

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

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| **Code assigned:** | **2020.002P** |  |
| **Short title:** Create nine new species and three new genera (*Alphasatellitidae*) | | |
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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* SG |

**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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| --- |
| 2020.002P.R.Alphasatellitidae\_3ng\_9nsp.xlsx |

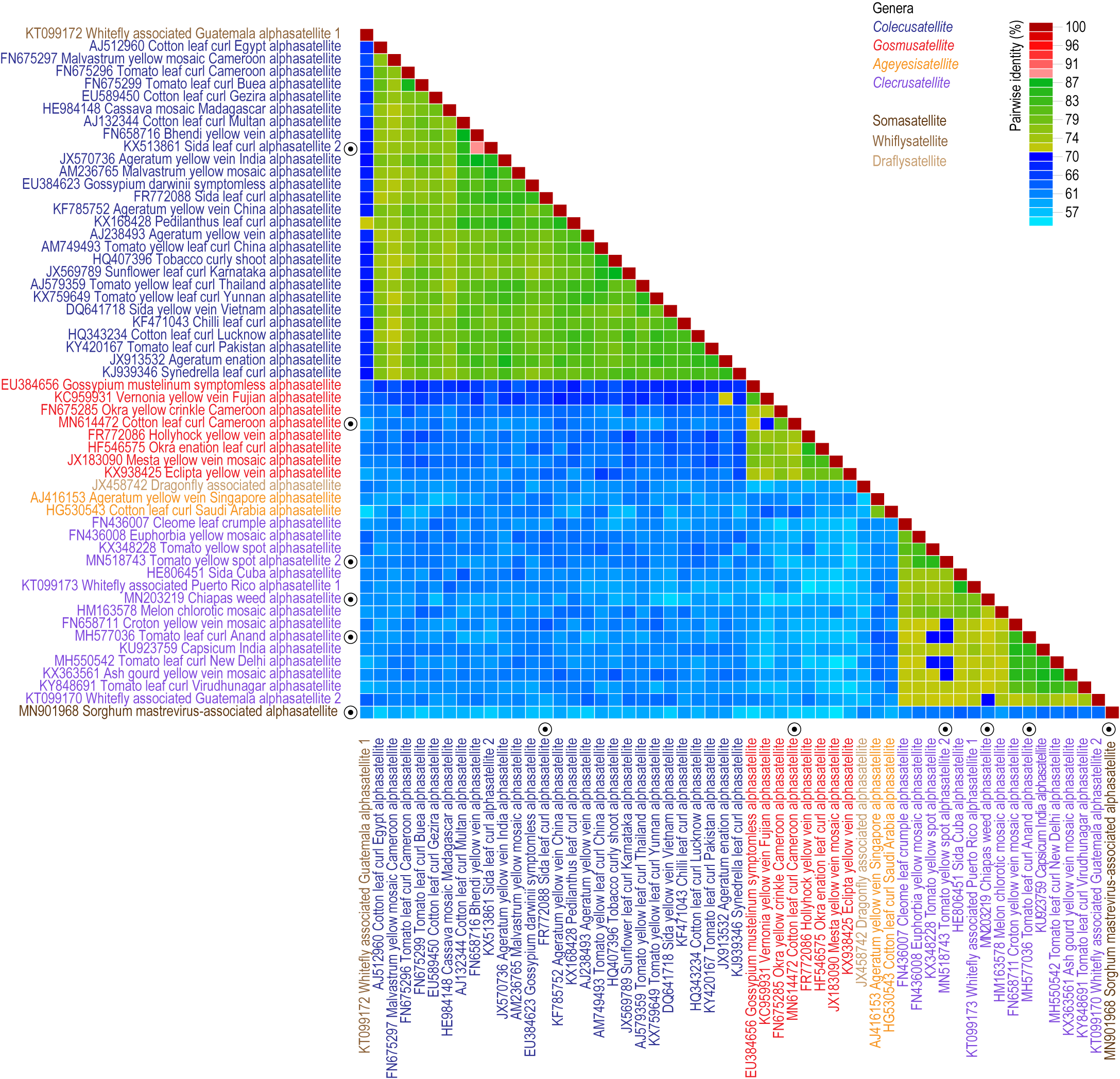
**Abstract**

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| Here we propose to classify new geminialphasatellites into six new species and nanoalphasatellites into three new species based on species demarcation guidelines already established for the family *Alphasatellitidae.* Furthermore, we propose to establish three new genera in the subfamily *Geminialphasatellitinae* to accommodate one new species identified here and two previously classified species that were not assigned to any genera. |

