

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

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| **Code assigned:** | **2020.007P** |  |
| **Short title:** Create one species in the genus *Deltasatellite* (*Tolecusatellitida*e) | | |
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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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| *Geminiviridae* and *Tolecusatellitidae* 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 31, 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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| 2020.007P.R.Deltasatellite\_1nsp.xlsx |

**Abstract**

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| In this TP we propose to create 1 species in the genus *Deltasatellite*, family *Tolecusatellitidae*. This proposal has been prepared following the taxonomic criteria established for this genus. |

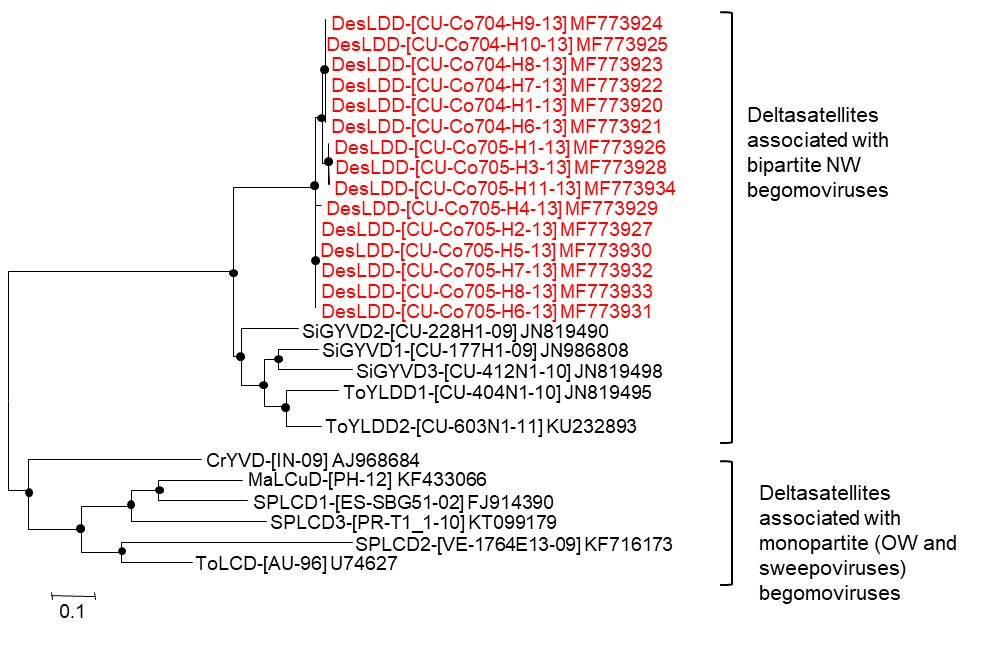
**Text of proposal**

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| |  | | --- | | Deltasatellites (genus *Deltasatellite*, family *Tolecusatellitidae*) are non-coding DNA satellites associated with begomoviruses, of about a quarter size of begomoviral genome components. All deltasatellites contain common features; they share a small region with some sequence identity to a conserved region present in the betasatellites, an A-rich sequence, a predicted stem-loop structure containing the nonanucleotide TAATATTAC, and a predicted secondary stem-loop (Fiallo-Olivé *et al*., 2012; Lozano *et al*., 2016).  The genus *Deltasatellite* comprises 11 species (Briddon *et al*., 2016; Adams *et al*., 2016), five of them reported associated with bipartite New World begomoviruses. Recently, 15 deltasatellites (Table 1) were cloned and sequenced from *Corchorus siliquosus* plants from Cuba. They share a nucleotide identity of 96.4–100% between them and showed the highest nucleotide identity (74.4–75.7%) with five isolates of *Sida golden yellow vein deltasatellite 2* (JN819490-JN819494) (Fiallo-Olivé *et al*., 2012). According to the proposed 91% deltasatellite species demarcation criteria (Briddon *et al*., 2016), the deltasatellites isolated in this work belong to a new species. Based on the fact that the New World begomovirus Desmodium leaf distortion virus, present in samples where the novel deltasatellite was found, was also able to maintain the deltasatellite in *N. benthamiana*, the name *Desmodium leaf distortion deltasatellite* is proposed for this species.  Phylogenetic analysis (Figure 1) showed that all Desmodium leaf distortion deltasatellite isolates clustered together and are separated from the rest of New World deltasatellites, supporting that this deltasatellite constitutes a novel species. | |

