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:** | ***2018.003M*** | | | | (to be completed by ICTV officers) |
| **Short title:** Three new species in the genus *Dichorhavirus*, family *Rhabdoviridae* | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
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| Juliana Freitas-Astúa [juliana.astua@embrapa.br](mailto:juliana.astua@embrapa.br) | | | | | |
| **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) | | | ICTV *Rhabdoviridae* Study Group | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
| Reviewed and supported by the Study Group (8 supporters and 4 non-responders). | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | | June 6, 2018 | |
| Date of this revision (if different to above): | | | |  | |

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

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

|  |
| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet:** 2018.003M.N.v1.Dichorhavirus\_3sp |

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.

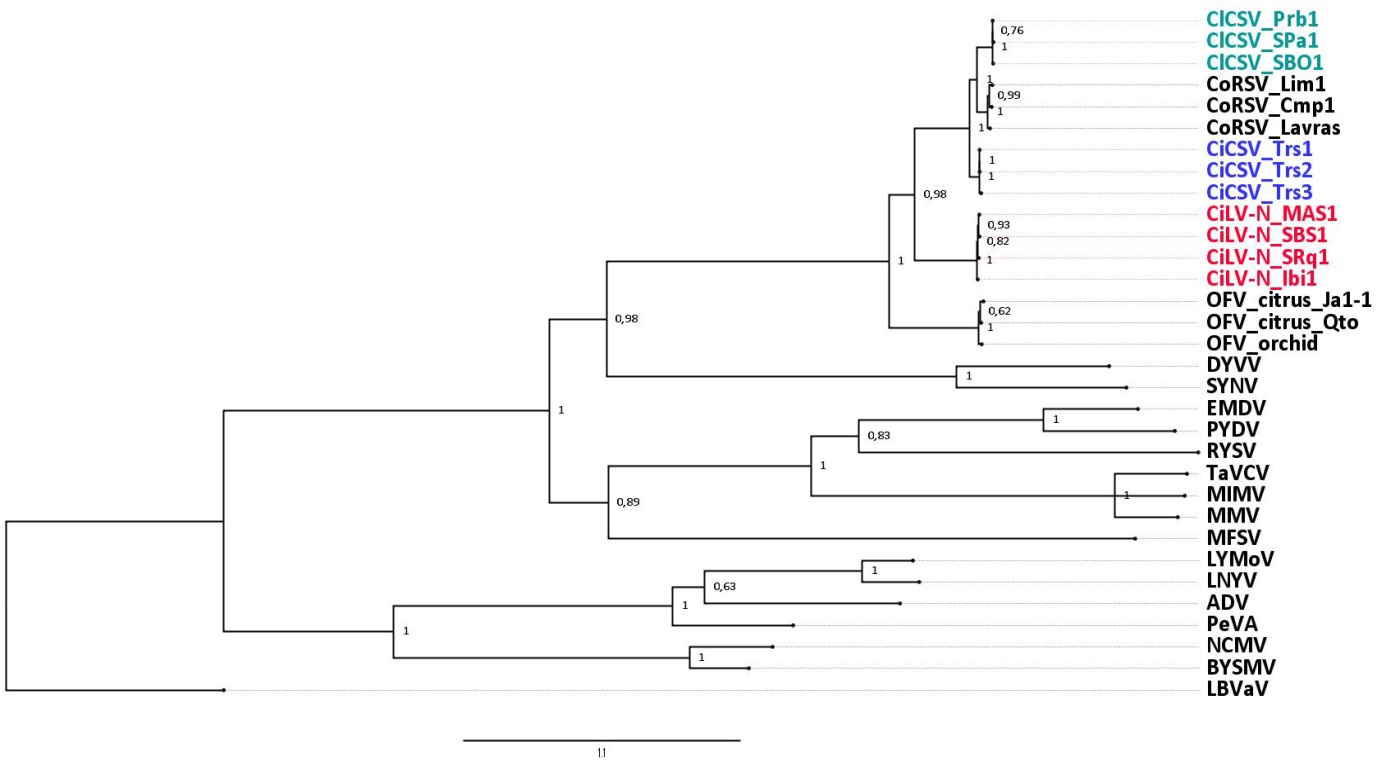
**Part 4:** **APPENDIX**: supporting material

| additional material in support of this proposal |
| --- |

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.