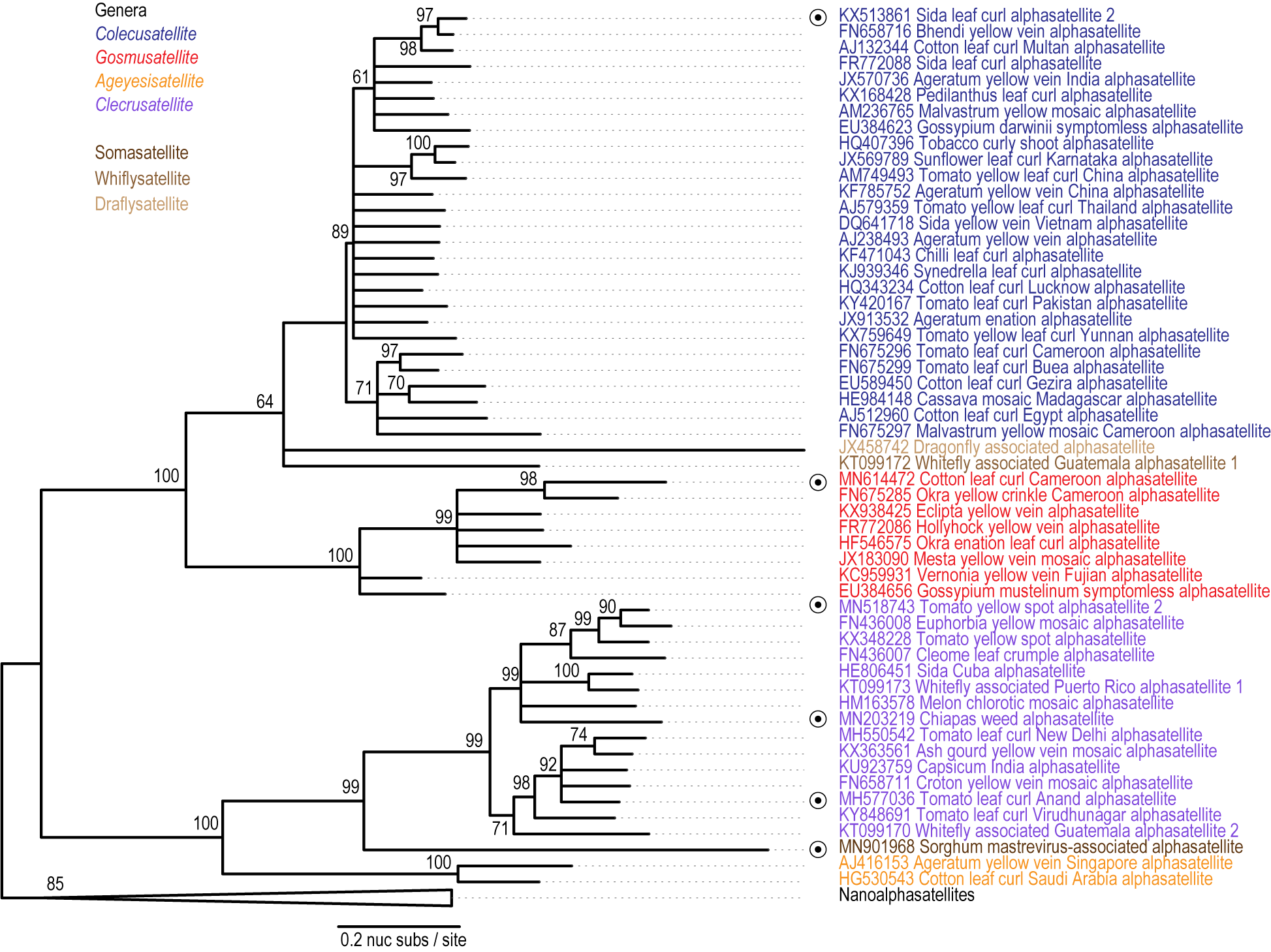
**Text of proposal**

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Currently there are four genera in the subfamily *Geminialphasatellitinae* and seven genera in the subfamily *Nanoalphasatellitinae*.  ***Geminialphasatellitinae***  A genera demarcation threshold of 70% and a species demarcation threshold of 88% based on genome-wise pairwise identity, was recommended by Briddon et al. [1]. Currently there are 49 species in this subfamily. Of these two are not assigned to any genera. In the last year, 17 geminialphasatellites have been identified that can not be assigned to the currently established species. These 17 can be classified into six new species (see summary below, Table 1). We also establish three new genera following the guideline set by Briddon et al. [1] to accommodate the two previously unassigned species and one for a new species being proposed here.  **Table 1:** Summary of the six new proposed species in the subfamily *Geminialphasatellitinae* and three new genera. The new species and genera are highlighted in red font.   |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | | **Genera** | ***Species*** | **Accession #** | **Virus name** | **Acronym** | **Isolate** | **Country** | **host** | | *Gosmusatellite* | *Cotton leaf curl Cameroon alphasatellite* | MN614472 | Cotton leaf curl Gezira alphasatellite 3 | CLCuGeA3 | CM-OBKG-Okra-2007 | Cameroon | *Abelmoschus esculentum* | | *Colecusatellite* | *Sida leaf curl alphasatellite 2* | KX513861 | Sida leaf curl alphasatellite 2 | SLCuA2 | IN-Gandhinagar-Sida-2016 | India | *Sida* sp | |  |  | KX513858 | Sida leaf curl alphasatellite 2 | SLCuA2 | IN-Gandhinagar-Calotropis-2016 | India | *Calotropis* sp | | *Somasatellite* | *Sorghum mastrevirus associated alphasatellite* | MN901968 | Sorghum mastrevirus associated alphasatellite | SmaA | RE-Bassin plat-Sorghum arundinaceum-RE180\_a-2017 | Reunion | *Sorghum arundinaceum* | |  |  | MN901967 | Sorghum