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:** | ***2017.010P*** | | | | (to be completed by ICTV officers) |
| **Short title:** 66 new species in the genus *Begomovirus* | | | | | |
| **Modules attached**  (Modules 1, 4 and either 2 or 3 are required. | | **1**  **2  3  4** | | | |
| **Author(s):** | | | | | |
| F. Murilo Zerbini, Arvind Varsani, Jesus Navas-Castillo, Enrique Moriones, Darren Martin, Rob Briddon | | | | | |
| **Corresponding author with e-mail address:** | | | | | |
| zerbini@ufv.br | | | | | |
| **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: | | | | June 2017 | |
| Date of this revision (if different to above): | | | |  | |

|  |
| --- |
| **ICTV-EC comments and response of the proposer:** |
|  |

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

|  |
| --- |
| Present the proposed new taxonomy on accompanying spreadsheet |
| **Name of accompanying spreadsheet:** 2017.010P.N.v1.Begomovirus\_66sp |

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.

|  |
| --- |
| non-standard proposal |
| **Title of proposal:** |
| **Text of proposal:** |
|  |

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

Species demarcation criteria for the genus *Begomovirus* (family *Geminiviridae*) were recently revised (Brown et al., 2015). Pairwise sequence comparisons can now be used as the main criterion, although phylogenetic support is highly desirable due to frequent occurrence of recombination among begomoviruses. Using these criteria, 66 new species are being proposed in the genus (see the accompanying Excel file). Members of these 66 species have <91% nucleotide sequence identity for the complete genome (or the complete DNA-A in the case of bipartite viruses) with members of existing species (Table 1), which is the cut off value established after the exhaustive analysis described in Brown et al. (2015). Also, excellent phylogenetic support can be observed in all 66 cases (Figure 1A, B).

The remarkable species diversity of begomoviruses is a reflection of the easiness with which their genomes can be cloned and completely sequenced. Begomoviruses have a very small (2.6 kb) circular, ssDNA genome which replicates using a dsDNA intermediate. Both forms (ss and ds) can be readily amplified using rolling-circle amplification (RCA), a sequence-unbiased method which has been widely embraced by the geminivirus community since it was shown to be applicable to these viruses (Inoue-Nagata et al., 2004). RCA allows the rapid and cost-effective (since no reverse transcription step is required) cloning of begomovirus genomes from cultivated and non-cultivated plants. Thus, many new species are reported from non-cultivated plants (36 out of the 66 in this proposal).

This proposal also includes six new species whose sequences were obtained in a metagenomic study (whitefly-associated begomoviruses 1, 2, 3, 4, 6 and 7; Rosario et al., 2016). The ICTV EC has recently established clear guidelines for the classification of viruses from such studies (Simmonds et al., 2017). The six species listed here are were initially detected by assembly of 100-nt HTS reads, however the complete genomes were later PCR-amplified with abutting primers, clones and Sanger sequenced (Rosario et al., 2016).

