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:** | ***2017.009P*** | | | | (to be completed by ICTV officers) |
| **Short title:** A new species in the genus *Turncurtovirus* | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| Arvind Varsani and Darren P. Martin | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| Arvind.varsani@asu.edu | | | | | |
| **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) | | | ***Geminiviridae* SG** | | |
| **ICTV Study Group comments (if any) and response of the proposer:** | | | | | |
|  | | | | | |
|  | | | | | |
| Date first submitted to ICTV: | | | |  | |
| Date of this revision (if different to above): | | | |  | |

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| **ICTV-EC comments and response of the proposer:** |
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**Part 2**: **PROPOSED TAXONOMY**

|  |
| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet:** 2017.009P.N.v1.Turncurtovirus\_sp |

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 3:** **NON-STANDARD**

Template for any proposal regarding ICTV procedures, rules or policy, not involving the creation of new taxonomy.

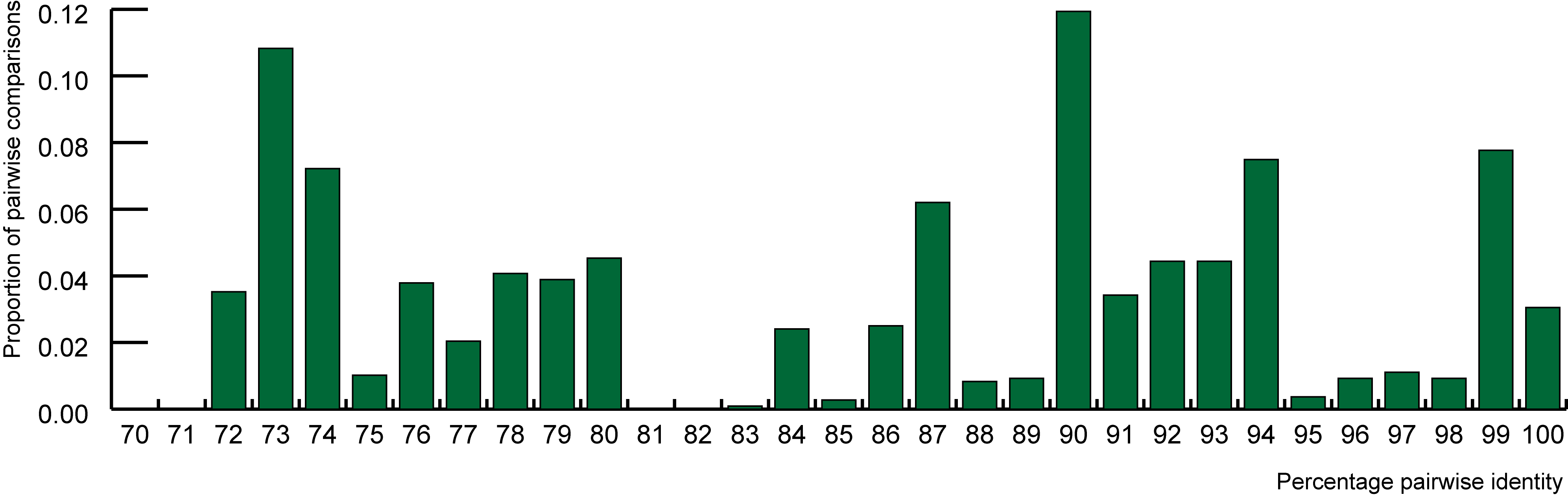
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| non-standard proposal |
| **Title of proposal:** |
| **Text of proposal:** |
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**Part 4:** **APPENDIX**: supporting material

The genus *Turncurtovirus* in the family *Geminiviridae* currently has one species, *Turnip curly top virus* (Varsani et al., 2014). Hence, currently, there is no official species demarcation criteria for this genus. Accordingly, we propose to establishment an official species demarcation criterion of less than 80% genome-wide nucleotide sequence between isolates of distinct turncurtovirus species. Formal establishment of such metrics will allow classification of growing number of sequence-based data on these viruses.

