017.001P*** | | | | (to be completed by ICTV officers) |
| **Short title:** Two new genera in family *Potyviridae* | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1** **X 2 X 3  4 X** | | | |
| **Author(s):** | | | | | |
| |  |  | | --- | --- | | Wylie, Stephen (Chair) | [s.wylie@murdoch.edu.au](mailto:s.wylie@murdoch.edu.au) | | Adams, Michael J. | [mike.adams.ictv@gmail.com](mailto:mike.adams.ictv@gmail.com) | | Chalam, Celia | mailcelia@gmail.com | | Kreuze, Jan F. | [j.kreuze@cgiar.org](mailto:j.kreuze@cgiar.org) | | Lopez-Moya, Juan Jose | [juanjose.lopez@cragenomica.es](mailto:juanjose.lopez@cragenomica.es) | | Ohshima, Kazusato | [ohshimak@cc.saga-u.ac.jp](mailto:ohshimak@cc.saga-u.ac.jp) | | Praveen, Shelly | shellypraveen@hotmail.com | | Rabenstein, Frank | frank.rabenstein@jki.bund.de | | Wang, Aiming | [aiming.wang@agr.gc.ca](mailto:aiming.wang@agr.gc.ca) | | Zerbini, F. Murilo | [zerbini@ufv.br](mailto:zerbini@ufv.br) | | | | | | |
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| **List the ICTV study group(s) that have seen this proposal:** | | | | | |
| A list of study groups and contacts is provided at <http://www.ictvonline.org/subcommittees.asp> . If in doubt, contact the appropriate subcommittee chair (there are six virus subcommittees: animal DNA and retroviruses, animal ssRNA-, animal ssRNA+, fungal and protist, plant, bacterial and archaeal) | | | *Potyviridae* | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
|  | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | | 2017 | |
| Date of this revision (if different to above): | | | |  | |

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

**Part 2**: **PROPOSED TAXONOMY**

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| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet: 2017.001P.N.v1.Potyviridae\_2gen** |

Please display the taxonomic changes you are proposing on the accompanying spreadsheet module 2017\_TP\_Template\_Excel\_module. Submit both this and the spreadsheet to the appropriate ICTV Subcommittee Chair.

**Part 4:** **APPENDIX**: supporting material

| additional material in support of this proposal |
| --- |
| **References:** |
| Lockhart B, Zlesak D, Fetzer J (2011) Identification and partial characterization of six new viruses of cultivated roses in the USA. *Acta Horticulturae* 901:139–147  Mollov D, Lockhart B, Zlesak D (2013) Complete nucleotide sequence of rose yellow mosaic virus, a novel member of the family *Potyviridae*. *Archives of Virology*, *158*:1917-1923  Seo, J.K., Kwak, H.R., Kim, M.K., Kim, J.S. and Choi, H.S., 2017. The complete genome sequence of a novel virus, bellflower veinal mottle virus, suggests the existence of a new genus within the family *Potyviridae*. *Archives of Virology*, DOI 10.1007/s00705-017-3374-5 |

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| --- |
| **Annex:**  Please explain the reasons for the taxonomic changes you are proposing and provide evidence to support them. The following information should be provided, where relevant:   * **Species demarcation criteria**: Explain how new species differ from others in the genus and demonstrate that these differences meet the criteria previously established for demarcating between species. If no criteriahave previously been established, and if there will now be more than one species in the genus, please state the demarcation criteria you are proposing. * **Higher taxa**:   + There is no formal requirement to state demarcation criteria when proposing new genera or other higher taxa. However, a similar concept should apply in pursuit of a rational and consistent virus taxonomy.   + Please indicate the **origin of names** assigned to new taxa at genus level and above.   + For each new genus a **type species** must be designated to represent it. Please explain your choice. * **Supporting evidence**: The use of Figures and Tables is strongly recommended (note that copying from publications will require permission from the copyright holder). For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance. |

**Proposal to create a new species in a new genus, *Bevemovirus***

A new virus was isolated from a bellflower (*Campanula takesimana*) plant located in a public park in Suwon, South Korea (Seo et al., 2017). The plant showed veinal mottle symptoms, and its complete genome sequence was determined after high-throughput sequencing of a transcriptome library of the infected plant. The assembled sequence was 8259 nt (KY491536). The termini of the genome were determined by RACE. Presence of the virus in the host plant was confirmed using specific primers. There was one large ORF of 7416 nt, predicted to be processed into nine mature proteins. The polyprotein is notable in that it lacks the P1 of most potyvirids. Although its genome architecture resembles that of macluraviruses, pairwise analysis of the polyprotein sequence with those of four macluravirus species it shared only 26-27% aa identity with them, and 22-23% aa identity with three bymovirus species. It shared 14-18% aa with the complete polyproteins of other potyvirids. Phylogenetic analysis of the aa sequence of this isolate placed the virus, named by the authors Bellflower veinal mottle virus (BVMoV) isolate SW, basal to *Macluravirus* and *Bymovirus* (Fig 1). The vector is unknown. The HC-Pro lacks the conserved potyvirus aphid transmission motifs R/KITC and PTK, but the coat protein has DTG near its N-terminus, possibly analogous to the conserved DAG motif of potyviruses that is also involved in aphid transmission. We propose that *Bellflower veinal mottle virus* be created as the type species of a new genus named *Bevemovirus* (from bellflower veinal mottle virus).

