

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

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| **Code assigned:** | **2020.030P** |  |
| **Short title:** Abolish one species in the genus *Potexvirus* (*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 | August 2, 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**

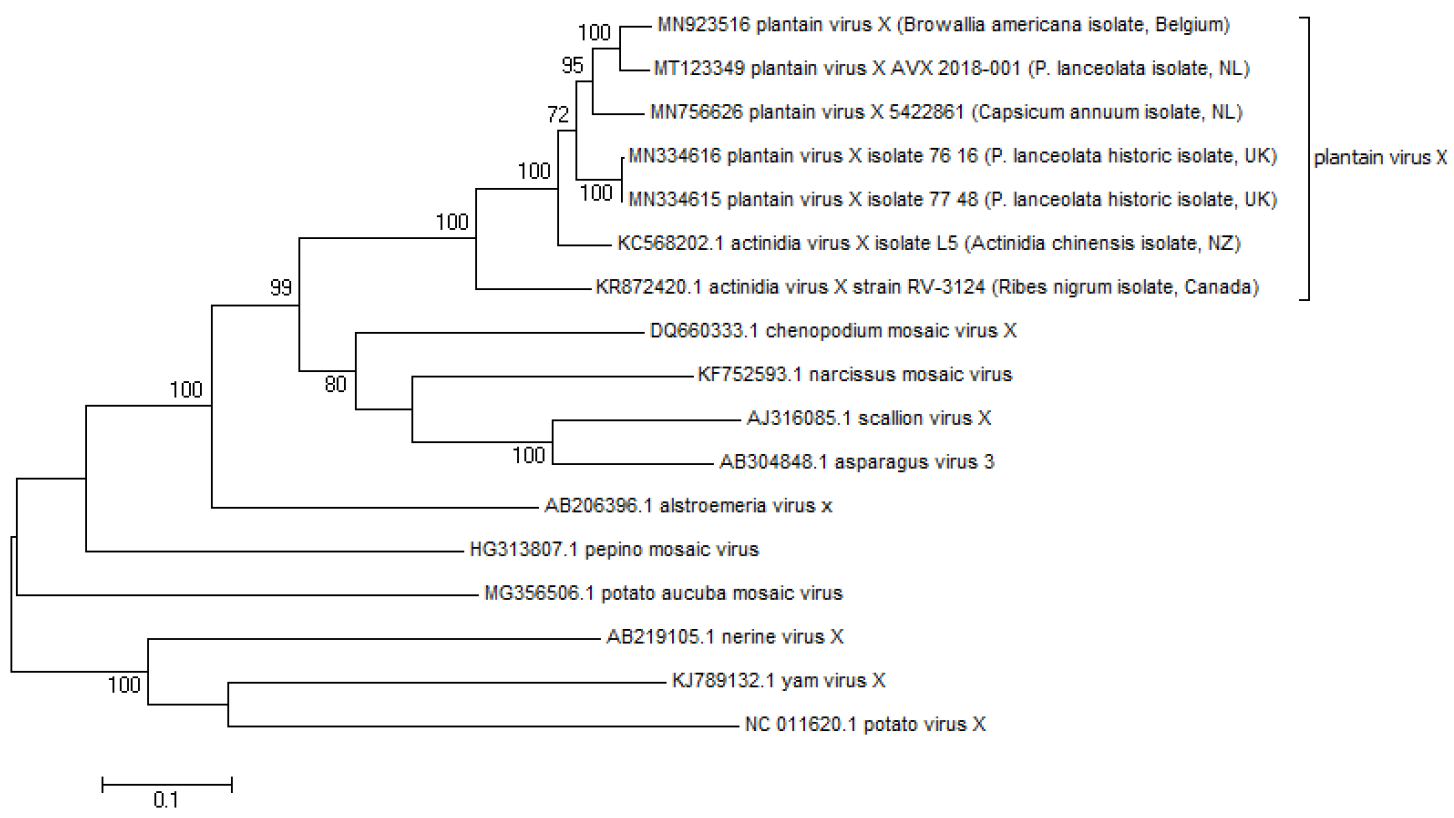
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**Abstract**

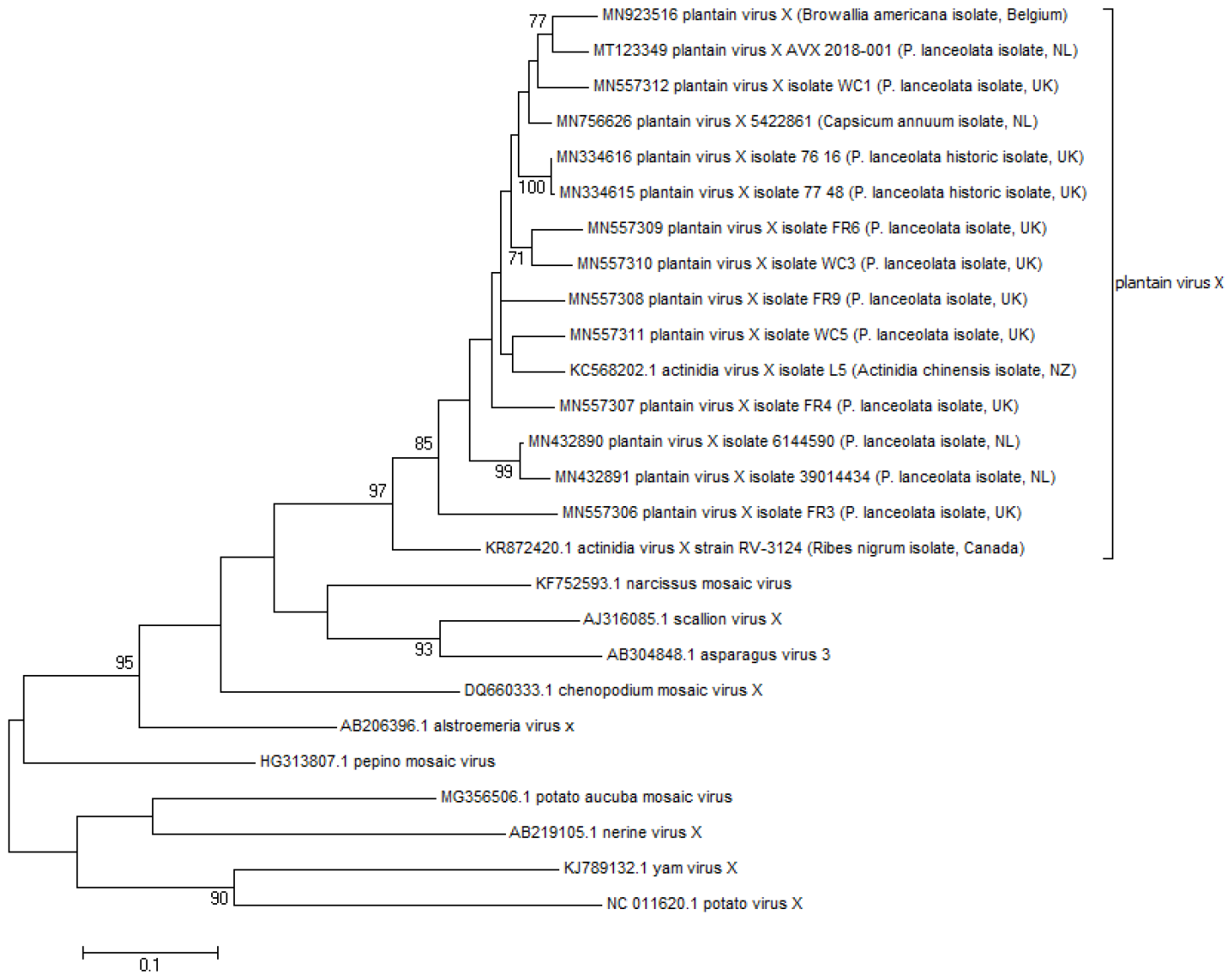
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| Sequences of two historic (>40 years old) isolates of plantain virus X(PlVX), and multiple contemporary isolates from *Plantago lanceolata* from the United Kingdom (UK) and the Netherlands, *Browallia americana* from Belgium, and *Capsicum* *annuum* from Ethiopia share high nucleotide and amino acid identities with isolates of actinidia virus X (AVX) from *Actinidia chinensis* and *Ribes nigrum*. Variability of contemporary isolates of PlVX from the UK encompasses all but the *Ribes* isolate of AVX, which is closely related, such that PlVX and AVX are clearly