|  |
| --- |
| Citrus leprosis virus N (CiLV-N), citrus chlorotic spot virus (CiCSV), and Clerodendrum chlorotic spot virus (ClCSV) are unassigned negative-sense, single-stranded (**−**)ssRNA short bacilliform plant viruses. CiLV-N and ClCSV were previously suggested as tentative members of genus *Dichorhavirus*, family *Rhabdoviridae*, order *Mononegavirales* (1,2,3). CiCSV was recently identified, characterized, and is also proposed as a new member of the same genus (4). These three viruses cause only localized lesions on their hosts under natural conditions, are transmitted by mites of the genus *Brevipalpus,* have similarparticle morphology (non-enveloped bacilliform particles), induce typical symptoms and nuclear cytopathic effects, exhibit sequence similarity, and share similar genome organization with viruses belonging to the two accepted species of the genus*,* namely *Orchid fleck dichorhavirus* and *Coffee ringspot dichorhavirus* (1,2,4).  CiLV-N infects *Citrus sinensis* (sweet orange) plants in São Paulo state, Brazil. Three complete and one near-complete (3' and 5' ends were not sequenced) genome sequences have been determined for four isolates of the virus (1).  ClCSV was identified in two *Clerodendrum* sp. plants and one *Hibiscus rosa-sinensis* plant from different municipalities of the state of São Paulo, Brazil. The two isolates from *Clerodendrum* had their genomes fully sequenced, while the isolate from hibiscus has a near complete genome sequence (2).  CiCSV was originally found in two sweet orange plants and one beach hibiscus plant (*Hibiscus tiliaceus* syn. *Talipariti tiliaceum*) from Teresina, state of Piauí, Brazil. One of the citrus isolates had its genome completely sequenced, while near-complete sequences are available for the other two isolates (4).  The available biological and nucleotide sequence data indicate that CiLV-N, ClCSV, and CiCSV are related, but distinct, *Brevipalpus* mite-transmitted, (**−**)ssRNA viruses and should be classified taxonomically as members of three novel species within the genus *Dichorhavirus*.  While isolates of the same virus share >89% whole genome nucleotide sequence identity, comparisons between the accepted and proposed dichorhaviruses yield > 20% divergence in the *L* gene, as well as any other gene sequence of their genomes (Tables 1 and 2). Additionally, all accepted and proposed species form distinct phylogenetic clades (Figure 1).  Finally, the dichorhaviruses display differences in hosts and, mainly, in vectors (orchid fleck virus (OFV) seems to be transmitted only by *B. californicus*, coffee ringspot virus (CoRSV) has been reported so far as transmitted by *B. papayensis*, CiLV-N is transmitted by *B. phoenicis*, and ClCSV and CiCSV are transmitted by *B. yothersi* and/or *B. aff. yothersi*. Some of these viruses are found in particular niches (although both CiLV-N and CiCSV infect citrus plants in Brazil, the first one has been identified only under cooler weather conditions, while the latter only in much warmer situation, probably due to vector specificity (1,4). Therefore, we propose the creation of three new species within genus *Dichorhavirus* to accommodate these new viruses. **Species demarcation criteria** Currently, the criterion for demarcation of species within the genus is 25% divergence in the *L* gene (3,5). We propose expanding the species demarcation criteria for the genus *Dichorhavirus*, in line with the accepted criteria in other genera of the *Rhabdoviridae*, as follows:  “Viruses assigned to different species within the genus Dichorhavirus have at least two of the following characteristics: A) minimum nucleotide sequence divergence of 20% in *L* genes; B) minimum nucleotide sequence divergence of 20% in RNA1; C) can be distinguished in serological tests; and D) occupy different ecological niches as evidenced by differences in plant hosts and/or arthropod vectors.”  CiLV-N and CiCSV meet demarcation criteria A, B and D. ClCSV meets the four criteria. OFV and CoRSV meet demarcation criteria A, B and D.   * **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. |



