

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

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| **Code assigned:** | **2020.031P** |  |
| **Short title:** Abolish the genus *Mandarivirus*, create one new subgenus (*Mandarivirus*) in the genus *Potexvirus* and one new subgenus (*Acarillexivirus*)in the genus *Allexivirus* (*Tymovirales*: *Alphaflexiviridae*) | | |
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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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| *Alphaflexiviridae* 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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| **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 | July 30, 2020 |
| Date of this revision (if different to above) |  |

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

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**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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| 2020.031P.R.Alphaflexiviridae\_ab1gen\_2nsg.xlxs |

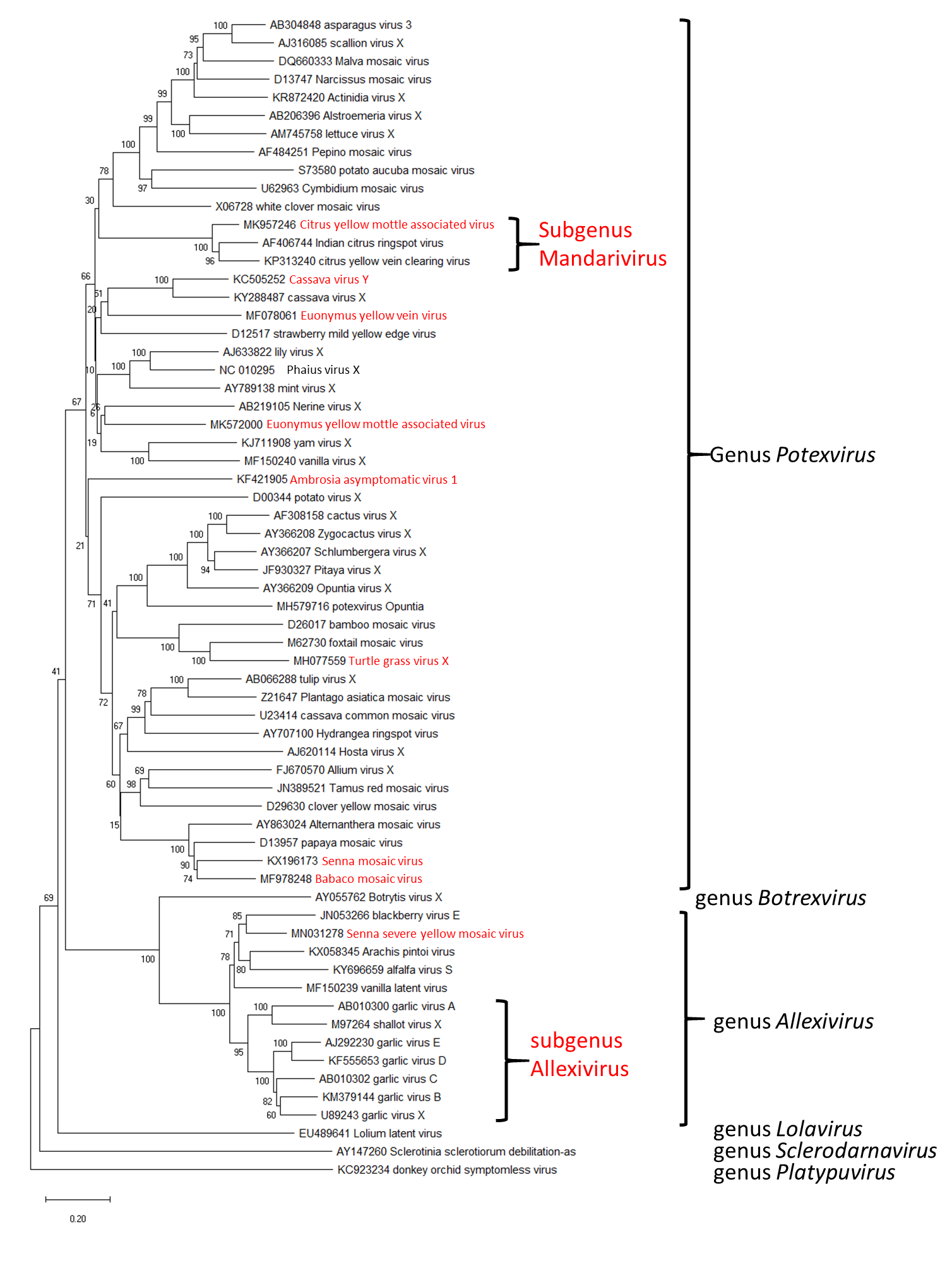
**Abstract**

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| The two species in the genus *Mandarivirus* have an additional ORF6, as compared to potexviruses, to which they are most closely related. However, they do not form a separate phylogenetic lineage from potexviruses. Likewise, in the genus *Allexivirus*, a subgroup of viruses infecting *Allium* species encode an additional ORF at the 3’ end of their genomes compared to the remaining viruses. To resolve these inconsistencies, we propose to abolish the genus *Mandarivirus* and create a new subgenus *Mandarivirus* within the genus *Potexvirus*, and to create subgenus *Acarallexivirus* within the existing genus *Allexivirus*. |

