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:** | ***2017.004P*** | | | | (to be completed by ICTV officers) |
| **Short title:** Establishment of a family, two subfamilies, 11 genera and 63 species for geminivirus- and nanovirus-associated satellites. | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1  2  3  4** | | | |
| **Author(s):** | | | | | |
| Rob W. Briddon and Arvind Varsani | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| [rob.briddon@gmail.com](mailto:rob.briddon@gmail.com); [Arvind.varsani@asu.edu](mailto: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* and *Nanoviridae* SGs** | | |
| **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:** |
|  |

**Part 2**: **PROPOSED TAXONOMY**

|  |
| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet:** 2017.004P.N.v1.Alphasatellitidae |

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:** |
|  |

**Part 4:** **APPENDIX**: supporting material

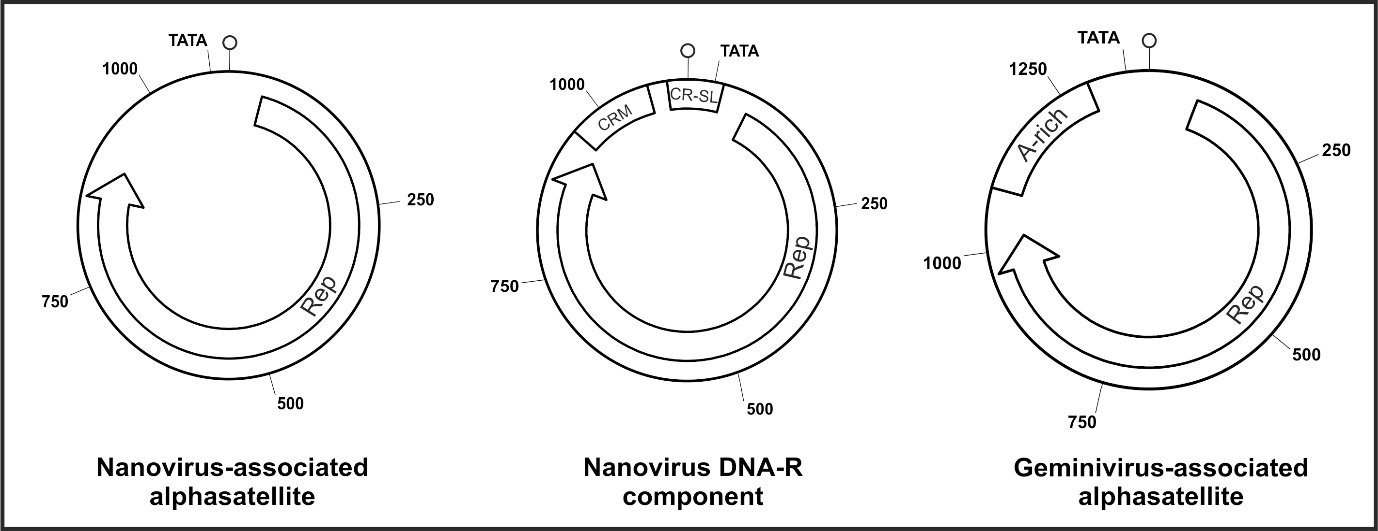
A new family is proposed to encompass the satellite-like molecules that are associated with geminiviruses and nanoviruses. Based on the proposed genus and species demarcation thresholds the new family will include two subfamilies, 11 genera and 63 species.

The family *Geminiviridae* consists of viruses with either monopartite or bipartite single-stranded (ss)DNA genomes, with each component individually encapsidated in twinned quasi-isometric (geminate) 22-38 nm virions. The family contains nine genera, of which two are relevant to the discussion here - *Begomovirus* and *Mastrevirus*; viruses transmitted by the whitefly *Bemisia tabaci* and by leafhoppers, respectively, in a circulative, non-propagative manner. The genomes/genomic components of geminiviruses are typically 2600-3100 nucleotides (Brown et al., 2012).

The family *Nanoviridae* encompasses viruses with multicomponent ssDNA genomes that are individually encapsidated within isometric 17-20 nm virions. The family contains two genera, *Nanovirus* and *Babuvirus*, of viruses transmitted by aphids in a circulative, non-propagative manner. Members of the genus *Nanovirus* infect dicotyledonous host plants whereas those of the genus *Babuvirus* infect monocotyledonous plants. Typically the genomes of nanoviruses have eight components and the genomes of babuviruses consist of six components; the components of both range in size from 970 to 1116 nucleotides (Vetten et al., 2012). The *bona fide* genome components of a nanovirus genome share two regions of sequence similarity known as the common region stem-loop (CR-SL) and the common region major (CRM; Figure 1). The DNA-R component of nanoviruses encodes a replication-associated protein (Rep) (Burns et al., 1995; Hafner et al., 1997; Harding et al., 1993; Heydarnejad et al., 2017) which is involved in replicating all *bona fide* genome components.