**Table 1.** Details of the proposed new begomovirus species.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Species name** | **Isolate name** | **Access #** | **Reference** | **Highest nt seq identity with (%)** |
| *Allamanda leaf mottle distortion virus* | AllLMoDV-[IN-Al\_K1-12] | KC202818 | unpublished | KT948069 (89%) |
| *Andrographis yellow vein leaf curl virus* | AnYVLCV-[IN-A64-12] | KM359406 | Khan et al., 2015 | LK028570 (88%) |
| *Asystasia mosaic Madagascar virus* | AsMMV-[MG-MG493-11] | KP663485 | De Bruyn et al., 2015 | JF694484 (73%) |
| *Bean white chlorosis mosaic virus* | BWCMV-[VE-Rubio932-07] | JN848772 | Fiallo-Olivé et al., 2013 | KT099120 (88%) |
| *Cnidoscolus mosaic leaf deformation virus* | CnMLDV-[BR-Mes3-15] | KT966771 | Melo et al., 2016 | FJ972767 (86%) |
| *Coccinia mosaic Tamil Nadu virus* | CMTNV-[IN-TDVCoc1-13] | KM244719 | Nagendran et al., 2016 | AF509739 (77%) |
| *Common bean mottle virus* | CBMoV-[CU-May6-14] | KX011473 | Chang-Sidorchuk et al., 2017 | FJ944019 (87%) |
| *Common bean severe mosaic virus* | CBSMV-[CU-May99-14] | KX011477 | Chang-Sidorchuk et al., 2017 | HM236368 (88%) |
| *Cotton leaf curl Barasat virus* | CLCuBarV-[IN-14] | LC080677 | unpublished | KY001641 (90%) |
| *Cotton yellow mosaic virus* | CYMV-[BN-Gos\_San2-14] | KU683748 | Leke et al., 2016b | AM701760 (80%) |
| *Deinbollia mosaic virus* | DMV-[TZ-DB\_T1A-15] | KT878829 | Kyallo et al., 2017 | AM701764 (78%) |
| *Desmodium mottle virus* | DesMoV-[UG-Ki\_UG5-15] | KY294725 | Mollel et al., 2017b | GQ472984 (80%) |
| *Duranta leaf curl virus* | DuLCV-[PK-57SA-14] | KT948069 | unpublished | LK028570 (90%) |
| *Euphorbia mosaic Peru virus* | EuMPV-[PE-07] | AM886131 | Shepherd et al., 2008 | FJ619507 (90%) |
| *Euphorbia yellow leaf curl virus* | EuYLCV-[PK-PK1A-12] | KT159766 | unpublished | AJ558121 (90%) |
| *Hollyhock yellow vein mosaic virus* | HoYVMV-[PK-2YI-14] | LM645009 | unpublished | DQ116884 (90%) |
| *Jacquemontia yellow mosaic virus* | JacYMV-[VE-RC1250-09] | KF661331 | Fiallo-Olivé et al., 2014 | AF068636 (78%) |
| *Jatropha leaf curl Gujarat virus* | JLCGV-[IN-Gujarat-13] | KM411359 | unpublished | HM230683 (86%) |
| *Jatropha leaf yellow mosaic virus* | JLYMV-[IN-Katerniaghat2-11] | JN698954 | Srivastava et al., 2015 | HM230683 (89%) |
| *Lisianthus enation leaf curl virus* | LELCV-[TW-BG1-15] | LC091538 | unpublished | AF141922 (86%) |
| *Lycianthes yellow mosaic virus* | LyYMV-[CN-GD-15] | KT582302 | Tang et al., 2017 | FJ237617 (86%) |
| *Macroptilium bright mosaic virus* | MacBMV-[BR-ALM33\_5B-14] | KX691400 | unpublished | JN419013 (82%) |
| *Macroptilium common mosaic virus* | MacCMV-[BR-ALM2\_5B-09] | KX691396 | unpublished | JN419021 (87%) |
| *Malvastrum bright yellow mosaic virus* | MaBYMV-[US-Ma8S-14] | KU058856 | Alabi et al., 2016 | DQ520944 (88%) |
| *Malvastrum yellow vein Cambodia virus* | MaYVCV-[KH-08-14] | KP188831 | unpublished | KU954385 (87%) |
| *Melochia mosaic virus* | MelMV-[BR-CorB25-14] | KT201151 | Fiallo-Olivé et al., 2015 | KT201153 (87%) |
| *Melochia yellow mosaic virus* | MelYMV-[BR-CorB26-14] | KT201153 | Fiallo-Olivé et al., 2015 | EF016486 (81%) |
| *Mirabilis leaf curl virus* | MirLCV-[IN-Pragpur-13] | LK054801 | Kulshreshtha et al., 2017 | DQ116884 (87%) |
| *Okra leaf curl Oman virus* | OLCOV-[OM-OK2-12] | HE862273 | unpublished | AF155064 (88%) |
| *Oxalis yellow vein virus* | OxYVV-[US-LA01-12] | KM887907 | Herrera et al., 2015 | AY090555 (87%) |
| *Passionfruit leaf distortion virus* | PLDV-[CO-Valle-14] | KT899302 | Vaca-Vaca et al., 2017 | M88179 (87%) |
| *Pavonia mosaic virus* | PavMV-[BR-Cor40-14] | KT948785 | Pinto et al., 2016 | KT948787 (88%) |