**Text of proposal**

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| |  | | --- | | **Abolish the genus *Mandarivirus* and create a new subgenus *Mandarivirus* within the genus *Potexvirus* of the family *Alphaflexiviridae***  The genus *Mandarivirus* was created in 2003 within the then existing family *Flexiviridae* based on its having an additional ORF6, encoding a putative nucleic acid binding protein (NAB), as compared to potexviruses, to which it was most closely related based on the phylogeny of the replicase protein and also serology. However, since then, as more potexvirus species have been discovered it has become clear that the genus *Mandarivirus*, which currently includes two species, does not form a separate phylogenetic lineage as compared to the viruses of the genus *Potexvirus*, regardless of which gene or predicted protein is used for analysis (Figure 1). A similar situation currently exists in the genus *Allexivirus*, where a subgroup of viruses infecting *Allium* species encode an addition NAB at the 3’ end of their genomes compared to the remaining viruses.  To resolve this inconsistency, we propose to abolish the genus *Mandarivirus* and create a new subgenus *Mandarivirus* within the genus *Potexvirus*. The species assigned to the abolished genus *Mandarivirus* are then re-assigned to the new subgenus *Mandarivirus*.  **Create a new subgenus *Acarallexivirus* within the genus *Allexivirus***  A new subgenus, *Acarallexivirus*, within the genus *Allexivirus* is proposed for the following reasons:   1. All *Allium* infecting allexiviruses group together phylogenetically, separate from those infecting other host species; 2. All *Allium* infecting allexiviruses have an additional nucleic acid binding protein as opposed to those infecting other plant species (Figure 2).     The original name of the genus originated from this group of viruses and is derived from **All**ium and Fl**exivirus**. Since mite transmission has only been confirmed in species belonging to the proposed new subgenus, the proposed name is *Acarallexivirus*, where Acar derives from Acari, the subclass containing mite species. | |