Isolates of turnip curly top virus (TCTV; Table 1) have been identified in *Beta vulgaris* (n=2), *Brassica rapa* (n=25), *Lactuca sativa* (n=1), *Ocimum basilicum* (n=1) and *Raphanus sativus* (n=2) (Kamali et al., 2015). In addition to these, two TCTVs have been identified in leafhoppers (Kamali et al., 2017). These 34 isolates share >83% pairwise identity with one another.

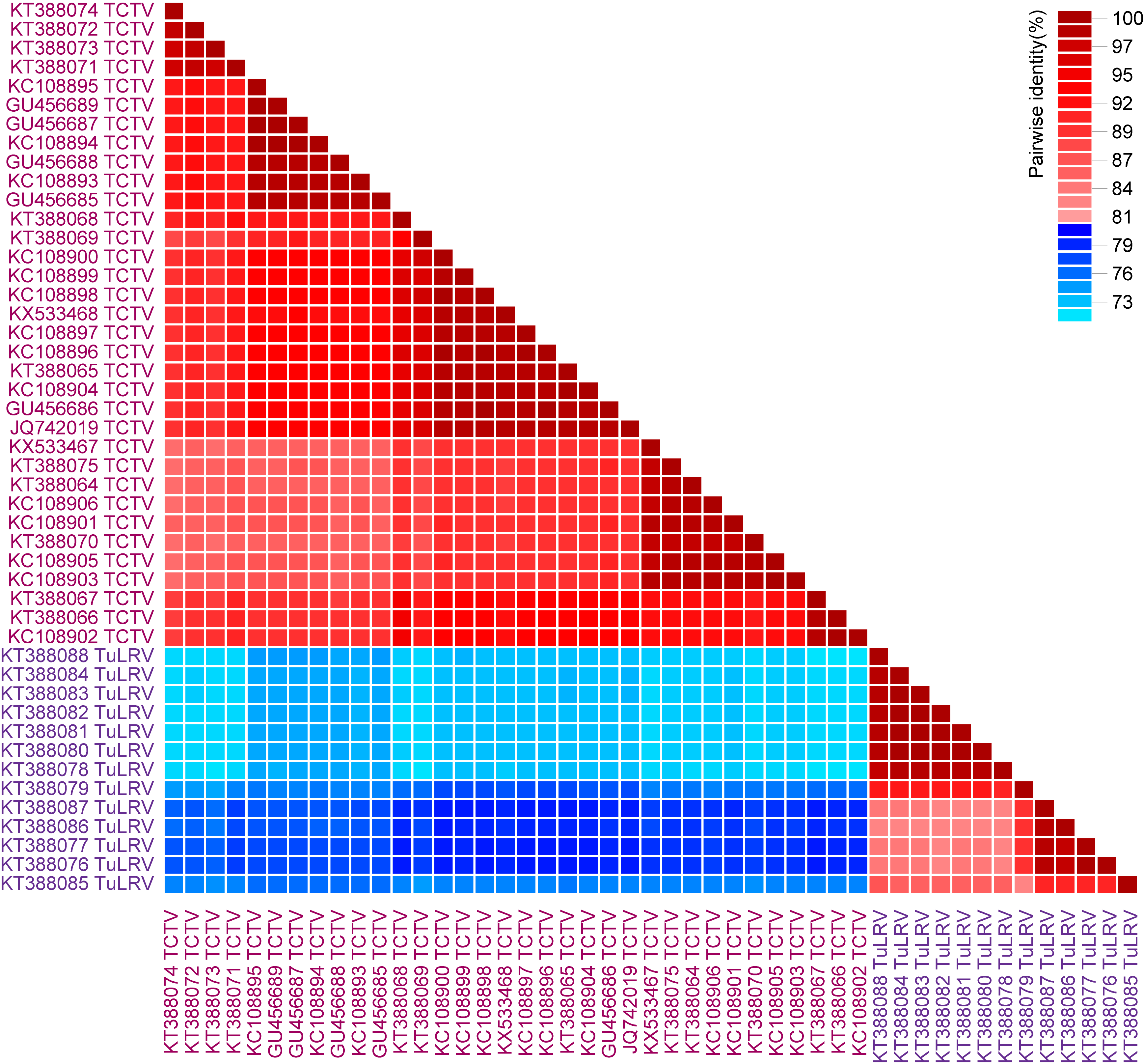
A group of viruses (n=13) that share <80% identity with turnip curly top viruses were identified from *Beta vulgaris* (n=3), *Brassica rapa* (n=7) and *Lactuca sativa* (n=3) (Table 1). Genome-wide pairwise comparisons of these 13 viruses with TCTV indicates a trough of pairwise identity values between 81 and 82% (Figure 1). Based on these analyses and coupled with phylogenetic support (Figure 2) for two distinct clusters, it is proposed that turncurtoviruses sharing less than 80% pairwise identity to other known turncurtoviruses be considered new species. Therefore, the 13 viruses (Figures 2 and 3) identified in Kamali et al. (2015) should be considered members of a new species, *Turnip leaf roll virus* according to the proposed criterion. Furthermore, this classification aligns with the recommendations set out in Varsani et al. (2014).