| *Pavonia yellow mosaic virus* | PavYMV-[BR-Alb51-14] | KT948787 | Pinto et al., 2016 | HM585445 (83%) |
| *Pea leaf distortion virus* | PeLDV-[NP-N36\_41-10] | KY001635 | Shahid et al., 2017 | JQ897969 (90%) |
| *Pepper yellow leaf curl Thailand virus* | PepYLCTHV-[TH-WF\_SPN\_Pep-15] | KX943290 | unpublished | AF414287 (90%) |
| *Ramie mosaic Yunnan virus* | RMYnV-[CN-4819\_5-15] | KU522485 | unpublished | EU596959 (81%) |
| *Senna leaf curl virus* | SenLCuV-[IN-Mohali-13] | KU852742 | Kumar et al., 2016 | JQ866297 (89%) |
| *Sida angular mosaic virus* | SiAMV-[BR-ALS30\_4C-14] | KX691407 | Passos et al., 2017 | KX691402 (83%) |
| *Sida bright yellow mosaic virus* | SiBYMV-[BR-Tac720-10] | KX348184 | Ferro et al., 2017 | AJ557451 (85%) |
| *Sida chlorotic mottle virus* | SiCMoV-[BR-Trm531.1-10] | KX348183 | Ferro et al., 2017 | JN564749 (85%) |
| *Sida chlorotic vein virus* | SiCVV-[BR-BALS15\_2C-08] | KX691402 | Passos et al., 2017 | EU710749 (82%) |
| *Sida golden yellow spot virus* | SiGYSV-[BR-Sab889-10] | KX348185 | Ferro et al., 2017 | HM585443 (73%) |
| *Solanum mosaic Bolivia virus* | SoMBoV-[BO-07] | HM585435 | Wyant et al., 2011 | EF016486 (86%) |
| *Sweet potato golden vein Korea virus* | SPGVKRV-[SK-102-12] | KT992056 | unpublished | FJ529203 (86%) |
| *Sweet potato leaf curl Guangxi virus* | SPLCGV-[CN-Guangxi5-11] | KJ476510 | unpublished | KU323597 (90%) |
| *Synedrella yellow vein clearing virus* | SyYVCV-[IN-NCBS\_PS\_1-13] | KX363443 | unpublished | AF314144 (89%) |
| *Telfairia golden mosaic virus* | TelGMV-[CM-BBT20-14] | KT454832 | Leke et al., 2016a | AM701760 (80%) |
| *Tomato chlorotic mottle Guyane virus* | ToCMoGV-[GF-Mon2-GF455-09] | KR263181 | Lett et al., 2015 | KX691400 (79%) |
| *Tomato enation leaf curl virus* | ToELCV-[IN-TC14-08] | KP195260 | unpublished | LT716984 (89%) |
| *Tomato golden leaf spot virus* | ToGLSV-[UY-TO83-Araguaina-13] | KC626021 | unpublished | KC791691 (88%) |
| *Tomato latent virus* | ToLV-[CU-T2+-11] | KM926624 | Fuentes et al., 2016 | DQ875868 (83%) |
| *Tomato leaf curl Burkina Faso virus* | TLCBFV-[BF-Loumbila-Tomate51B1-13] | KX853168 | Ouattara et al., 2017 | AY502935 (85%) |
| *Tomato mottle wrinkle virus* | ToMoWV-[AR-Pichanal\_400-08] | JQ714137 | Vaghi-Medina et al., 2015 | KC136337 (86%) |
| *Tomato yellow leaf curl Shuangbai virus* | TYLCShV-[CN-Y4536-14] | KT962229 | unpublished | AJ512761 (88%) |
| *Tomato yellow leaf curl Yunnan virus* | TYLCYnV-[CN-YN2013-11] | KC686705 | Ding et al., 2016 | DQ641697 (85%) |
| *Triumfetta yellow mosaic virus* | TrYMV-[BR-Msj1-10] | KU131588 | Nascimento et al., 2016 | JX871376 (85%) |
| *Velvet bean golden mosaic virus* | VBGMV-[TW-bgv6\_5-14] | KU569583 | unpublished | FN543425 (85%) |
| *Whitefly-associated begomovirus 1* | WfaBV1-[GT-GtSq11-12] | KT099124 | Rosario et al., 2016 | KT201151 (80%) |
| *Whitefly-associated begomovirus 2* | WfaBV2-[GT-GtSq5-12] | KT099125 | Rosario et al., 2016 | FN543425 (85%) |
| *Whitefly-associated begomovirus 3* | WfaBV3-[GT-GtSq10-12] | KT099127 | Rosario et al., 2016 | DQ875868 (83%) |
| *Whitefly-associated begomovirus 4* | WfaBV4-[GT-GtSq8-12] | KT099128 | Rosario et al., 2016 | HM236370 (86%) |
| *Whitefly-associated begomovirus 6* | WfaBV6-[PR-PR10-10] | KT099139 | Rosario et al., 2016 | JN411687 (88%) |
| *Whitefly-associated begomovirus 7* | WfaBV7-[ES-Sp5\_4-11] | KT099156 | Rosario et al., 2016 | AM701764 (80%) |
| *Vernonia crinkle virus* | VeCrV-[UG-Na\_UG7-15] | KX831132 | Mollel et al., 2017a | DQ641698 (73%) |
| *Vinca leaf curl virus* | VinLCV-[IN-RK-15] | KR612272 | unpublished | AM948961 (87%) |
| *Wissadula yellow mosaic virus* | WYMV-[BR-ALW35\_5B-14] | KX691411 | unpublished | KC430935 (82%) |