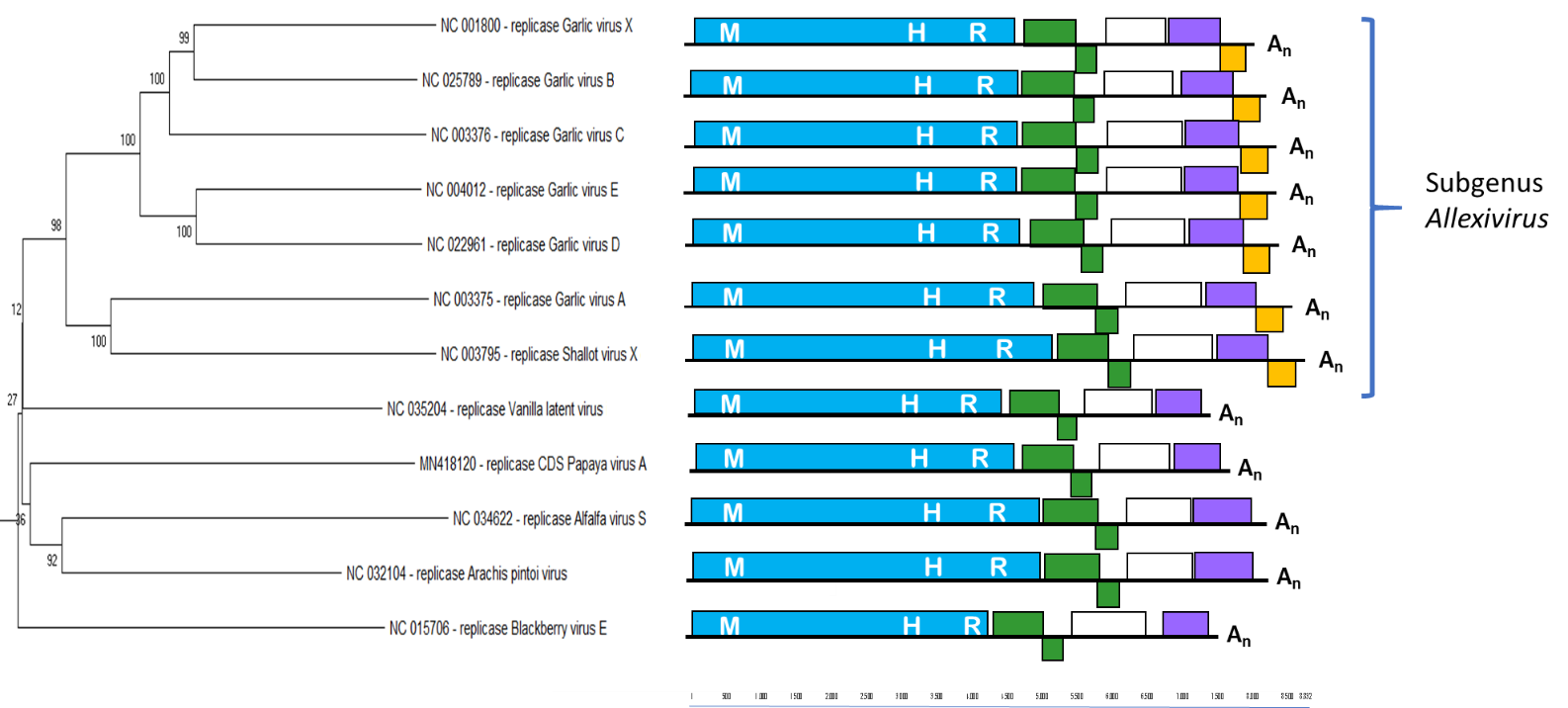
**Supporting evidence**



*Mandarivirus*

*Acarallexivirus*

**Figure 1.** Phylogenetic tree of replication protein of members of the family *Alphaflexiviridae* showing the monophyletic origin of the suggested new subgenera *Acarallexivirus* and *Mandarivirus* nested within the genera *Allexivirus* and *Potexvirus*, respectively. Other proposed new species submitted as a separate proposal are indicated in red. Tree was generated using neighbor-joining and JTT distance matrix with 500 bootstrap replicates. Numbers on nodes indicate the percentage of bootstrap support for the corresponding node.



*Acarallexivirus*

**Figure 2.** Phylogenetic tree of replication protein encoding genes and genome structures of members of the genus *Allexivirus* showing the monophyletic origin and distinct genome structure of the suggested new subgenus *Acarallexivirus*. Light blue: replication protein gene; green triple gene block protein 1 and 2 genes respectively; white: ORF4; purple: Coat Protein; orange: Nucleic acid binging protein. Tree was generated using neighbor-joining and the maximum composite likelihood algorithm with 500 bootstrap replicates. Numbers on nodes indicate the % of bootstrap support for the corresponding node.