

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

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| **Code assigned:** | **2020.029P** |  |
| **Short title:** Create eight new species in the genus *Potexvirus* and one new species in the genus *Allexivirus* (*Tymovirales*: *Alphaflexiviridae*) | | |
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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**

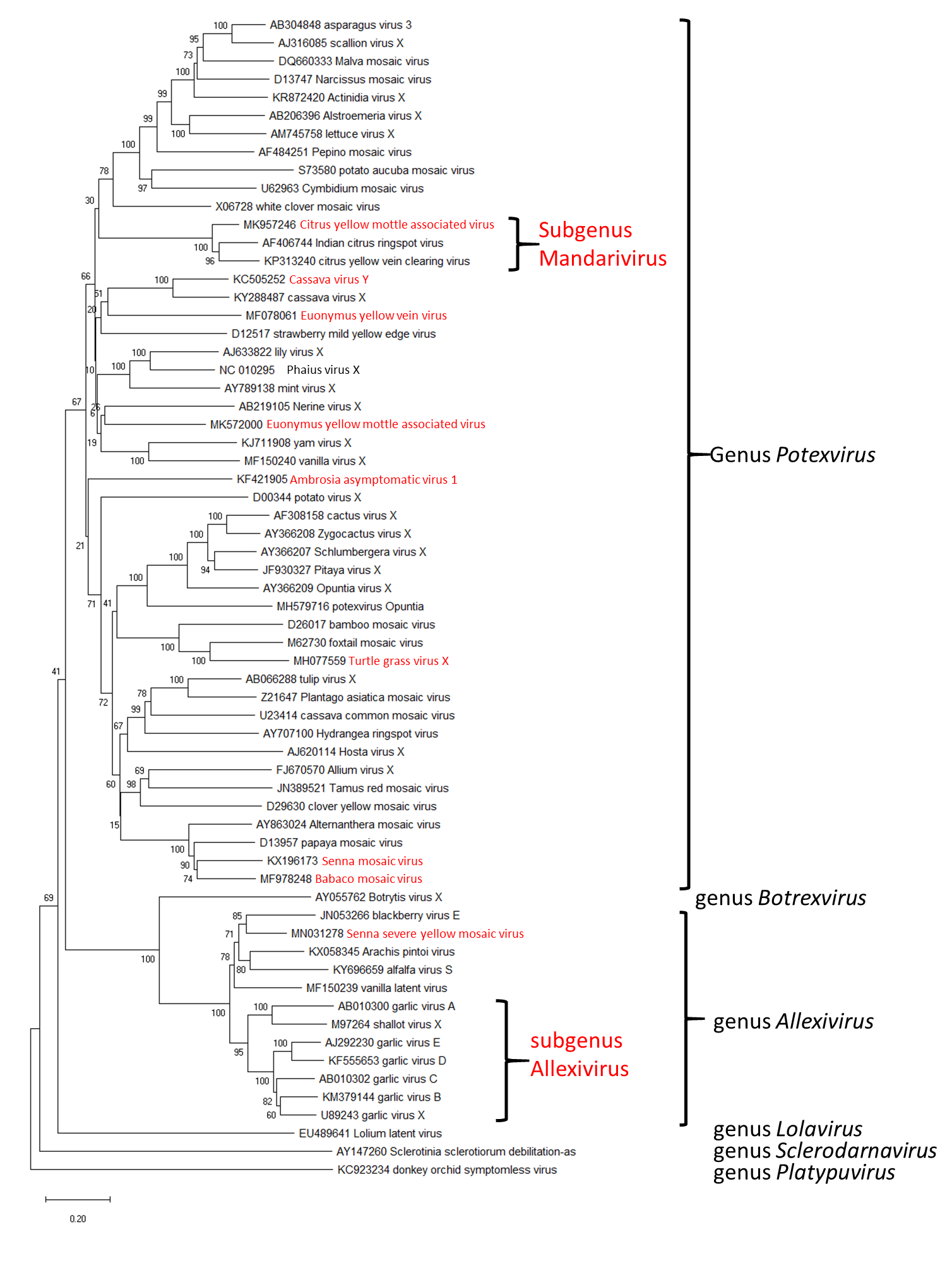
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**Abstract**

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| This proposal describes nine unambiguous cases of reported novel viruses that should be considered as new species in the genera *Potexvirus* and *Allexivirus*. |