Viruses of the family *Nanoviridae,* and some begomoviruses and mastreviruses may be associated with additional ssDNA components that resemble the DNA-R components of nanoviruses; these will be referred to as alphasatellites. In common with the DNA-R component of nanoviruses, the alphasatellites encode a Rep gene and have a predicted stem-loop structure with, in most cases, the nonanucleotide sequence TAGTATTAC forming part of the loop (Figure 1). However, alphasatellites associated with nanoviruses are the size of typical nanovirus components (~1100 nucleotides), lack the CR-SL and CRM of their helper viruses and are unable to trans-replicate the *bona fide* genome components of the virus with which they are associated (Horser et al., 2001; Timchenko et al., 1999; Timchenko et al., 2006; Timchenko et al., 2000). Alphasatellites have also been identified in association with begomoviruses and, for one reported case, a mastrevirus (Briddon et al., 2004; Kumar et al., 2014). The geminivirus associated alphasatellites are typically ~1380 nucleotides (Briddon et al., 2004), significantly larger than nanovirus components or nanovirus alphasatellites. This size increase, due mostly to the presence of a region of sequence rich in adenine and encoding a larger Rep gene, is thought to have been necessitated for encapsidation by the helper geminivirus. Geminiviruses have a strict size range for encapsidation and a ssDNA molecule of half the geminivirus genome length (~1400 nucleotides) could possibly be encapsidated in isometric (half geminate) virions. For both nanovirus- and geminivirus-associated alphasatellites the sequence relatedness and similarity in structure to nanovirus DNA-R components has led to the hypothesis that the satellites evolved from DNA-R components “captured” following co-infections.

It is interesting to note that the vast majority of geminivirus-associated alphasatellites identified in the Old World have been identified in association with infections of monopartite begomoviruses with betasatellites. This contrasts with the situation in the New World where monpartite begomoviruses are very rare, betasatellites have not been identified and alphasatellites are reported to occur in association with bipartite begomovirus infections (Paprotka et al., 2010; Romay et al., 2010; Ferro et al., 2017). The precise biological significance of the presence of alphasatellites in virus infections remains unclear. Timchenko et al. (2006) have shown that the presence of one of the additional Rep-encoding components (alphasatellite) of faba bean necrotic yellows virus reduced infectivity of the virus. This suggests that the alphasatellite interferes with virus multiplication. For the geminivirus-associated alphasatellites analyses have produced conflicting results which may suggest that alphasatelites from different genera have evolved slightly differently.



**Figure 1.** Illustration of the Rep-encoding DNA molecules of nanovirus- and geminivirus-associated alphasatellites in comparison to the DNA-R components of nanoviruses. The diagrams include the position of the replication-associated protein (Rep), the TATA box of the presumed Rep promoter, an adenine rich sequence (A-rich) in geminivirus-associated alphasatellites and the common region major (CRM) and common region stem-loop (CR-SL) of nanovirus DNA-R components. All components have a predicted stem-loop structure (at position zero) with, in most cases, the nonanucleotide sequence TAGTATTAC forming part of the loop. This likely forms the origin of virion-strand DNA replication that is nicked by Rep to initiate rolling-circle replication.

Idris et al. (2011) showed the unusual geminivirus-associated alphasatellite (*Ageratum yellow vein Singapore alphasatellite*; proposed genus *Ageyesisatellite*) to reduce symptom severity of infections, likely by reducing the DNA levels of the betasatellite associated with the begomovirus complex; betasatellites encode a dominant symptom determinant. Kon et al. (2009) showed a begomovirus-associated alphasatellite (*Cotton leaf curl Gezira alphasatellite*, proposed genus *Colecusatellite*) to reduce helper virus DNA levels, but not attenuate symptoms, in the absence of the cognate betasatellite. In the presence of the betasatellite no significant effects were noted. Two distinct begomovirus-associated alphasatellites, *Gossypium darwinii symptomless alphasatellite* and *Gossypium mustelinium symptomless alphasatellite* (proposed genera *Colecusatellite* and *Gosmusatellite*, respectively) were shown to encode Rep proteins with suppressor of post-transcriptional gene silencing activity; thus they are involved in overcoming host defences. In contrast, for six alphasatellites associated with begomoviruses (proposed genus *Colecusatellite*) no post-transcriptional gene silencing activity of the Rep could be shown (Abbas and Briddon - manuscript in preparation); instead the Rep proteins exhibited suppressor of transcriptional gene silencing activity (Abbas et al., 2017). For a begomovirus-associated alphasatellite originating from the New World (*Euphorbia yellow mosaic alphasatellite*; proposed genus *Clecrusatellite*) the presence of the alphasatellite exacerbated virus symptoms in plants (Paprotka et al., 2010; Mar et al., 2017).

Due to the rising number of alphasatellites being described, owing mainly to the increasing interest in begomoviruses and nanoviruses as well as the ease with which they can be isolated and characterized, there is an urgent need for a robust and workable system of nomenclature and classification of these components. Since these satellite-like molecules are not independent entities, relying on a helper virus for their spread, the biological data useful for their classification that can unequivocally be attributed to the satellite-like molecule are limited and uninformative. It is thus necessary to base a classification system entirely on their nucleotide sequences, which could potentially be adjusted once biological evidence becomes available.