**(A)**

**Figure 1.** Midpoint-rooted, maximum likelihood phylogenetic trees based on the complete nucleotide sequences (genomic DNA for monopartite viruses, DNA-A component for bipartite viruses) of (**A**) New World and (**B**) Old World begomoviruses. The trees were inferred with RAxML v. 8.2 (Stamatakis, 2014) and the GTR+G nucleotide substitution model. Numbers at the nodes incidate bootstrap values (2000 replications; only values >50% are shown). The new species listed in this proposal are highlighted in blue. Full-size, high resolution trees can be visualized at https://1drv.ms/b/s!Al3X713NJlYTrjPeh4W08x0j1Qki (NW tree) and https://1drv.ms/b/s!Al3X713NJlYTrjLkzvkhVQ4PjVV5 (OW tree).



**(B)**

**References**

Alabi OJ, Villegas C, Gregg L, Murray KD (2016) Complete nucleotide sequences of a new bipartite begomovirus from *Malvastrum* sp. plants with bright yellow mosaic symptoms in South Texas. Arch Virol 161:1729-1733.

Brown JK, Zerbini FM, Navas-Castillo J, Moriones E, Ramos-Sobrinho R, Silva JC et al. (2015) Revision of *Begomovirus* taxonomy based on pairwise sequence comparisons. Arch Virol 160:1593-1619

Chang-Sidorchuk L, González-Alvarez H, Navas-Castillo J, Fiallo-Olivé E, Martínez-Zubiaur Y (2017) Complete genome sequences of two novel bipartite begomoviruses infecting common bean in Cuba. Arch Virol 162:1431-1433.

De Bruyn A, Harimalala M, Hoareau M, Ranomenjanahary S, Reynaud B, Lefeuvre P, Lett JM (2015) Asystasia mosaic Madagascar virus: a novel bipartite begomovirus infecting the weed *Asystasia gangetica* in Madagascar. Arch Virol 160:1589-1591.

Ding M, Li T, Fang Q, Zhang Z, Zhou X (2016) Tomato yellow leaf curl yunnan virus, a new begomovirus species associated with tomato yellow leaf curl disease in China. J Plant Pathol 98:337-340.

Ferro CG, Silva JP, Xavier CAD, Godinho MT, Lima ATM, Mar TB, Lau D, Zerbini FM (2017) The ever increasing diversity of begomoviruses infecting non-cultivated hosts: new species from *Sida* spp. and *Leonurus sibiricus*, plus two New World alphasatellites. Ann Appl Biol 170:204-218.

Fiallo-Olivé E, Chirinos DT, Geraud-Pouey F, Moriones E, Navas-Castillo J. (2014) Complete genome sequence of Jacquemontia yellow mosaic virus, a novel begomovirus from Venezuela related to other New World bipartite begomoviruses infecting Convolvulaceae. Arch Virol 159:1857-1860.

Fiallo-Olivé E, Marquez-Martin B, Hassan I, Chirinos DT, Geraud-Pouey F, Navas-Castillo J, Moriones E (2013) Complete genome sequences of two novel begomoviruses infecting common bean in Venezuela. Arch Virol 158:723-727

Fiallo-Olivé E, Zerbini FM, Navas-Castillo J (2015) Complete nucleotide sequences of two new begomoviruses infecting the wild malvaceous plant *Melochia* sp. in Brazil. Arch Virol 160:3161-3164

Fuentes A, Carlos N, Ruiz Y, Callard D, Sánchez Y, Ochagavía ME, Seguin J, Malpica-López N, Hohn T, Lecca MR, Pérez R, Doreste V, Rehrauer H, Farinelli L, Pujol M, Pooggin MM (2016) Field trial and molecular characterization of RNAi-transgenic tomato plants that exhibit resistance to tomato yellow leaf curl geminivirus. Mol Plant-Microbe Interact 29:197-209.

Herrera F, Aboughanem-Sabanadzovic N, Valverde RA (2015) A begomovirus associated with yellow vein symptoms of *Oxalis debilis*. Eur J Plant Pathol 142:203-208.

Inoue-Nagata AK, Albuquerque LC, Rocha WB, Nagata T (2004) A simple method for cloning the complete begomovirus genome using the bacteriophage phi29 DNA polymerase. J Virol Met 116:209-211

Khan A, Saeed ST, Samad A (2015) New record of Catharanthus yellow mosaic virus and a betasatellite associated with lethal leaf yellowing of kalmegh (*Andrographis paniculata*) in Northern India. Plant Dis 99:292.