synonymous. The whole genomes have sequence identity of ~83-91%, with 82.01% and 84.54% (nt identity) and 93.72% and 97.98% (aa identity) for the polymerase and CP respectively. Therefore, PlVX and AVX should be considered isolates of the same species. It is proposed that *Actinidia virus X* should be abolished as it is a synonym of the earlier described and accepted species *Plantain virus X*. |

**Text of proposal**

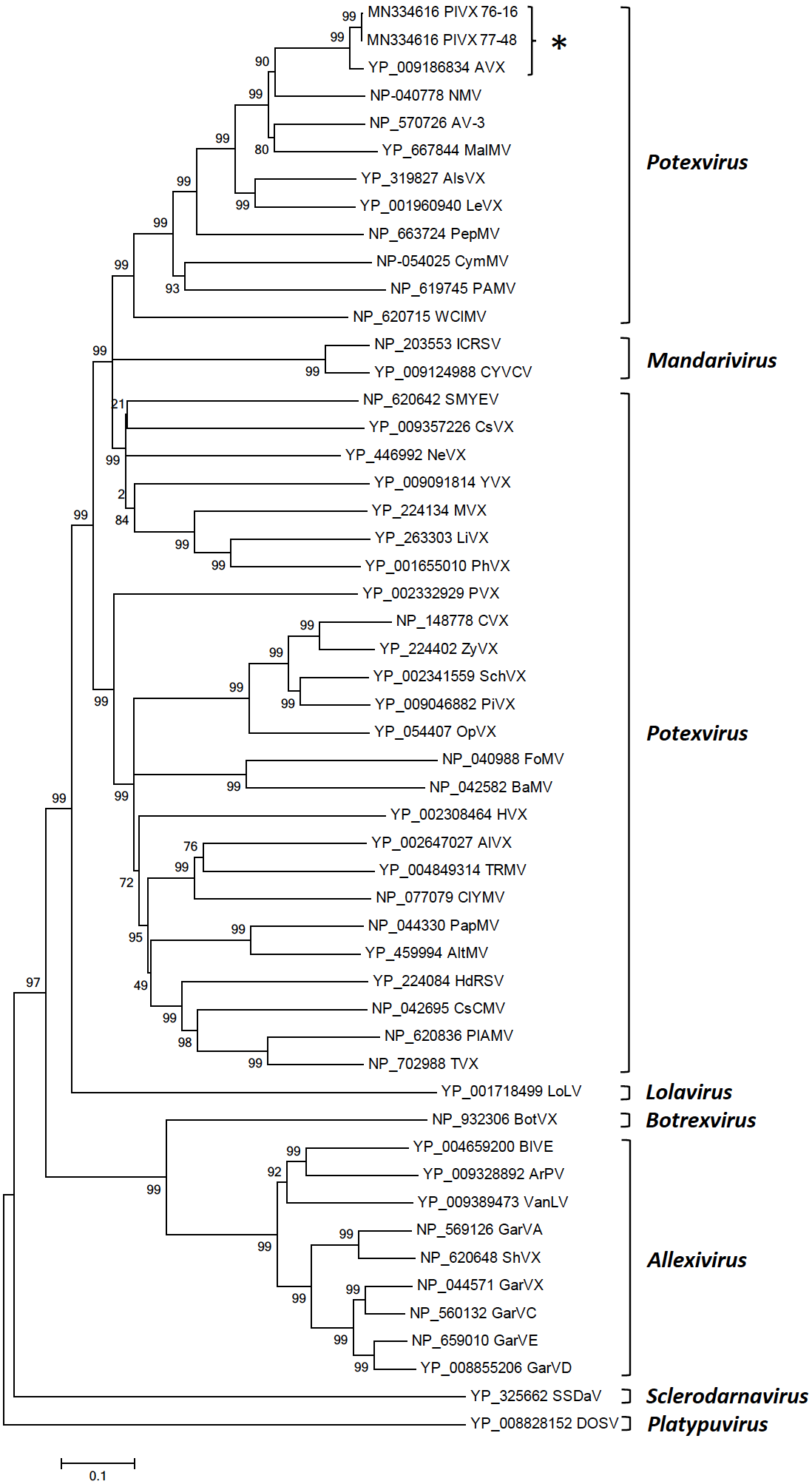
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| |  | | --- | | *Plantain virus X* (plantain virus X; PlVX) was isolated from *Plantago lanceolata* in the United Kingdom, biologically and serologically characterized, and reported as a distinct new potexvirus (Hammond and Hull, 1981), and accepted as a species in the Potexvirus group in the ICTV 4th Report (1982), initially as *Plantago virus X*, corrected to *Plantain virus X* in the ICTV 5th Report (1991). At that time no sequence information was generated.  *Actinidia virus X* (Actinidia virus X; AVX) was initially detected from an *Actinidia chinensis* cultivar imported to New Zealand (Pearson et al., 2011, Blouin et al., 2013), with a partial sequence of this isolate available (KC568202); the full sequence on an isolate from *Ribes nigrum* imported to Canada (KR872420; James and Phelan, 2016) showed; this sequence has c.80.8% identity to the Actinidia isolate, and was the basis for acceptance of *Actinidia virus X* as a species at the ICTV EC 49 in Singapore (2017) and ratified in 2018 (MSL #32). It was determined that *A. chinensis* is not a preferred host (Blouin et al., 2013), as when *A. chinensis* was mechanically infected with the virus the titer fell rapidly and could not be detected after 2 months (Pearson et al., 2011).  Recently two original isolates of PlVX (from 1976 and 1977) were recovered from a plant virus collection held at the University of Warwick (UK), and nearly full-length sequences determined for each (MN334616, MN334615 respectively). Multiple current isolates were also obtained from *P. lanceolata* collected from one of the original UK PlVX sampling sites; additional samples of *P. lanceolata* were collected in the Netherlands, and the virus also detected in *Browallia americana* in Belgium, and in a sample of *Capsicum annuum* imported to the Netherlands from Ethiopia in 2011. Essentially full genome sequences were also determined for an isolate from *P. lanceolata* from the Netherlands (MT123349), *B. americana* in Belgium (MN923516), and from *Capsicum annuum* (MN756626); partial polymerase sequences were also determined from several contemporary isolates from *P. lanceolata* from the UK (MN557306-MN557312) and from the Netherlands (MN432890, MN432891). The genomic sequences of PlVX and AVX group together in phylogenetic trees, and distinguished from other potexvirus species (**Figure 1**).  The genome sequences of the various PlVX and AVX isolates have nucleotide sequence identity of ~83-91%, with **82.01%** and **84.54%** (nt identity) and **93.72%** and **97.98%** (aa identity) **for the polymerase and CP respectively** of PlVX 77/48 (MN334615) and AVX RV3124 (KR872420). The sequence variation among partial polymerase sequence of contemporary PlVX isolates from the UK encompasses that of the equivalent region of all other PlVX/AVX isolates except for the *Ribes nigrum* isolate of AVX, which is still more closely related than that of other potexviruses (**Figure 2**).  **The sequence-based species differentiation criteria for the genus *Potexvirus* are that isolates of different species have less than 72% nt identity (or 80% aa identity) between their CP or Rep genes.** Therefore, PlVX and AVX should be considered isolates of the same species; this is also supported by results of submitting the PlVX 77/48 genomic sequence (MN334615) to the PAirwise Sequence Comparison tool (PASC) (<https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=overview>), which shows PlVX and AVX at the ‘same species’ level of 82.73% identity.  Neighbor-Joining trees of both the polymerase (**Figure 3**)and CP (**Figure 4**)amino acid sequences of the two historical isolates of PlVX (77/48 and 76/16), the *Ribes nigrum* isolate of AVX (RV3124), and other currently recognized species of the genus *Potexvirus* and other genera in the *Alphaflexiviridae* also clearly show that PlVX and AVX are grouped closely together and differentiated from the other potexvirus species and members of the other genera; the potexvirus species most closely group in the polymerase and CP trees (*Narcissus mosaic virus*, *Asparagus virus 3*, and *Malva mosaic virus*) are also those identified by PASC as being most closely related at the full genome level (**Figure 5**).  Based on the identities between isolates described as AVX and PlVX being above the established level for distinction of species in the genus *Potexvirus,* PlVX and AVX represent a single species. It is therefore proposed that *Actinidia virus X* should be abolished as it is a synonym of the earlier described and accepted species *Plantain virus X.* In addition to its earlier report and biological characterization, PlVX was previously known to be naturally present in *P. lanceolata* in multiple regions of the UK (Hammond and Hull, 1981, Hammond, 1981), and has now been found in *P. lanceolata* in several locations in the Netherlands (Hammond et al., in review), whereas *Actinidia chinensis* has been found not to be a preferred host of the isolate initially described as