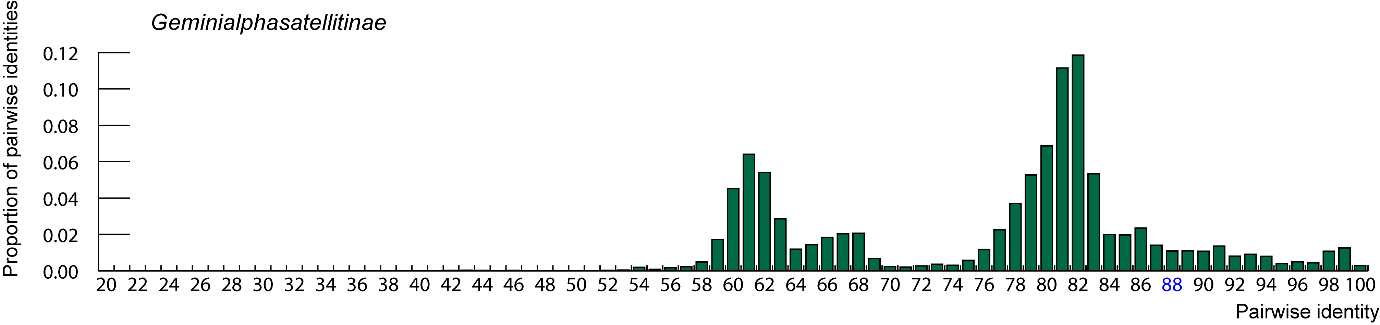
We propose the creation of two subfamilies based on the fact that there are clear differences between geminivirus- and nanovirus-associated alphasatellites. These include genome length and an A-rich region downstream of the Rep coding region for alphasatellites associated with geminiviruses. The two sub families are:

1. *Geminialphasatellitinae*: geminivirus-associated alphasatellites
2. *Nanoalphasatellitinae*: nanovirus-associated alphasatellites

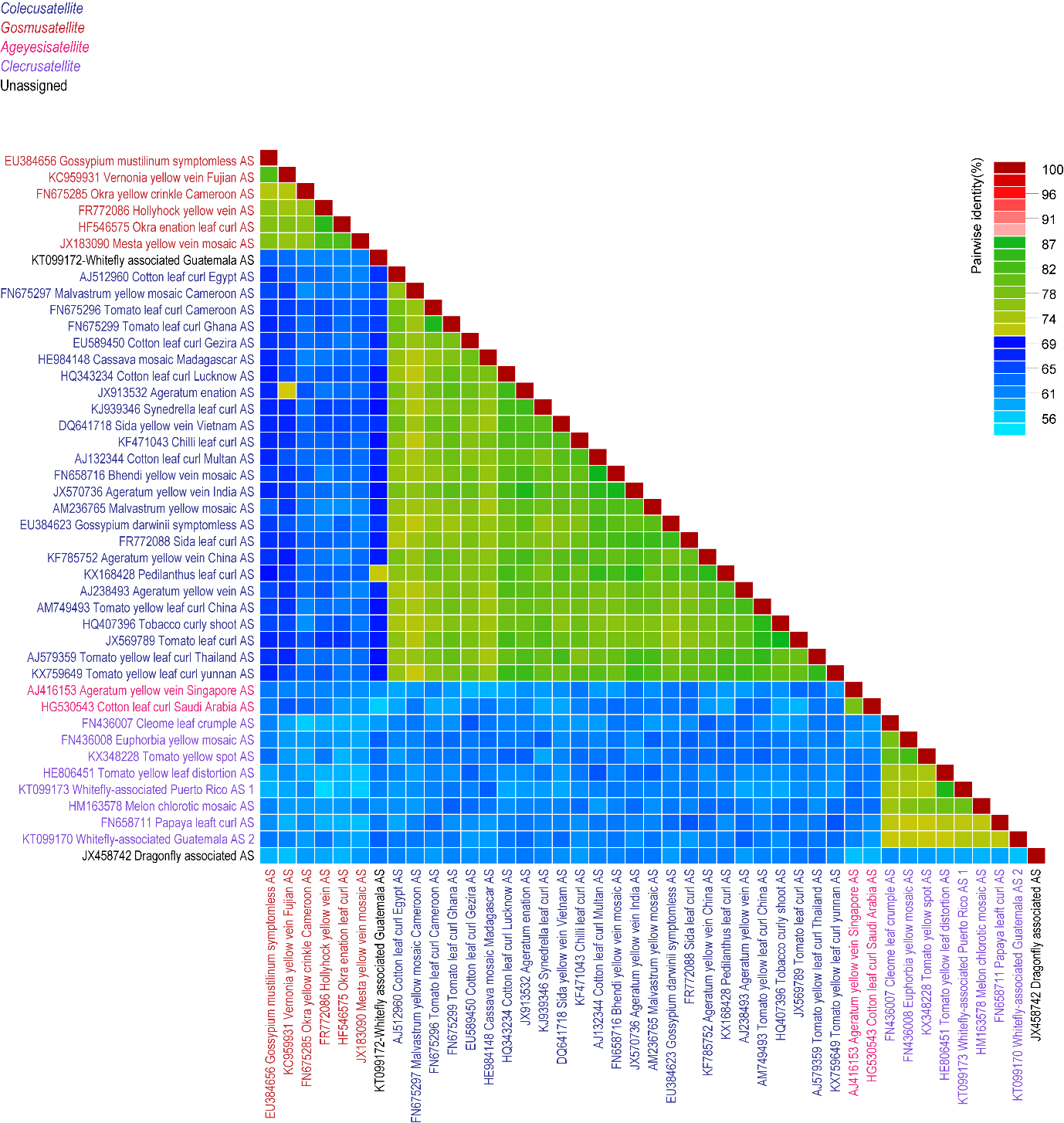
***Geminialphasatellitinae***

Sequences of geminivirus-associated alphasatellites were downloaded from GenBank (1st May 2017). These sequences were checked to make sure they were unit length molecules (complete), had intact Rep open reading frames and were not sub-genomic begomoviruses. The filtered 629 geminivirus-associated alphasatellites were analysed with SDT v1.2. The 629 taxa were aligned using MUSCLE (Edgar, 2004) and the resulting alignment was used to infer a maximum likelihood phylogenetic tree using IQ-TREEE (Nguyen et al., 2015) with TIM2+I+G4 as the best fit substitution model and the tree was rooted with DNA-R sequences of nanoviruses.