*Dichorhavirus*

*Nucleorhabdovirus*

*Cytorhabdovirus*

*Varicosavirus*

**Figure 1.** Bayesian phylogenetic reconstruction using the L protein deduced amino acid sequence of a number of plant-infecting rhabdoviruses. A Gblocks-edited Clustal alignment containing 71% of the original 2,284 positions was analyzed under the lowest BIC scores substitution model (LG + G + I + F) calculated in MEGA7. MCMC convergence was obtained for four independent runs of 2 million generations, which were sufficient to obtain a proper sample for posterior probability, assessed by effective sample sizes (ESS) above 200. A majority-rule (50%) consensus tree was obtained using the Geneious package v. R11.2 and visualized using Figtree v. 1.4.3. Gblocks parameters were as follows: min. number of sequences for a conserved position = 17, min. number of sequences for a flanking position = 17, max. number of contiguous nonconserved positions = 30, min. length of a block = 8, half allowed gap positions, and using similarity matrices. Bar size below the tree indicates the average number of amino acid substitutions per site

**Table 1**. Percentage of nucleotide sequence identity – *L* gene. In red: isolates of the same species ( > 80% identity).

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **CiLV-N**  **Ibi1** | **CiLV-N SRq1** | **CiLV-N MAS1** | **CiLV-N**  **SBS1** | **CiCSV**  **Trs1** | **CiCSV**  **Trs3** | **CiCSV**  **Trs2** | **CoRSV**  **Cmp1** | **CoRSV**  **Lim1** | **CoRSV**  **Lavras** | **ClCSV**  **Prb1** | **ClCSV**  **SBO1** | **ClCSV**  **SPa1** | **OFV**  **citrus\_Jal-1** | **OFV**  **citrus\_Qto** | **OFV**  **So** | **OFV**  **NHHS1** |
| **CiLV-N\_SRq1** | 97..8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **CiLV-N\_MAS1** | 98.0 | 97.8 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **CiLV-N\_SBS1** | 97.7 | 97.6 | 98.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **CiCSV\_Trs1** | 62.0 | 62.0 | 61.9 | 62.0 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **CiCSV\_Trs3** | 61.7 | 61.7 | 61.6 | 61.7 | 98.6 |  |  |  |  |  |  |  |  |  |  |  |  |
| **CiCSV\_Trs2** | 61.8 | 61.8 | 61.7 | 61.8 | 98.5 | 98.3 |  |  |  |  |  |  |  |  |  |  |  |
| **CoRSV\_Cmp1** | 61.2 | 61.4 | 61.5 | 61.4 | 77.1 | 76.7 | 77.0 |  |  |  |  |  |  |  |  |  |  |
| **CoRSV\_Lim1** | 61.6 | 61.6 | 61.7 | 61.5 | 77.1 | 76.7 | 76.9 | 94.0 |  |  |  |  |  |  |  |  |  |
| **CoRSV\_Lavras** | 61.5 | 61.6 | 61.7 | 61.6 | 77.1 | 76.7 | 76.8 | 93.4 | 92.9 |  |  |  |  |  |  |  |  |
| **ClCSV\_Prb1** | 62.6 | 62.7 | 62.6 | 62.5 | 75.8 | 75.5 | 75.8 | 77.2 | 77.0 | 77.5 |  |  |  |  |  |  |  |
| **ClCSV\_SBO1** | 62.6 | 62.7 | 62.6 | 62.4 | 75.7 | 75.4 | 75.6 | 77.3 | 76.9 | 77.4 | 99.4 |  |  |  |  |  |  |
| **ClCSV\_SPa1** | 62.7 | 62.8 | 62.6 | 62.5 | 75.9 | 75.7 | 75.9 | 77.2 | 76.8 | 77.5 | 98.1 | 98.2 |  |  |  |  |  |
| **OFV\_citrus\_Jal-1** | 59.1 | 59.0 | 58.9 | 59.2 | 59.7 | 59.4 | 59.4 | 58.9 | 59.2 | 58.7 | 59.1 | 59.0 | 59.0 |  |  |  |  |
| **OFV\_citrus\_Qto** | 59.2 | 59.1 | 59.1 | 59.3 | 60.1 | 59.8 | 59.8 | 59.2 | 59.6 | 59.1 | 59.4 | 59.3 | 59.4 | 96.2 |  |  |  |
| **OFV\_Cym07** | 59.0 | 58.8 | 58.8 | 58.9 | 59.7 | 59.5 | 59.5 | 59.3 | 59.4 | 59.2 | 59.0 | 59.0 | 59.1 | 88.8 | 89.8 |  |  |
| **OFV\_So** | 58.9 | 58.6 | 58.7 | 58.8 | 59.8 | 59.6 | 59.6 | 59.3 | 59.4 | 59.2 | 59.2 | 59.2 | 59.2 | 89.1 | 90.0 | 98.7 |  |
| **OFV\_NHSS1** | 58.9 | 58.8 | 58.8 | 58.9 | 59.8 | 59.5 | 59.5 | 59.1 | 59.3 | 59.0 | 58.9 | 58.9 | 59.0 | 88.8 | 89.8 | 98.5 | 98.6 |