**Text of proposal**

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| ***Ambrosia asymptomatic virus 1* (AAV1; *Potexvirus*; Dutta et al. 2014; KF421905)**  This virus was obtained from *Ambrosia psilostachya* DC (western ragweed) (Asteraceae)by enriching in viral particles, generic PCR amplification, cloning and sanger sequencing. No symptoms were detected, but AAV1was found in ambrosia during different years. A 7408 bp sequence was determined including RNA-dependent RNA polymerase, putative triple gene block protein 1, 2 and 3, putative coat protein and putative nucleic acid binding protein genes. Near-complete genome (5’RACE not successful, likely at least the first three nucleotides are missing). Suggested as a new species inside the genus *Potexvirus*. BlastN analysis using the near-full genome shows about 67% identity with several potexvirus species. There is a 78% identity (nt, CP gene) with Alstroemeria virus X CP but is related to only 8% coverage. Similar results are obtained with White clover mosaic virus and Asparagus virus 3. An issue is that the AAV1 genome, according to Authors, shows a putative NABP at the 3’-end of its genome, however based on a separate proposal to reclassify the genus *Mandarivirus* to a subgenus within the genus *Potexvirus*, this would not anymore be unique among potexviruses. BlastN analysis of putative AAV1 NABP shows it has 80% identity with 3’ CP genes of Pitaya virus X and Cactus virus X. More interestingly, BlastP analysis shows 35-40% identity with NBPs of several Allexiviruses. CP and RdRp aa sequences of AAV1 place it in the potexvirus group upon phylogenetic analysis (see **Fig. 1**) distant from the species of the genus *Mandarivirus*, where Dutta et al 2014 are proposing to place AAV1. BlastP analysis of CP aa sequence (AHB87037) reveals 44-49% identity with EYMaV, NVX, PVX, VanillaVX (all potexviruses) and BlastP analysis of RdRP aa sequence (AHB87033) reveals a best match of 42% identity with a 99% coverage and very high score with CYVCV (Mandarivirus); a little less coverage and 52-54% identity with EYMaV, NVX, LVX, PepMV (potexviruses)  ***Cassava Colombian symptomless virus* (CsCSV; *Potexvirus*; Lozano et al. 2017; KC505252)**  Host: cassava (*Manihot esculenta* Crantz, *Euphorbiaceae*). No symptoms detected – difficult transmission to *Nicotiana benthamiana*. Often in mixed infection – detected in 6 out of 15 samples collected in center/south and Amazonas area in Colombia. Suggested as new species in the genus *Potexvirus*. TGB3 ORF is missing in the isolate sequenced and confirmed in two additional isolates; BLASTn of available genome seq: 68% identity with KY288487 Cassava virus X (CsVX) also missing TGB3. The authors propose the name cassava new alphaflexivirus and suggest they may include two earlier named putative potexviruses, cassava Caribbean mosaic virus (CsCaMV) and cassava Colombian symptomless virus (CsCSV), for which no sequence data was available at the time. Personal communication with the corresponding author of the Lozano et al. (2017) has since confirmed that sequence was obtained from a historic isolate of CsCSV and was found to be the same virus, thus the name cassava Colombian symptomless virus is proposed as a name for this virus.  CCoSV and CsVX are not serologically correlated. RdRp: aa seq (AHA91819), 69% identity with YP\_009357226 Cassava virus X CP: aa seq (AHA91822), 78,1% identity with YP\_009357229 Cassava virus X, 46% identity with PVX CP and 45% identity with Nerine virus X. CP nt seq shows 72,38% identity with KY288487 (Cassava virus X) and with other potexviruses 76-77%, with garlic virus C: 82,5% RdRp nt seq shows 68,04% identity with KY288487 (Cassava virus X). CCoSV and CsVX appear to be supported as distinct species (**Fig. 1**); moreover they are NOT serologically related. A separate subgenus could be proposed listing CCoSV and CsVX,. Authors (Lozano et al 2017) suggest creation of a new genus inside *Alphaflexivirideae*, the *Euphorbiavirus* genus, due to common and peculiar genome arrangement/biologic characteristics (TGB3 ORF missing, tricky transmission to *N. benthamiana*, no symptoms on cassava) ot the two species, similarly to the situation of *Mandarivirus*. Considering our separately proposal to change the status of Mandarivirus from genus, to a subgenus within the genus Potexvirus, instead a subgenus could be considered if more viruses with similar characteristics and relatednes are discovered in the future.  ***Euonymus yellow mottle associated virus* (EYMaV; *Potexvirus*; Yang et al. 2019; MK572000)**  This virus is described by Yang et al (2019). The full genome sequence was obtained by RNAseq NGS and 5’ and 3’ RACE and is 6,784 nucleotides. Host: *Euonymus bungeanus* Maxim (Celastraceae), Symptoms: yellow mottle leaf disease in Shenyang of Liaoning Province, China. Particles visualized by TEM. Two additional plants showing the same symptoms were positive for EuYMaV. Proposed as a new species in the genus *Potexvirus*. Typical potexvirus genome arrangement, with five ORFs. Full genome seq shows best identity (80%) with Euonymus yellow vein associated virus, but with very low % query coverage (14%); 65-70% identity for several other potexviruses and CYVCV, always with low % query coverage (RdRp seq); the RdRp aa sequence forms a clade with NerineVX, YamVX, and VanVX (**Fig. 1**). EuYMaV CP aa seq (BlastP) shows 44-50% identity with AAV1 and several other potexviruses (YamVX, NerineVX, VanillaVX, CsVX, PVX) EuYMaV CP nt seq (BlastN) shows 69-73% identity with various potexviruses (YamVX, AAV1, WCMV, VanillaVX, PepMV, CactusVX)  ***Euonymus yellow vein virus* (EYVV; *Potexvirus*; Yang et al. 2018; MF078061)**  Full genome (7279 nt) was determined by smallRNA sequencing, then amplified, cloned and sequenced, including 5’ and 3’ RACE. Host: *Euonymus bungeanus* Maxim (Euonymus, Celastraceae) in Liaoning, Northern China showing yellow vein disease. Particles visualized by TEM. EuYVAV was detected in three *E. bungeanus* samples showing yellow vein symptoms but in none of three *E. bungeanus* samples exhibiting either no symptoms or leaf curling symptoms.  Suggested as a new species in Potexvirus genus. EYVV has the typical genomic organization of potexviruses, with five ORFs. Full genome seq shows 66-68% identity with several potexviruses as HostaVX, CsVX, YamVX, AltMV, TamusRedMV, VanillaVX, CactusVX, PitayaVX, with low % query coverage (11-19% in RdRp seq). The RdRp aa sequence forms a clade with strawberry mild yellow edge virus, cassava virus X, and ‘cassava new alphaflexivirus’ (**Fig. 1**). EuYVaV CP aa seq (BlastP) shows 36-44% identity with several potexviruses as CsNAV, NerineVX, CsVX, EuYMV, AAV1, CsCMV, YamVX. EuYVaV CP nt seq (BlastN) shows the best score and 72% identity with PepMV. Name: in the paper is EuYVaV (associated) in NCBI database in EuYVV: the name proposed in the paper (Euonymus yellow vein associated virus) is recommended.  ***Babaco mosaic virus* (BabMV; *Potexvirus*; Alvarez-Quinto et al. 2017; MF978248)**  Complete genome, 6692 nt sequences encoding an RNA-dependent RNA polymerase, three triple gene blocks proteins, and a coat protein. It was isolated from babaco plants (Vasconcellea x heilbornii) showing leaf mottling and mosaic symptoms (Alvarez-Quinto et al., 2017). Its genome organization is the genome structure of typical potexvirus. This virus was grouped with *Alternathera mosaic virus*, *Papaya mosaic virus* and *Senna mosaic virus* that belong to the genus *Potexvirus* (**Fig. 1**).  ***Senna mosaic virus* (SenMV; *Potexvirus*; Rezende et al., 2017; KX196173)**  Complete genome (Illumina HiSeq) of 6775 bp; [NOTE: there is an apparent direct repeat of 102 bp in the 3'-terminal domain following a 42 bp stretch between the 1st and 2nd iteration, and an 11 bp 3'-terminal poly(G); no 3'-RACE was performed to confirm; the authors will attempt to resolve the true 3’-end structure and update the GenBank accession]. Host: *Senna occidentalis*. Typical potexvirus genome structure and phylogeny, most closely related (full genome) to papaya mosaic virus (79% coverage, 69.79%nt identity), babaco mosaic virus (75% coverage, 69.64% identity), alternanthera mosaic virus (81% coverage, 68.77% identity),lagenaria mild mosaic virus (partial sequence;43% coverage, 70.98% nt identity). RdRP AA - babaco mosaic virus (70.49%), papaya mosaic virus (70.07%), alternanthera mosaic virus (69.49%)(**Fig. 1**). CP AA -lagenaria mild mosaic virus (77.83%), papaya mosaic virus (76.10%), alternanthera mosaic virus (77.39%), babaco mosaic virus (74.37%).  ***Turtle grass virus X* (TGVX; *Potexvirus*; van Bogeart et al. 2018; MH077559)**  Complete genome was determined through traditional methods (Sanger) from the sea grass species *Thalassia testudinum*, from Tampa Bay, Florida. Potexvirus-like virus particles were seen by electron microscopy and prevalence studied during one year in small area. TGVX has a typical potexvirus genome structure and phylogeny and is most closely related to foxtail mosaic virus (65% nt identity in Rep protein and 66% over entire genome) and bamboo mosaic virus (**Fig. 1**).  ***Cnidium virus X* (CnVX; *Potexvirus*; Honma et al., 2019; LC460456)**  A flexuous virus was detected in a *Cnidium officinale* plant in Japan showing mosaic symptoms. The genomic RNA of the virus was 5,964 nucleotides in length, excluding the 3′-terminal poly(A) tail. It contained five open reading frames (ORFs), consistent with other members of the genus *Potexvirus*. The ORF sequences differ from those of previously reported potexviruses. Phylogenetic analysis indicated that the polymerase of the virus is closely related to that of strawberry mild yellow edge virus; and the CP, to those of both yam virus X and vanilla virus X (**Fig 1**). We propose that this virus be designated as “cnidium virus X” (CnVX).    ***Senna severe yellow mosaic virus* (SSYMV; *Allexivirus*; Alves et al. 2020; MN031278)**  Described as Cassia mild mosaic virus in Alves et al. (2020) but deposited as Senna severe yellow mosaic virus GenBank accession MN031278. Near-complete genome sequence and biological properties of an allexivirus found in *Senna rizzinii* in Brazil. Near complete genome with partial 5' and 3' NCR (respectively 103 and 306nt). Genome sequence contains a total of 143 degenerate positions, making the search of ORFs complicated and uncertain. Reported in publication with typical allexivirus genome organization and unambiguously represents a novel Allexivirus that is found in non-*Allium* hosts (**Fig. 1**).  There are some uncertainties about the validity of the name. Cassia mild mosaic is an old name given in the 1970's to a virus found in *Senna* (= *Cassia*) *macranthera* and *Cassia sylvestris* (Lin et al., 1979; 1980). On the basis of particle morphology and a few other properties it was suggested to be a carlavirus, but no sequence available.  Beserra et al. (2011) concludes that Senna virus X has similar host range of that reported for Cassia mild mosaic virus (restricted to *Senna* species, necrotic LL in *Gomphrena* *globosa*) but still does not accept a synonymy. Authors changed their mind and deposited it in GenBank as Senna mild mosaic.  Reverse situation for Senna severe yellow mosaic, deposited as such in GenBank but interpreted in publication as Cassia mild mosaic. Host range info is hard to interpret. Lin et al. (1980) report no infection in *Chenopodium amaranticolor* but Beserra et al. (2011) do (but presence of a potyvirus may have confounded results), and Alves et al. (2020) report necrotic local lesions in this host. All three reports note NLL in *G. globosa*.  As it is not clear if the virus reported here is the same as the virus reported in the late 70's as cassia mild mosaic virus, the name Senna severe yellow mosaic virus is preferred, both as descriptive of the symptoms in the isolation host, *S. rizzinii*, and the name used for the GenBank accession MN031278. |

**Supporting evidence**

*Mandarivirus*

*Acarallexivirus*

**Fig. 1.** Phylogenetic tree of replication protein of members of the family Alphaflexiviridae showing the proposed new species and subgenera of this and accompanying proposals in red. Tree was generated using neighbor-joining and JTT distance matrix with 500 bootstrap replicates. Numbers on nodes indicate the % of bootstrap support for the corresponding node.

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