The distribution of the pairwise identities shows that there is a trough at ~88% pairwise identity and this was chosen as a species cut off (Figure 2). Additionally the trough in distribution of percent identity values at 70% was found to divide the known geminivirus-associated alphasatellites into groups (genera) which mirrors their phylogenetic/geographic distributions, sequence divergence and range of helper viruses. The species threshold of 88% and genus threshold of 70% (Figure 3) are supported by the phylogenetic analysis (Figure 4).



**Figure 2.** Distribution of pairwise identities of geminivirus-associated alphasatellites determined using SDT v1.2 (Muhire et al., 2014).



**Figure 3.** A ‘three color’ pairwise identity matrix inferred using SDT v1.2 (Muhire et al., 2014) showing that both the genera demarcation threshold of 70% and that for species at 88% are supported.



**Figure 4.** Maximum likelihood phylogenetic tree of representative geminivirus-associated alphasatellite sequences from each species inferred using IQ-TREE (Nguyen et al., 2015) with GTR+I+G4 chosen as the best fit model. Branches with less than 60% bootstrap support have been collapsed.

A previous incarnation of the *Geminiviridae* Study Group sought to establish a taxonomy and nomenclature for alphasatellites. This was presented at geminivirus meetings but was not submitted to ICTV or published. Nevertheless, many of the species names established by this earlier effort are now in widespread use in the geminivirus community. Every effort has been made to maintain these names here so as to avoid confusion and maintain consistency. The name *Alphasatellitidae* derives from the name alphasatellite which is now in common usage for this group of satellites. The begomovirus alphasatellites, upon first identification were called DNA 1 in recognition of their being related to the Rep-encoding components of nanoviruses (DNA-R) which at the time were called DNA 1 (Mansoor et al., 1999). Following the identification of the DNA 1 (alpha)satellites, the betasatellites were identified and were originally referred to as DNA β satellites (Saunders et al., 2000), to indicate that they are not (apparently) related to nanoviruses and to indicate that they are begomovirus DNA-B component-like (a second component), which became “betasatellites” to avoid the use of Greek symbols. As a consequence the then DNA 1 satellites were named alphasatellites. The alphasatellite genera names are derived from the names of the type species so, for example, the genus name *Colecusatellite* derives from the name of the first begomovirus alphasatellite identified, Cotton leaf curl Multan alphasatellite. The alphasatellite species names are, whenever possible, derived from the name of the helper virus with which they were first identified; so Cotton leaf curl Multan alphasatellite was first identified in an infection of cotton with cotton leaf curl Multan virus.

Based on the above criteria, 4 genera are established in the subfamily *Geminialphasatellitinae* and 43 species. The classification of the genera and species in the subfamily *Geminialphasatellitinae* is summarized in Table 1.