**Table 1.** Details of the proposed deltasatellite species.

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| **Species name** | **Virus acronym** | **GenBank Acc. No.** | **Isolate** | **Size (nt)** |
| *Desmodium leaf distortion deltasatellite* | DesLDD | MF773920 | CU-Co704-H1-13 | 666 |
| MF773921 | CU-Co704-H6-13 | 666 |
| MF773922 | CU-Co704-H7-13 | 666 |
| MF773923 | CU-Co704-H8-13 | 666 |
| MF773924 | CU-Co704-H9-13 | 666 |
| MF773925 | CU-Co704-H10-13 | 666 |
| MF773926 | CU-Co705-H1-13 | 666 |
| MF773927 | CU-Co705-H2-13 | 665 |
| MF773928 | CU-Co705-H3-13 | 666 |
| MF773929 | CU-Co705-H4-13 | 665 |
| MF773930 | CU-Co705-H5-13 | 665 |
| MF773931 | CU-Co705-H6-13 | 665 |
| MF773932 | CU-Co705-H7-13 | 665 |
| MF773933 | CU-Co705-H8-13 | 665 |
| MF773934 | CU-Co705-H11-13 | 666 |

**Supporting evidence**

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**Figure 1.** Phylogenetic tree illustrating the relationships of isolates of the proposed species, *Desmodium leaf distortion deltasatellite* (DesLDD in the tree) and one isolate per recognized deltasatellites species. The tree was constructed by the maximum-likelihood method (1000 replicates) with the MEGA 7 program using the best fit model, T92+G. CrYVD, *Croton yellow vein deltasatellite*; MaLCuD, *Malvastrum leaf curl deltasatellite*; SiGYVD1, *Sida golden yellow vein deltasatellite 1*; SiGYVD2, *Sida golden yellow vein deltasatellite* *2*; SiGYVD3, *Sida golden yellow vein deltasatellite 3*; SPLCD1, *Sweet potato leaf curl deltasatellite 1*; SPLCD2, *Sweet potato leaf curl deltasatellite 2*; SPLCD3, *Sweet potato leaf curl deltasatellite 3*; ToLCD, *Tomato leaf curl deltasatellite*; ToYLDD1, *Tomato yellow leaf distortion deltasatellite 1*; ToYLDD2, *Tomato yellow leaf distortion deltasatellite 2*. The bar below each tree indicates the number of nucleotide substitutions per site.

**References**

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2. Briddon RW, Navas-Castillo J, Fiallo-Olivé E (2016) ICTV taxonomic Proposal 2016.021a-kP.A.v2.Tolecusatellitidae. Create the *Tolecusatellitidae*, a new family of single-stranded DNA satellites with two genera. Available online at: http://www.ictv.global/proposals-16/2016.021a-kP.A.v2. Tolecusatellitidae.pdf (accessed July 20, 2020).
3. Fiallo-Olivé E, Navas-Castillo J (2020) Molecular and biological characterization of a New World mono-/bipartite begomovirus/deltasatellite complex infecting *Corchorus siliquosus*. Front Microbiol 11:1755. PMID: 32793176 DOI: 10.3389/fmicb.2020.01755
4. Lozano G, Trenado HP, Fiallo-Olivé E, Chirinos D, Geraud-Pouey F, Briddon RW, et al. (2016) Characterization of non-coding DNA satellites associated with sweepoviruses (genus *Begomovirus*, *Geminiviridae*) – definition of a distinct class of begomovirus-associated satellites. Front Microbiol 7:162. PMID: 26925037 DOI: 10.3389/fmicb.2016.00162