**Table 2.** Percentage of nucleotide sequence identity – RNA1. In red: isolates of the same species (> 80% identity).

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **CiLV-N**  **Ibi1** | **CiLV-N SRq1** | **CiLV-N MAS1** | **CiLV-N**  **SBS1** | **CiCSV**  **Trs1** | **CiCSV**  **Trs2** | **CiCSV**  **Trs3** | **CoRSV**  **Lavras** | **CoRSV**  **Lim1** | **ClCSV**  **Prb1** | **ClCSV**  **SBO1** | **ClCSV**  **SPa1** | **OFV**  **citrus\_Jal-1** | **OFV**  **citrus\_Qto** | **OFV**  **So** | **OFV**  **NHHS1** |
| **CiLV-N\_SRq1** | 97.9 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **CiLV-N\_MAS1** | 92.6 | 92.2 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **CiLV-N\_SBS1** | 92.2 | 92.6 | 90.3 |  |  |  |  |  |  |  |  |  |  |  |  |  |
| **CiCSV\_Trs1** | 49.9 | 49.7 | 51.0 | 50.2 |  |  |  |  |  |  |  |  |  |  |  |  |
| **CiCSV\_Trs2** | 51.5 | 51.5 | 51.3 | 51.8 | 96.6 |  |  |  |  |  |  |  |  |  |  |  |
| **CiCSV\_Trs3** | 51.3 | 51.3 | 51.2 | 51.6 | 95.6 | 95.3 |  |  |  |  |  |  |  |  |  |  |
| **CoRSV\_Lavras** | 51.6 | 51.5 | 52.1 | 51.5 | 70.4 | 71.4 | 71.4 |  |  |  |  |  |  |  |  |  |
| **CoRSV\_Lim1** | 50.9 | 50.7 | 51.1 | 50.8 | 68.4 | 71.4 | 70.0 | 92.0 |  |  |  |  |  |  |  |  |
| **ClCSV\_Prb1** | 50.6 | 50.5 | 51.4 | 50.1 | 70.9 | 70.0 | 70.7 | 71.5 | 68.8 |  |  |  |  |  |  |  |
| **ClCSV\_SBO1** | 50.7 | 50.6 | 51.5 | 50.2 | 70.9 | 70.7 | 70.7 | 71.6 | 69.0 | 98.8 |  |  |  |  |  |  |
| **ClCSV\_SPa1** | 52.2 | 52.1 | 51.6 | 51.6 | 70.8 | 70.6 | 70.7 | 72.1 | 69.9 | 99.5 | 98.7 |  |  |  |  |  |
| **OFV\_citrus\_Jal-1** | 47.0 | 47.0 | 47.9 | 47.3 | 47.2 | 48.3 | 48.1 | 46.6 | 45.8 | 47.1 | 47.1 | 46.6 |  |  |  |  |
| **OFV\_citrus\_Qto** | 47.6 | 47.6 | 48.0 | 47.8 | 47.3 | 48.1 | 47.9 | 46.8 | 46.4 | 47.1 | 47.2 | 46.8 | 96.0 |  |  |  |
| **OFV\_So** | 47.1 | 47.2 | 48.0 | 47.4 | 47.2 | 48.4 | 48.0 | 46.4 | 46.0 | 46.8 | 46.9 | 46.4 | 89.5 | 90.1 |  |  |
| **OFV\_NHHS1** | 47.2 | 47.3 | 48.1 | 47.4 | 47.2 | 48.5 | 48.0 | 46.4 | 46.0 | 46.9 | 47.0 | 46.4 | 89.4 | 90.0 | 99.3 |  |
| **OFV\_Cym07** | 48.3 | 48.3 | 48.6 | 48.1 | 47.7 | 48.8 | 48.7 | 47.0 | 46.4 | 47.4 | 47.3 | 47.0 | 81.4 | 81.8 | 82.8 | 82.2 |