**Table 1:** Summary of the genera and species in subfamily *Geminialphasatellitinae.* Representative species of each genus is in bold font.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Genus** | **Species** | **Accession #** | **Acronym** | **Isolate** |
| *Ageyesisatellite* | ***Ageratum yellow vein Singapore alphasatellite*** | AJ416153 | AYVSGA | AYVSGA-[SG:98] |
|  | *Cotton leaf curl Saudi Arabia alphasatellite* | HG530543 | CLCuSAA | CLCuSAA-[SA:Jazan:13] |
| *Clecrusatellite* | ***Cleome leaf crumple alphasatellite*** | FN436007 | ClLCrA | ClLCrA-[BR:Mato Grosso do Sul:07] |
|  | *Papaya leaf curl alphasatellite* | FN658711 | PaLCUA | PaLCuA-[IN:Haryana:Acalypha:07] |
|  | *Euphorbia yellow mosaic alphasatellite* | FN436008 | EuYMA | EuYMA-[BR:Mato grosso do sul:1:07] |
|  | *Tomato yellow spot alphasatellite* | KX348228 | ToYSA | ToYSA-[BR:Dou1095.1:11] |
|  | *Melon chlorotic mosaic alphasatellite* | HM163578 | MeCMA | MeCMA-[VE:2009-02-04-0:09] |
|  | *Tomato yellow leaf distortion alphasatellite* | HE806451 | ToYLDA | ToYLDA-[CU:Trinidad:07] |
|  | *Whitefly-associated Guatemala alphasatellite 2* | KT099170 | WfaGTA 2 | WfaGTA 2-[GT:GtTo2-1:10] |
|  | *Whitefly-associated Puerto Rico alphasatellite 1* | KT099173 | WfaPRA 1 | WfaPRA 1-[PR:PR3-6:10] |
| *Colecusatellite* | *Ageratum enation alphasatellite* | JX913532 | AEA | AEA-[IN:Luc:12] |
|  | *Ageratum yellow vein alphasatellite* | AJ238493 | AYVA | AYVA-[SG:98] |
|  | *Ageratum yellow vein China alphasatellite* | KF785752 | AYVCNA | AYVCNA-[PH:Davao:SN3:Synedrella nodiflora:12] |
|  | *Ageratum yellow vein India alphasatellite* | JX570736 | AYVIA | AYVIA-[IN:Luc:parthenium:12] |
|  | *Bhendi yellow vein mosaic alphasatellite* | FN658716 | BhYVMA | BhYVMA-[IN:Har:07] |
|  | *Cassava mosaic Madagascar alphasatellite* | HE984148 | CMMGA | CMMGA-[MG:Diana:635A1:11] |
|  | *Chilli leaf curl alphasatellite* | KF471043 | ChLCA | ChLCA-[IN:273:06] |
|  | *Cotton leaf curl Egypt alphasatellite* | AJ512960 | CLCuEA | CLCuEA-[EG:SB45:95] |
|  | *Cotton leaf curl Gezira alphasatellite* | EU589450 | CLCuGeA | CLCuGeA-[ML:Bamako:okra:06] |
|  | *Cotton leaf curl Multan alphasatellite* | AJ132344 | CLCuMuA | CLCuMuA-[PK:Fai01:98] |
|  | *Cotton leaf curl Lucknow alphasatellite* | HQ343234 | CLCuLuA | CLCuLuA-[IN:Luc:10] |
|  | *Gossypium darwinii symptomless alphasatellite* | EU384623 | GDarSLA | GDarSLA-[PK:Mul:Dav7C:06] |
|  | *Malvastrum yellow mosaic Cameroon alphasatellite* | FN675297 | MaYMCMA | MaYMCMA-[CM:Mundemba:UMU1D1:08] |
|  | *Malvastrum yellow mosaic alphasatellite* | AM236765 | MaYA | MaYA-[CN:Hn39] |
|  | *Pedilanthus leaf curl alphasatellite* | KX168428 | PeLCA | PeLCA-[IN:carrot] |
|  | *Sida leaf curl alphasatellite* | FR772088 | SiLCuA | SiLCuA-[PK:Lahore:Alcea rosea:06] |
|  | *Sida yellow vein Vietnam alphasatellite* | DQ641718 | SiLCuA | SiYVVA-[VN:Han:05] |
|  | *Tomato leaf curl alphasatellite* | JX569789 | ToLCA | ToLCA-[IN:tomato:11] |
|  | *Synedrella leaf curl alphasatellite* | KJ939346 | SyLCA | SyLCA-[IN:Por:synf-1:09] |
|  | *Tobacco curly shoot alphasatellite* | HQ407396 | TbCSA | TbCSA-[IN:WSF1:Helianthus:10] |
|  | *Tomato leaf curl Ghana alphasatellite* | FN675299 | ToLCuGHA | ToLCuBuA-{CM:Buea:TOS2D1:07] |
|  | *Tomato leaf curl Cameroon alphasatellite* | FN675296 | ToLCuCMA | ToLCuCMA-[CM:Buea:OMHD3:08] |
|  | *Tomato yellow leaf curl Thailand alphasatellite* | AJ579359 | TYLCTHA | TYLCTHA-[TH:Y70:03] |
|  | *Tomato yellow leaf curl China alphasatellite* | AM749493 | TYLCCNA | TYLCCNA-[PK:Fai:09] |
|  | *Tomato yellow leaf curl Yunnan alphasatellite* | KX759649 | TYLCYnA | TYLCYnA-[CN:YN4368-69:14] |
| *Gosmusatellite* | ***Gossypium mustilinum symptomless alphasatellite*** | EU384656 | GMusSLA | GMusSLA-[PK:Mul:2:06] |
|  | *Hollyhock yellow vein alphasatellite* | FR772086 | HoYVA | HoYVA-[PK:Lahor:17-5:06] |
|  | *Mesta yellow vein mosaic alphasatellite* | JX183090 | MeYVMA | MeYVMA-[IN:Ludhiana:Okra:10] |
|  | *Okra enation leaf curl alphasatellite* | HF546575 | OEnLCuA | OEnLCuA-[IN:Surat:11] |
|  | *Okra yellow crinkle Cameroon alphasatellite* | FN675285 | OkYCCMA | OkYCCMA-[CM:Lys1sp3:08] |
|  | *Vernonia yellow vein Fujian alphasatellite* | KC959931 | VeYVFA | VeYVFA-[IN:Vamban:blackgram:12] |
| Unassigned | ***Whitefly associated Guatemala alphasatellite 1*** | KT099172 | WfaGTA 1 | WfaGTA 1-[GT:GtTo2-2:12] |
| Unassigned | ***Dragonfly associated alphasatellite*** | JX458742 | DaA | DaA-[PR:09] |

The 43 *Geminialphasatellitinae* species described here:

1. All have the distinctive organization consisting of a single conserved coding sequence in the virion-sense, encoding a Rep (a rolling-circle replication initiator protein), and predicted stem-loop structure containing, in most cases, a TAGTATTAC sequence.