**Figure 1.** Distribution of 47 full turncurtovirus genomes based on genome-wide identities calculated using SDT v1.2 (Muhire et al., 2014).



**Figure 2.** Neighbor-joining phylogenetic tree depicting the degrees of relatedness of turncurtovirus complete genome sequences. The tree is rooted with the genome sequences of eragroviruses (not shown). Clear distinction between isolates of two species is indicated by the presence of two distinct groups. Branches with <60% bootstrap support have been collapsed



**Figure 3:** A pairwise identity matrix of turncurtoviruses calculated using SDT v1.2 (Muhire et al., 2014).

**Table 1.** Details of turncurtovirus species and isolates.

|  |  |  |  |
| --- | --- | --- | --- |
| **Species name** | **GenBank accession #** | **Isolate name** | **Host** |
| *Turnip curly top virus* | GU456687 | TCTV-[IR: Hom2:8K:09] | *Brassica rapa* |
|  | GU456688 | TCTV-[IR: Hom3:4K:09] | *Brassica rapa* |
|  | GU456689 | TCTV-[IR: Hom3:7K:09] | *Brassica rapa* |
|  | KC108893 | TCTV-[IR:Lap:L13:Tur:12] | *Brassica rapa* |
|  | KC108895 | TCTV-[IR:Lap:L2-P:Tur:12] | *Brassica rapa* |
|  | GU456685 | TCTV-[IR:Zaf:B11:06] | *Brassica rapa* |
|  | KC108894 | TCTV-[IR:Zaf:Z8:Tur:12] | *Brassica rapa* |
|  | KC108899 | TCTV-[IR:Hom:H6:Tur:12] | *Brassica rapa* |
|  | KC108904 | TCTV-[IR:Hom:H8:Tur:12] | *Brassica rapa* |
|  | JQ742019 | TCTV-[IR:Hom:T57K:Tur:10] | *Raphanus sativus* |
|  | KT388065 | TCTV-[IR:Hom:Th8:Tur:12] | *Brassica rapa* |
|  | GU456686 | TCTV-[IR:Hom1:2K:09] | *Brassica rapa* |
|  | KC108896 | TCTV-[IR:Lap:L16:Tur:12] | *Brassica rapa* |
|  | KC108898 | TCTV-[IR:Zaf:Z2-14:Tur:12] | *Brassica rapa* |
|  | KC108900 | TCTV-[IR:Zaf:Z2-18:Tur:12] | *Brassica rapa* |
|  | KT388069 | TCTV-[IR:Zaf:Z2-26:Let:12] | *Lactuca sativa* |
|  | KT388068 | TCTV-[IR:Zaf:Z2-4:Sug:12] | *Beta vulgaris* |
|  | KC108897 | TCTV-[IR:Zaf:Z9:Tur:12] | *Brassica rapa* |
|  | KC108901 | TCTV-[IR:Hom:H1:Tur:12] | *Brassica rapa* |
|  | KT388064 | TCTV-[IR:Lap:L14:Tur:12] | *Brassica rapa* |
|  | KC108903 | TCTV-[IR:Zaf:Z10:Tur:12] | *Brassica rapa* |
|  | KC108905 | TCTV-[IR:Zaf:Z2-1:Tur:12] | *Brassica rapa* |
|  | KT388070 | TCTV-[IR:Zaf:Z3:Tur:12] | *Brassica rapa* |
|  | KC108906 | TCTV-[IR:Zaf:Z5-2:Tur:12] | *Brassica rapa* |
|  | KT388075 | TCTV-[IR:Zaf:Z6:Tur:12] | *Brassica rapa* |
|  | KC108902 | TCTV-[IR:Hom:H9:Tur:12] | *Brassica rapa* |