AVX (Blouin et al., 2013); to date there remain only reports of natural infection of three plants of *Actinidia chinensis* (Pearson et al., 2011; Blouin et al., 2013), and a few plants of *Ribes nigrum* (James and Phelan, 2016). | |

**Supporting evidence**

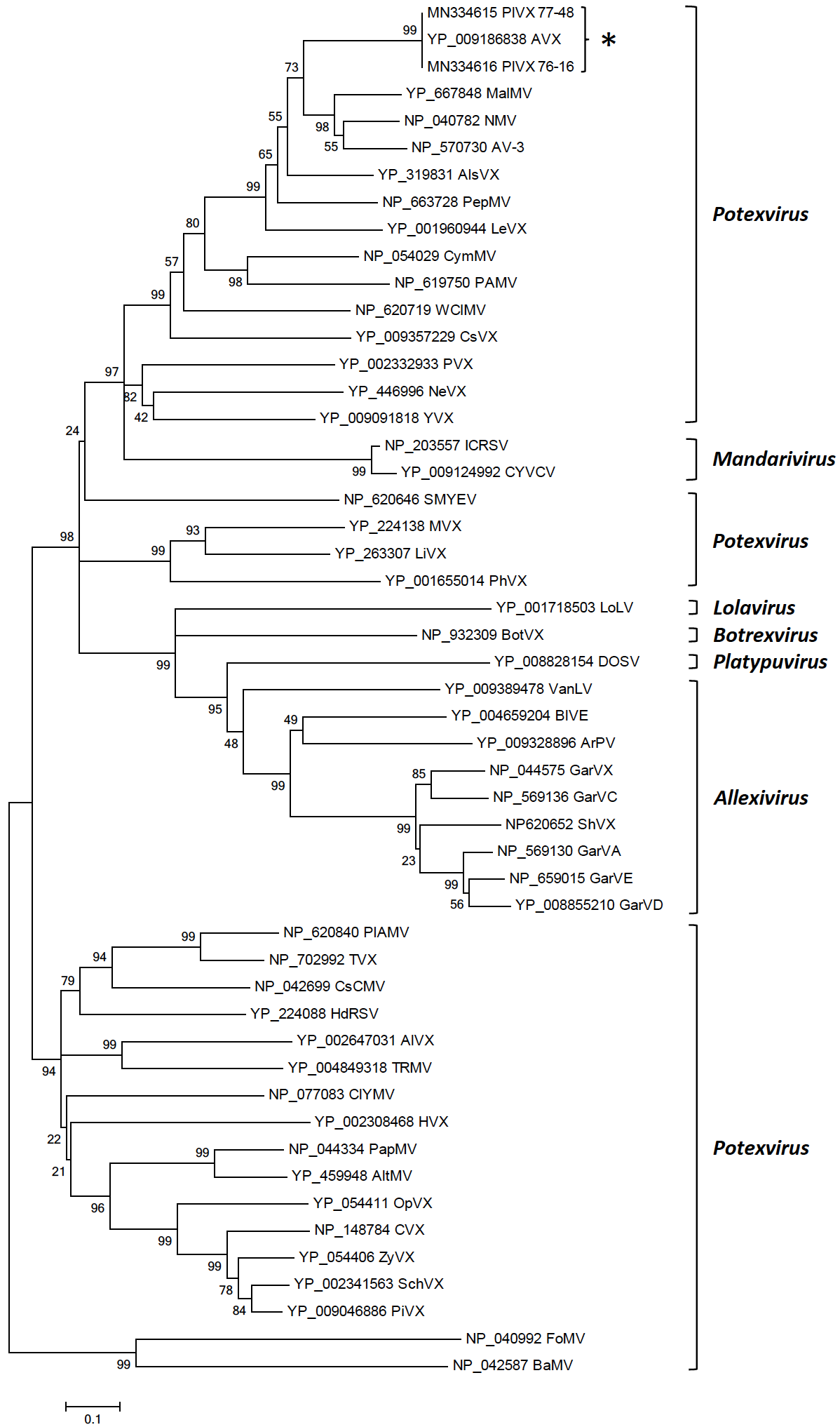
**Figure 1.** Maximum likelihood phylogenetic tree (500 bootstrap replications) produced from genomes of plantain virus X (PlVX), actinidia mosaic virus (AVX), and related genomes of the genus *Potexvirus*. PlVX and AVX isolate labels include host species and country of isolation (UK: United Kingdom; NL: The Netherlands; NZ: New Zealand).

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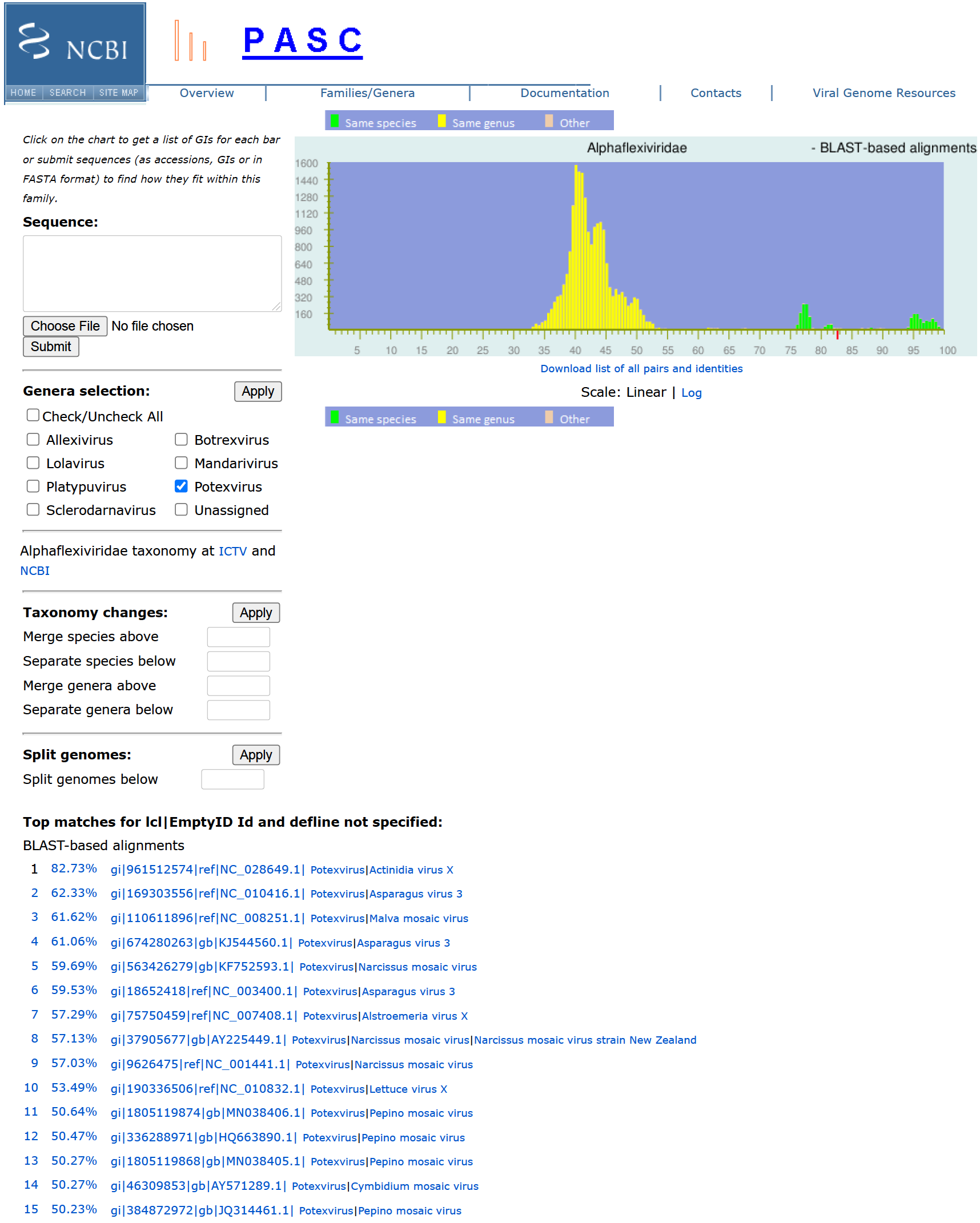
**Figure 2.**  Maximum likelihood phylogenetic tree (500 bootstrap replications) produced from partial polymerase nucleotide sequences of plantain virus X (PlVX), actinidia mosaic virus (AVX), and related genomes of the genus *Potexvirus*. PlVX and AVX isolate labels include host species and country of isolation (UK: United Kingdom; NL: The Netherlands; NZ: New Zealand).