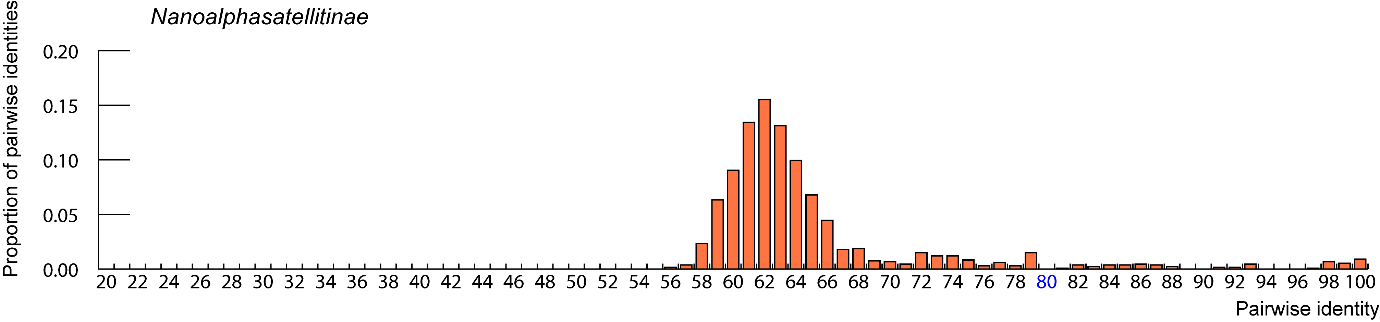
2. With the exception of two alphasatellites, all have been shown to be associated with a geminivirus.

For two putative alphasatellites included in the analysis no helper begomovirus is known. Sequence JX458742 (proposed *Dragonfly associated alphasatellite*) was isolated from a dragonfly caught in Puerto Rico and no virus could conclusively be shown to be associated with the molecule. Sequence KT099172 (proposed *Whitefly associated Guatemala alphasatellite 1*) was isolated from a *B. tabaci* whitefly originating from Guatemala and no virus could conclusively be shown to be associated with the molecule.

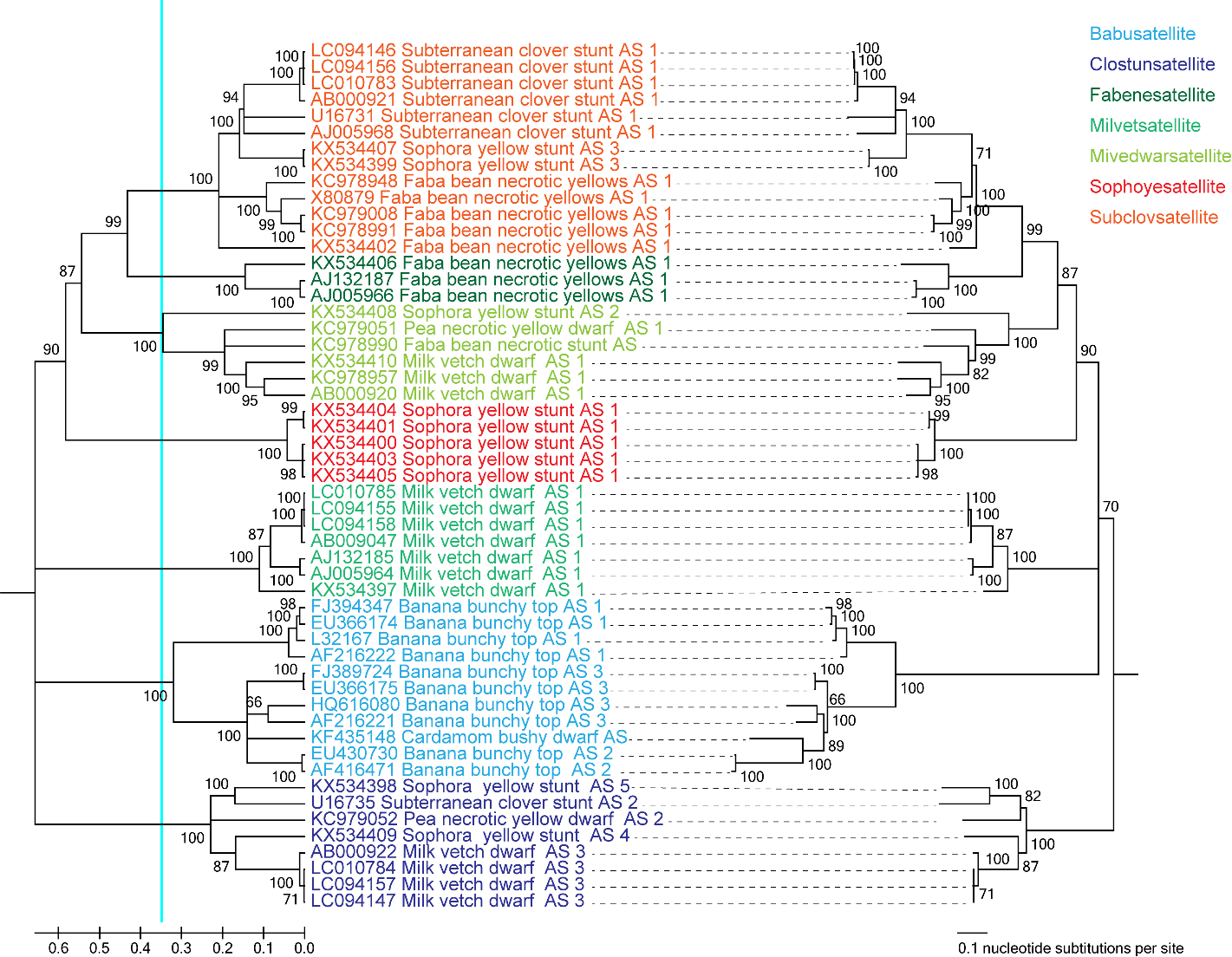
***Nanoalphasatellitinae***

Sequences of nanovirus-associated alphasatellites were downloaded from GenBank (1st May 2017). These sequences were checked to make sure they were unit length molecules (complete) and had intact Rep open reading frames. The 52 filtered nanovirus-associated alphasatellites were analysed with SDT v1.2 (Muhire et al., 2014). The 52 taxa were aligned using MUSCLE (Edgar, 2004) and the resulting alignment was used to infer a maximum likelihood phylogenetic tree using IQ-TREE (Nguyen et al., 2015) with TIM2+F+G4 as the best fit substitution model. The tree was rooted with DNA-R sequences of nanoviruses.