|  | KT388067 | TCTV-[IR:Hom:Th10:Tur:12] | *Brassica rapa* |
|  | KT388066 | TCTV-[IR:Hom:Th9:Tur:12] | *Brassica rapa* |
|  | KT388073 | TCTV-[IR:Zaf:Z4-15:Bas:12] | *Ocimum basilicum* |
|  | KT388074 | TCTV-[IR:Zaf:Z4-22:Rad:12] | *Raphanus sativus* |
|  | KT388071 | TCTV-[IR:Zaf:Z4-7:Rad:12] | *Raphanus sativus* |
|  | KT388072 | TCTV-[IR:Zaf:Z4-9:Sug12] | *Beta vulgaris* |
|  | KX533467 | TCTV-[IR:IR:CZ7:2013] | leafhopper |
|  | KX533467 | TCTV-[R:CZ1:2013] | leafhopper |
| *Turnip leaf roll virus* | KT388076 | TuLRV-[IR:Hom:Th2:Tur:12] | *Brassica rapa* |
|  | KT388077 | TuLRV-[IR:Hom:Th5:Tur:12]: | *Brassica rapa* |
|  | KT388087 | TuLRV-[IR:Zaf:Z11-4:Tur:12] | *Brassica rapa* |
|  | KT388086 | TuLRV-[IR:Zaf:Z11gl:Tur:12] | *Brassica rapa* |
|  | KT388085 | TuLRV-[IR:Zaf:Z7:Tur:12] | *Brassica rapa* |
|  | KT388079 | TuLRV-[IR:Zaf:Z2-22:Let:12] | *Lactuca sativa* |
|  | KT388088 | TuLRV-[IR:Ney:N8-5:Tur:14] | *Brassica rapa* |
|  | KT388078 | TuLRV-[IR:Zaf:Z2-15:Tur:12] | *Brassica rapa* |
|  | KT388080 | TuLRV-[IR:Zaf:Z2-23:Let:12] | *Lactuca sativa* |
|  | KT388081 | TuLRV-[IR:Zaf:Z2-24:Let:12] | *Lactuca sativa* |
|  | KT388082 | TuLRV-[IR:Zaf:Z2-49:Red beet:12] | *Beta vulgaris* subsp. *maritima* |
|  | KT388083 | TuLRV-[IR:Zaf:Z4-10:Sug:12] | *Beta vulgaris* |
|  | KT388084 | TuLRV-[IR:Zaf:Z4-12:Sug:12] | *Beta vulgaris* |

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| **References:** |
| Kamali, M., Heydarnejad, J., Massumi, H., Kvarnheden, A., Kraberger, S., Varsani, A. (2016) Molecular diversity of turncurtoviruses in Iran. Archives of Virology. 161, 551-561  Kamali, M., Heydarnejad, J., Pouramini, N., Masumi, H., Farkas, K., Kraberger, S., Varsani, A. (2017) Genome sequences of beet curly top Iran virus, Oat dwarf virus, Turnip curly top virus, and Wheat dwarf virus identified in leafhoppers. Genome Announcements. 5: e01674-16  Muhire, B.M., Varsani, A., Martin, D.P. (2014) SDT: A Virus Classification Tool Based on Pairwise Sequence Alignment and Identity Calculation. PLoS One 9 (9): e108277  Varsani, A., Navaz-Castillo, J., Moriones, E., Hernández-Zepeda, C., Idris, A., Brown, J.K., Zerbini, F.M., Martin, D.P. (2014) Establishment of three new genera in the family *Geminiviridae*: *Becurtovirus, Eragrovirus* and *Turncurtovirus*. Archives of Virology 159:2193-2203 |

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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. |