**Proposal to create a new genus, *Roymovirus* for a species currently unassigned in the family**

A virus with filamentous 720- to 750-nm particles associated with a disease of roses distinguished by yellow mosaic, premature leaf senescence and necrotic stem lesions was collected in 2008 from *Rosa* hybrid cv Ballerina. The virus was found to occur naturally in New York in rose cultivars Ballerina, Buff Beauty, Mozart, Cornelia, Nastarana, Dorothy Perkins, and Sir Thomas Lipton and in Minnesota in rose cultivars June Bride and Captain Harry Stebbings (Lockhart et al., 2011). Later, the complete nucleotide sequence of the whole genome of the virus, provisionally named rose yellow mosaic virus (RoYMV) isolate Minnesota was obtained from nine overlapping cDNA clones obtained from virion RNA extracted from rose cv. Ballerina (Mollov et al., 2013). The sequence of the RoYMV genomic RNA was 9508 nt excluding the 3′ poly-A end (JF280796). The nt sequence and deduced amino acid sequence of the polyprotein shared greatest identities with viruses in family *Potyviridae*, but they were not clearly closer to members of any one genus. Comparison of the deduced amino acid sequence of the large ORF revealed identities with other viruses of the family to be low, ranging from 13% (some bymoviruses) to 23% (some potyviruses). Some of the individual proteins shared up to 34% aa identity with other potyvirids. Phylogenetic analysis of the coat protein and ORF placed RoYMV basal to viruses of *Tritimovirus*, *Poeacevirus*, and *Ipomovirus* (Fig 1).

Potyviruses are aphid-transmitted, and this transmission is mediated by conserved HC-Pro and coat protein motifs. The conserved KITC and PTK motifs were not present in the RoYMV HC-Pro. Instead, a putative C-2x-C eriophyid mite transmission motif is found at amino acid residues 48-51 at the N-terminus of the protein. The coat protein DAG motif found in most aphid-transmitted potyvirids was also lacking. Together this information suggests RoYMV may be transmitted by eriophyid mites, although this was not proven experimentally.

*Rose yellow mosaic virus* was ratified as a species in 2013, but it was not assigned a genus. We propose that a new genus be created, in which *Rose yellow mosaic virus* is the type species. We propose the new genus be named *Roymovirus* (from rose yellow mosaic virus).

**Figure 1** Estimated phylogeny of deduced polyprotein sequences of completely sequenced representative viruses of ratified species within family *Potyviridae*, genera *Brambyvirus, Bymovirus, Ipomovirus, Macluravirus, Poacevirus, Potyvirus, Rymovirus, Tritimovirus*, and two proposed new genera, Roymovirus and Bevemovirus (shown in red font), were used. The tree was deduced in Mega v7.0.21 after alignment in Muscle using the Neighbor-joining method with 1000 bootstrap replications. Bootstrap support for branches is shown at the junctions of branches where it was >60%. Evolutionary distances were calculated using the Poisson correction method and branch lengths are proportional to genetic distance in units of amino acid substitutions per site.

Accession codes corresponding to the nucleotide sequence of each virus genome sequence used in the tree are: Agropyron mosaic virus, AY623626; artichoke latent virus, KP405232; barley mild mosaic virus (RNA1), D83408; bellflower veinal mottle virus, KY491536; blackberry virus Y, AY994084; broad-leafed dock virus A, KU053507; brome streak mosaic virus, Z48506; Caladenia virus A, JX156425; cassava brown streak virus, FN434437; Chinese yam necrotic mosaic virus, AB710145; Coccinia mottle virus, KU935732; cucumber vein yellowing virus, AY578085; Hordeum mosaic virus, AY623627; oat mosaic virus (RNA1), AJ306718; oat necrotic mottle virus, AY377938; rose yellow mosaic virus, JF280796; ryegrass mosaic virus, Y09854; squash vein yellowing virus, EU259611; sugarcane streak mosaic virus, GQ388116; sweet potato mild mottle virus, Z73124; Triticum mosaic virus, FJ669487; wheat yellow mosaic virus (RNA1), FJ361765; yam chlorotic mosaic virus, KT724961.