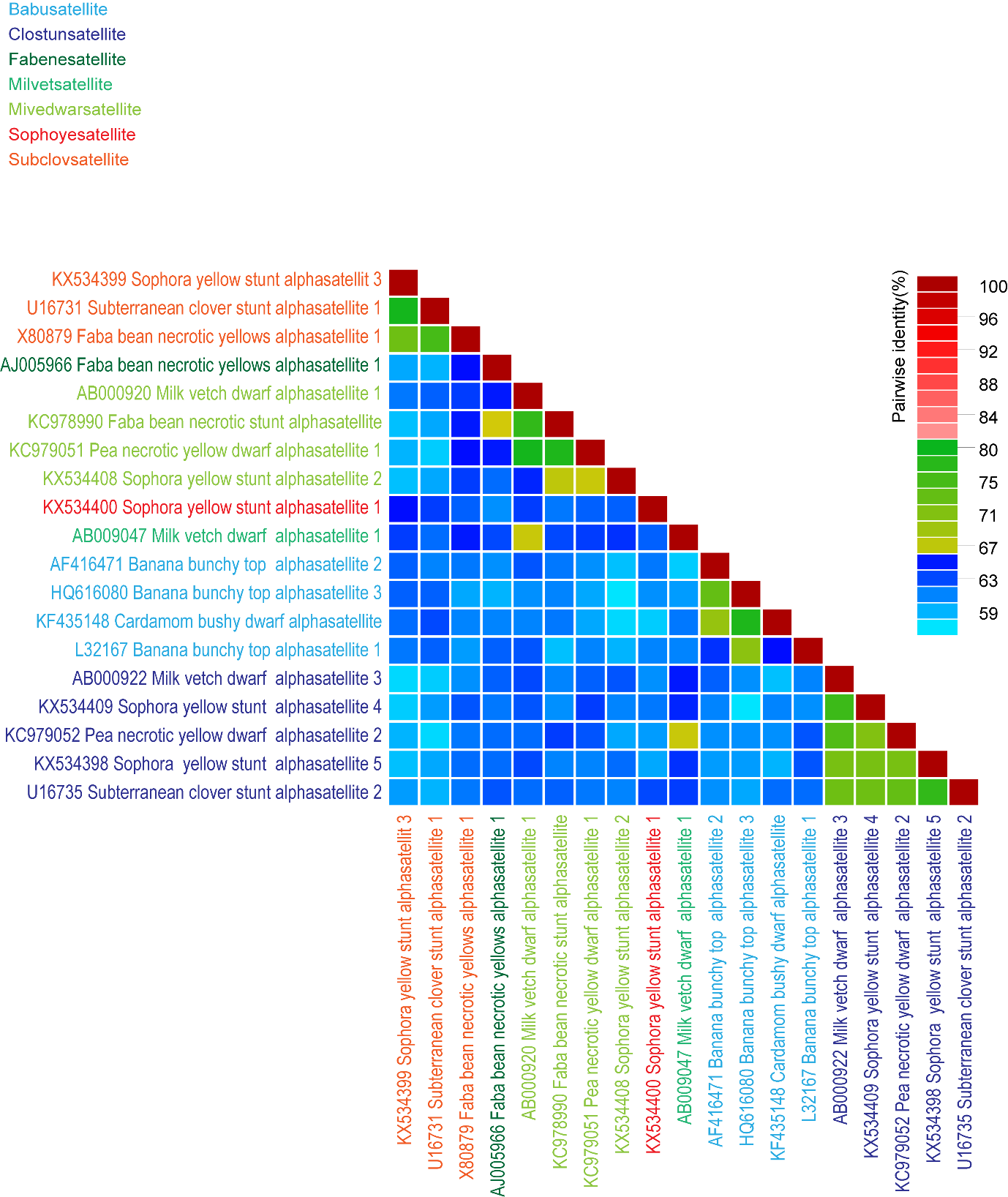
The distribution of the pairwise identities shows that there is a trough at ~80% pairwise identity and this was chosen as a species cut off (Figure 5). With the 80% species threshold, 19 new species need to be created to accommodate the current 52 taxa of nanovirus-associated alphasatellites. Furthermore, seven genera can be established based on the phylogenetic clustering of the nanovirus-associated alphasatellites (Figure 6). Pairwise identity analysis of this clustering suggests that an approx. 67% threshold (with a few exceptions; Figure 7) can be used as a guide towards inferring new genera, however, we recommend that this is supported by strong phylogenetic support. A summary of the genera and species in the subfamily *Nanoalphasatellitinae* is provided in Table 2.