| **References:** |
| --- |
| 1. Ramos-González, P.L., Chabi-Jesus, C., Guerra-Peraza, O., Tassi, A.D., Kitajima, E.W., Harakava, R., Salaroli, R.B., Freitas-Astúa, J. 2017. Citrus leprosis virus N: a new dichorhavirus causing citrus leprosis disease. Phytopathology 107(8): 963-976 (<http://dx.doi.org/10.1094/PHYTO-02-17-0042-R>). 2. Ramos-González, P.L., Chabi-Jesus, C., Banguela-Castillo, A., Tassi, A.D., Rodrigues, M., Kitajima, E.W., Salaroli, R., Harakava, R., Freitas-Astúa, J. 2018.Unveiling the complete genome sequence of *Clerodendrum* chlorotic spot virus, a putative dichorhavirus infecting ornamental plants (in press, Archives of Virology, DOI: 10.1007/s00705-018-3857-z). 3. Walker, P.J., Blasdell, K.R., Calisher, C.H., Dietzgen, R.G., Kondo, H., Kurath, G., Longdon, B., Stone, D.M., Tesh, R.B., Tordo, N., Vasilakis, N., Whitfield, A.E. 2018. ICTV Virus Taxonomy Profile: *Rhabdoviridae*. Journal of General Virology 99(4): 447-448. DOI 10.1099/jgv.0.001020 4. Chabi-Jesus, C., Ramos-González, P.L., Guerra-Peraza, O., Kitajima, E.W., Tassi, A.D., Harakava, R., Beserra Jr., E.A., Freitas-Astúa, J. 2018. Molecular characterization of Citrus chlorotic spot virus, a new dichorhavirus associated with citrus leprosis symptoms. Plant Disease in press (<https://doi.org/10.1094/PDIS-09-17-1425-RE>). 5. Dietzgen R.G., Kuhn J.H., Clawson A.N., Freitas-Astúa J., Goodin M.M., Kitajima E.W., Kondo H, Wetzel T., Whitfield A.E. 2014. *Dichorhavirus*: a proposed new genus for *Brevipalpus* mite-transmitted, nuclear, bacilliform, bipartite, negative-strand RNA plant viruses. Archives of Virology 159:607-619. |