mastrevirus associated alphasatellite | SmaA | RE-Bassin plat-Sorghum arundinaceum-RE179\_e-2017 | Reunion | *Sorghum arundinaceum* | |  |  | MN901969 | Sorghum mastrevirus associated alphasatellite | SmaA | RE-Bassin plat-Sorghum arundinaceum-RE183\_7d-2017 | Reunion | *Sorghum arundinaceum* | |  |  | MN901970 | Sorghum mastrevirus associated alphasatellite | SmaA | RE-Bassin plat-Sorghum arundinaceum-RE186\_9f-2017 | Reunion | *Sorghum arundinaceum* | |  |  | MN901971 | Sorghum mastrevirus associated alphasatellite | SmaA | RE-Bassin plat-Sorghum arundinaceum-RE552\_16a-2017 | Reunion | *Sorghum arundinaceum* | |  |  | MN901972 | Sorghum mastrevirus associated alphasatellite | SmaA | RE-Bassin plat-Sorghum arundinaceum-RE552\_31e-2017 | Reunion | *Sorghum arundinaceum* | |  |  | MN901973 | Sorghum mastrevirus associated alphasatellite | SmaA | RE-Bassin plat-Sorghum arundinaceum-RE552\_31f-2017 | Reunion | *Sorghum arundinaceum* | |  |  | MN901974 | Sorghum mastrevirus associated alphasatellite | SmaA | RE-Bassin plat-Sorghum arundinaceum-RE552\_32a-2017 | Reunion | *Sorghum arundinaceum* | |  |  | MN901975 | Sorghum mastrevirus associated alphasatellite | SmaA | RE-Bassin plat-Sorghum arundinaceum-RE552\_32j-2017 | Reunion | *Sorghum arundinaceum* | | *Clecrusatellite* | *Tomato leaf curl Anand alphasatellite* | MH577036 | Tomato leaf curl Anand alphasatellite | ToLCuAA | IN-Anand-2016 | India | *Solanum lycopersicum* | | *Clecrusatellite* | *Chiapas weed alphasatellite* | MN203219 | Begomovirus associated alphasatellite | BaA | MX-UHAsV-1-CD-W-2014 | Mexico | *Weed* | | *Clecrusatellite* | *Tomato yellow spot alphasatellite 2* | MN518743 | Tomato yellow spot alphasatellite 2 | ToYSA2 | AR-Jujuy-Yuto-Leonurus417-2008 | Argentina | *Leonurus japonicus Houtt* | |  |  | MN518744 | Tomato yellow spot alphasatellite 2 | ToYSA2 | AR-Jujuy-Yuto-Leonurus417-2008 | Argentina | *Leonurus japonicus Houtt* | |  |  | MN518745 | Tomato yellow spot alphasatellite 2 | ToYSA2 | AR-Jujuy-Yuto-Pepper423-2008 | Argentina | *Capsicum annuum* | | *Whiflysatellite* | *Whitefly associated Guatemala alphasatellite 1* | KT099172 | Whitefly associated Guatemala alphasatellite 1 | WfaGTA1 | GT-GtTo2-2-12 | Guatemala | Whiteflies | | *Draflysatellite* | *Dragonfly associated alphasatellite* | JX458742 | Dragonfly associated alphasatellite | DaA | PR-09 | Puerto Rico | *Erythrodiplax fusca* |   ***Nanoalphasatellitinae***  A genera demarcation threshold of 67% and species demarcation threshold of 80% based on genome-wise pairwise identity, was previously recommended by Briddon et al [1].  Currently there are 21 species in this subfamily. In the last year four nanoalphasatellites have been identified that cannot be assigned to established species. These four can be classified into three new species (see Table 2).  **Table 2:** Summary of the three new proposed species in the subfamily *Nanoalphasatellitinae.* The new species are highlighted in red font.   |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | | **Genera** | ***Species*** | **Accession #** | **Virus name** | **Acronym** | **Isolate** | **Country** | **host** | | *Mivedwarsatellite* | *Parsley severe stunt alphasatellite 3* | MK039141 | Parsley severe stunt alphasatellite 3 | PSSA3 | DE-Pa21-2017 | Germany | *Petroselinum crispum* | | *Mivedwarsatellite* | *Parsley severe stunt alphasatellite 4* | MK039142 | Parsley severe stunt alphasatellite 4 | PSSA4 | DE-Pa21-2017 | Germany | *Petroselinum crispum* | |  |  | MN531183 | Parsley severe stunt alphasatellite 4 | PSSA4 | IR-Bagh:39Ba-Pars:18 | Iran | *Petroselinum crispum* | | *Mivedwarsatellite* | *Milk vetch dwarf alphasatellite 4* | MN059431 | Milk vetch dwarf C1 alphasatellite | MVC1A | CN-G48-2017 | China | *Allium sativum* |   **NOTE: Please note that a separate TP has been submitted to establish a new sub-family within the *Alphasatellitidae* and that results in the move of the genus *Babusatellite* to the new genus.** | |