**Figure 5.** Distribution of pairwise identities of nanovirus-associated alphasatellites determined using SDT v1.2 (Muhire et al., 2014).



**Figure 6.** Maximum likelihood phylogenetic trees of the nanovirus-associated alphasatellite sequences inferred using IQ-TREE (Nguyen et al., 2015) with TIM2+F+I+G4 chosen as the best fit model. Branches with less than 60% bootstrap support have been collapsed. The Maximum likelihood phylogenetic tree on left is a guide for genera demarcation with the cyan line showing the rough 65% threshold.

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**Figure 7.** A ‘three color’ pairwise identity matrix inferred using SDT v1.2 (Muhire et al., 2014) showing that both the genera demarcation threshold of ~65% and that for species at 80% are supported.

**Table 2:** Summary of the genera and species in subfamily *Nanoalphasatellitinae.* Representative species of each genus is in bold font.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| ***Genus*** | ***Species*** | **Accession #** | **Acronym** | **Isolate** |
| *Babusatellite* | *Banana bunchy top alphasatellite 3* | HQ616080 | BBTA 3 | BBTA 3-[CN:Haikou:10] |
|  | ***Banana bunchy top alphasatellite 1*** | L32167 | BBTA 1 | BBTA 1-[93] |
|  | *Banana bunchy top alphasatellite 2* | AF416471 | BBTA 2 | BBTA 2-[VN:VB:sat3:00] |
|  | *Cardamom bushy dwarf alphasatellite* | KF435148 | CaBuDA | CaBuDA-[IN:Kalimpong:07] |
| *Fabenesatellite* | ***Faba bean necrotic yellows alphasatellite 1*** | AJ005966 | FBNYA 1 | FBNYA 1-[SY:C9:93] |
| *Milvetsatellite* | ***Milk vetch dwarf alphasatellite 1*** | AB009047 | MVDA 1 | MVDA 2-[JR:C10:97] |
| *Clostunsatellite* | *Milk vetch dwarf alphasatellite 3* | AB000922 | MVDA 3 | MVDA 3-[JR:C3:96] |
|  | *Pea necrotic yellow dwarf alphasatellite 2* | KC979052 | PNYDA 2 | PNYDA 2-[AT:Gross-Enzersdorf\_1:10] |
|  | *Sophora yellow stunt alphasatellite 4* | KX534409 | SYSA 4 | SYSA 4-[IR:Kerman:Ta1:14] |
|  | ***Subterranean clover stunt alphasatellite 2*** | U16735 | SCSA 2 | SCSA 2-[AU:C6:93] |
|  | *Sophora yellow stunt alphasatellite 5* | KX534398 | SYSA 5 | SYSA 5-[IR:Kerman:Ta1:14] |
| *Mivedwarsatellite* | ***Milk vetch dwarf alphasatellite 2*** | AB000920 | MVDA 1 | MVDA 2-[JR:C1:96] |
|  | *Pea necrotic yellow dwarf alphasatellite 1* | KC979051 | PNYDA 1 | PNYDA 1-[AT:Gross-Enzersdorf\_1:10] |
|  | *Sophora yellow stunt alphasatellite 2* | KX534408 | SYSA 2 | SYSA 2-[IR:Kerman:Ta1:14] |
|  | *Faba bean necrotic stunt alphasatellite* | KC978990 | FBNSA | FBNSA-[AZ:12b:10] |
| *Subclovsatellite* | *Faba bean necrotic yellows alphasatellite 1* | X80879 | FBNYA 1 | FBNYA 1-[SY:C1:88] |
|  | *Sophora yellow stunt alphasatellite 3* | KX534399 | SYSA 3 | SYSA 3-[IR:Kerman:Ta1:14] |
|  | ***Subterranean clover stunt alphasatellite 1*** | U16731 | SCSCA 1 | SCSCA 1-[AU:C2:93] |
| *Sophoyesatellite* | ***Sophora yellow stunt alphasatellite 1*** | KX534400 | SYSA 1 | SYSA 1-[IR:Kerman:Ta1:14] |

**Unassigned species in the family *Alphasatellitidae***

Sequence M29963 (Table 3; proposed species *Coconut foliar decay alphasatellite*) was isolated from a coconut palm affected by coconut foliar decay disease (Rohde et al., 1990), a disease earlier shown to be associated with a single-stranded circular DNA virus (Hanold et al., 1988; Randles et al., 1987; Randles et al., 1986). However, no virus has so far been identified or characterized infecting coconut even though virons were described by Randles and Hanold (1989). M29963 does not have all the hallmarks of alphasatellites of the *Geminialphasatellitinae*. It has a size (1291 nt) between that typical of alphasatellites of the *Geminialphasatellitinae* and *Nanoalphasatellitinae*. It lacks an A-rich sequence and was isolated from a monocot – only two other alphasatellites have been isolated from a monocot and both are typical of satellites of the *Geminialphasatellitinae* (Kumar et al., 2014). Thus we propose that this sequence to be an unclassified *Alphasatellitidae.* It is likely that this may be a member of a third sub-family in the future once more related sequences have been identified.

**Table 3.** Summary of unassigned species in the family *Alphasatellitidae*.

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| ***Genus*** | ***Species*** | **Accession #** | **Acronym** | **Isolate** |
| unassigned | ***Coconut foliar decay alphasatellite*** | M29963 | CFDA | CFDA-[89] |

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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. |