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**Figure 3.** Neighbor joining phylogenetic tree (1000 bootstrap replications) of the polymerase amino acid sequences of plantain virus X (PlVX), actinidia mosaic virus (AVX), and related species of the genus *Potexvirus* and other genera in the *Alphaflexiviridae*. The tree was generated using MEGA 6, with alignments created using MUSCLE. Other virus abbreviations: AlVX – Allium virus X; AlsVX – Alstroemeria virus X; AltMV – Alternanthera mosaic virus; ArPV – Arachis pintoi virus; AV-3 – asparagus virus 3; BaMV – bamboo mosaic virus; BlVE – blackberry virus E; BotVX – Botrytis virus X; ClYMV – clover yellow mosaic virus; CsCMV – cassava common mosaic virus; CsVX – cassava virus X; CVX – cactus virus X; CymMV – Cymbidium mosaic virus; CYVCV – citrus yellow vein clearing virus; DOSV – donkey orchid symptomless virus; FoMV – foxtail mosaic virus; GarVA – garlic virus A; GarVC – garlic virus C; GarVD – garlic virus D; GarVE – garlic virus E; GarVX – garlic virus X; HdRSV – hydrangea ringspot virus; HVX – hosta virus X; ICRSV – Indian citrus ringspot virus; LeVX – lettuce virus X; LiVX – Lily virus X; LoLV – Lolium latent virus; MalMV – Malva mosaic virus; MVX – mint virus X; NeVX – Nerine virus X; NMV – narcissus mosaic virus; OpVX – Opuntia virus X; PAMV – potato aucuba mosaic virus; PapMV – papaya mosaic virus; PepMV – pepino mosaic virus; PhVX – Phaius virus X; PiVX – pitaya virus X; PlAMV – Plantago asiatica mosaic virus; PVX – potato virus X; SchVX – Schlumbergera virus X; ShVX – shallot virus X; SMYEV – strawberry mild yellow edge virus; SSDaV - Sclerotinia sclerotiorum debilitation-associated virus; TRMV – Tamus red mosaic virus; TVX – tulip virus X; VanLV – vanilla latent virus; WClMV – white clover mosaic virus; YVX – yam virus X; ZyVX – Zygocactus virus X.

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**Figure 4.** Neighbor joining phylogenetic tree (1000 bootstrap replications) of the coat protein amino acid sequences of plantain virus X (PlVX), actinidia mosaic virus (AVX), and related species of the genus *Potexvirus* and other genera in the *Alphaflexiviridae*. The tree was generated using MEGA 6, with alignments created using MUSCLE. Other virus abbreviations: AlVX – Allium virus X; AlsVX – Alstroemeria virus X; AltMV – Alternanthera mosaic virus; ArPV – Arachis pintoi virus; AV-3 – asparagus virus 3; BaMV – bamboo mosaic virus; BlVE – blackberry virus E; BotVX – Botrytis virus X; ClYMV – clover yellow mosaic virus; CsCMV – cassava common mosaic virus; CsVX – cassava virus X; CVX – cactus virus X; CymMV – Cymbidium mosaic virus; CYVCV – citrus yellow vein clearing virus; DOSV – donkey orchid symptomless virus; FoMV – foxtail mosaic virus; GarVA – garlic virus A; GarVC – garlic virus C; GarVD – garlic virus D; GarVE – garlic virus E; GarVX – garlic virus X; HdRSV – hydrangea ringspot virus; HVX – hosta virus X; ICRSV – Indian citrus ringspot virus; LeVX – lettuce virus X; LiVX – Lily virus X; LoLV – Lolium latent virus; MalMV – Malva mosaic virus; MVX – mint virus X; NeVX – Nerine virus X; NMV – narcissus mosaic virus; OpVX – Opuntia virus X; PAMV – potato aucuba mosaic virus; PapMV – papaya mosaic virus; PepMV – pepino mosaic virus; PhVX – Phaius virus X; PiVX – pitaya virus X; PlAMV – Plantago asiatica mosaic virus; PVX – potato virus X; SchVX – Schlumbergera virus X; ShVX – shallot virus X; SMYEV – strawberry mild yellow edge virus; SSDaV - Sclerotinia sclerotiorum debilitation-associated virus; TRMV – Tamus red mosaic virus; TVX – tulip virus X; VanLV – vanilla latent virus; WClMV – white clover mosaic virus; YVX – yam virus X; ZyVX – Zygocactus virus X.

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**Figure 5.** Full genome nucleotide sequence comparison of plantain virus X against other potexviruses using the PAirwise Sequence Comparison tool (PASC) (<https://www.ncbi.nlm.nih.gov/sutils/pasc/viridty.cgi?textpage=overview>), which shows PlVX and AVX at the ‘same species’ level of 82.73% identity.

**References**

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