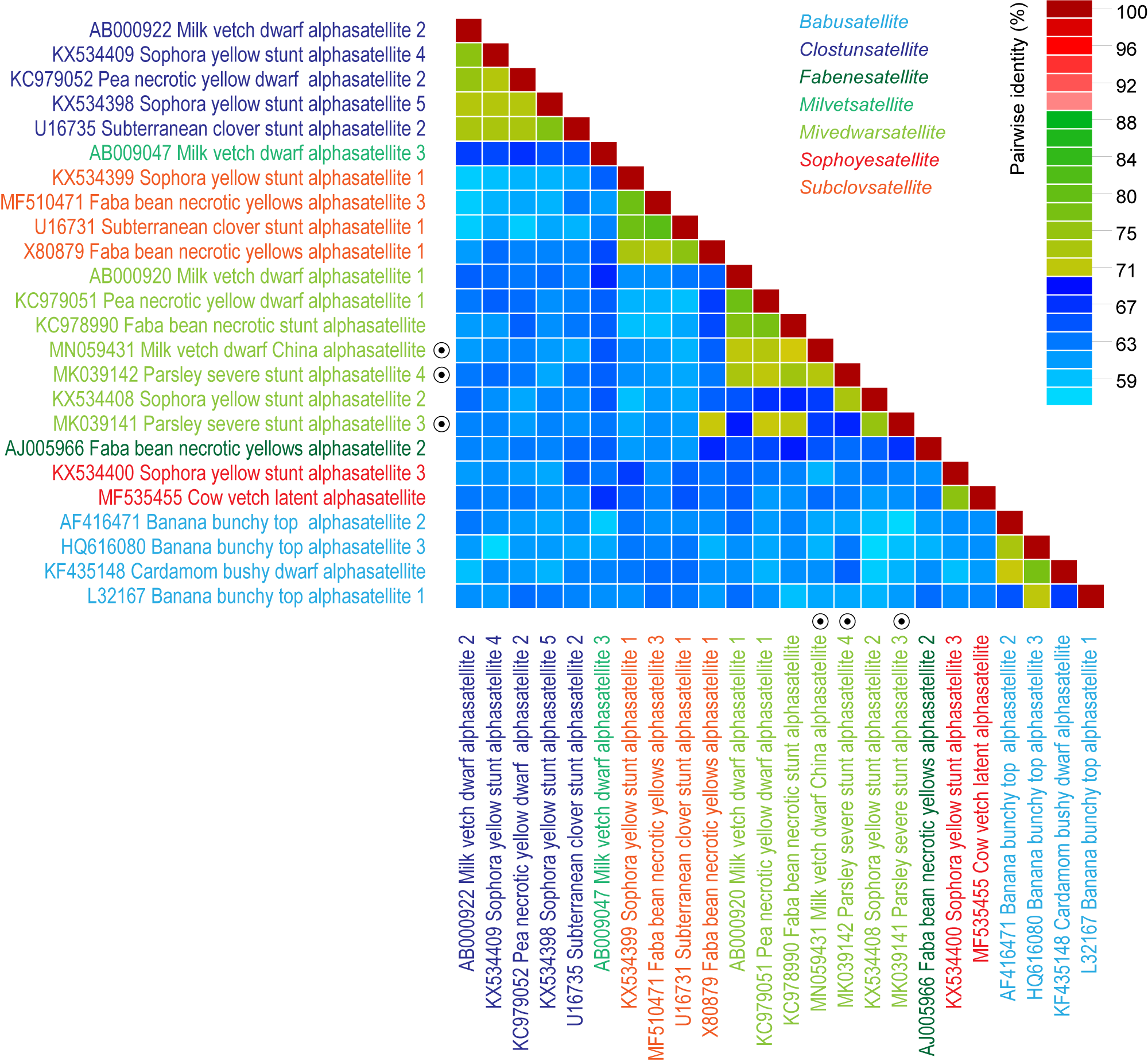
**Supporting evidence**

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**Figure 1:** A ‘three colour’ pairwise identity matrix inferred using SDT v1.2 [3] showing that both the genera demarcation threshold of 70% and the species demarcation threshold at 88% are supported. Representatives of new species are highlighted with a circle.

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**Figure 2:** Maximum likelihood phylogenetic tree of representative geminivirus-associated alphasatellite sequences from each species inferred using PHYML 3 [2] with GTR+I+G4 chosen as the best-fit model. Branches with <60% bootstrap support have been collapsed. Representatives of new species are highlighted with a circle.

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**Figure 3:** A ‘three colour’ pairwise identity matrix inferred using SDT v1.2 [3] showing that both the genera demarcation threshold of ~65% and the species demarcation threshold of 80% are supported. Representatives of new species are highlighted with a circle.

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**Figure 4:** Maximum likelihood phylogenetic tree of representative geminivirus-associated alphasatellite sequences from each species inferred using PHYML 3 [2] with GTR+I+G4 chosen as the best-fit model. Branches with <60% bootstrap support have been collapsed. Representatives of new species are highlighted with a circle.

**References**

1. Briddon RW, Martin DP, Roumagnac P, Navas-Castillo J, Fiallo-Olive E, Moriones E, Lett JM, Zerbini FM, Varsani A (2018) *Alphasatellitidae*: a new family with two subfamilies for the classification of geminivirus- and nanovirus-associated alphasatellites. Arch Virol 163:2587-2600. PMID: 29740680; DOI: 10.1007/s00705-018-3854-2

2. Guindon S, Dufayard JF, Lefort V, Anisimova M, Hordijk W, Gascuel O (2010) New algorithms and methods to estimate maximum-likelihood phylogenies: assessing the performance of PhyML 3.0. Syst Biol 59:307-321. PMID: 20525638; DOI: 10.1093/sysbio/syq010

3. Muhire BM, Varsani A, Martin DP (2014) SDT: a virus classification tool based on pairwise sequence alignment and identity calculation. PLoS One 9:e108277. PMID: 25259891; DOI: 10.1371/journal.pone.0108277