Kulshreshtha A, Roshan P, Sharma D, Hallan V (2017) Molecular characterization of a new begomovirus infecting *Mirabilis jalapa* in northern India. Arch Virol doi: 10.1007/s00705-017-3330-4

Kumar J, Alok A, Kumar J, Tuli R (2016) Senna leaf curl virus: a novel begomovirus identified in *Senna occidentalis*. Arch Virol 161:2609-2612.

Kyallo M, Sseruwagi P, Skilton RA, Ochwo-Ssemakula M, Wasswa P, Ndunguru J (2017) Deinbollia mosaic virus: a novel begomovirus infecting the sapindaceous weed *Deinbollia borbonica* in Kenya and Tanzania. Arch Virol 162:1393-1396.

Leke WN, Khatabi B, Fondong VN, Brown JK (2016a) Complete genome sequence of a new bipartite begomovirus infecting fluted pumpkin (*Telfairia occidentalis*) plants in Cameroon. Arch Virol 161:2347-2350.

Leke WN, Khatabi B, Mignouna DB, Brown JK, Fondong VN (2016b) Complete genome sequence of a new bipartite begomovirus infecting cotton in the Republic of Benin in West Africa. Arch Virol 161:2329-2333.

Lett JM, De Bruyn A, Hoareau M, Ouattara A, Claverie S, Dalmon A, Laplace D, Lefeuvre P, Hostachy B (2015) Tomato chlorotic mottle Guyane virus: a novel tomato-infecting bipartite begomovirus from French Guiana. Arch Virol 160:2887-2890.

Melo AM, Silva SJ, Ramos-Sobrinho R, Ferro MM, Assunção IP, Lima GS (2016) Cnidoscolus mosaic leaf deformation virus: a novel begomovirus infecting euphorbiaceous plants in Brazil. Arch Virol 161:2605-2608.

Mollel HG, Ndunguru J, Sseruwagi P, Alicai T, Colvin J, Navas-Castillo J, Fiallo-Olivé E (2017a) A novel East African monopartite begomovirus-betasatellite complex that infects *Vernonia amygdalina*. Arch Virol 162:1079-1082.

Mollel HG, Sseruwagi P, Ndunguru J, Alicai T, Colvin J, Navas-Castillo J, Fiallo-Olivé E (2017b) Desmodium mottle virus, the first legumovirus (genus *Begomovirus*) from East Africa. Arch Virol 162:1799-1803.

Nagendran K, Satya VK, Mohankumar S, Karthikeyan G (2016) Molecular characterization of a distinct bipartite *Begomovirus* species infecting ivy gourd (*Coccinia grandis* L.) in Tamil Nadu, India. Virus Genes 52:146-151.

Nascimento LD, Silva SJ, Ramos-Sobrinho R, Ferro MM, Oliveira MH, Zerbini FM, Assunção IP, Lima GS (2016) Complete nucleotide sequence of a new begomovirus infecting a malvaceous weed in Brazil. Arch Virol 161:1735-1738.

Ouattara A, Tiendrébéogo F, Lefeuvre P, Claverie S, Hoareau M, Traoré EV, Barro N, Traoré O, Lett JM (2017) Tomato leaf curl Burkina Faso virus: a novel tomato-infecting monopartite begomovirus from Burkina Faso. Arch Virol 162:1427-1429.

Passos LS, Teixeira JWM, Teixeira KJML, Xavier CAD, Zerbini FM, Araújo ASF, Beserra-Junior JEA (2017) Two new begomoviruses that infect non-cultivated malvaceae in Brazil. Arch Virol 162:1795-1797.

Pinto VB, Silva JP, Fiallo-Olivé E, Navas-Castillo J, Zerbini FM (2016) Novel begomoviruses recovered from *Pavonia* sp. in Brazil. Arch Virol 161:735-739.

Rosario K, Marr C, Varsani A, Kraberger S, Stainton D, Moriones E, Polston JE, Breitbart M (2016) Begomovirus-associated satellite DNA diversity captured through vector-enabled metagenomic (VEM) surveys using whiteflies (Aleyrodidae). Viruses 8:36

Shahid MS, Pudashini BJ, Khatri-Chhetri GB, Briddon RW, Natsuaki KT (2017) Molecular characterization of a distinct monopartite begomovirus associated with betasatellites and alphasatellites infecting *Pisum sativum* in Nepal. Virus Genes 53:300-306.

Shepherd DN, Martin DP, Lefeuvre P, Monjane AL, Owor BE, Rybicki EP, Varsani A (2008) A protocol for the rapid isolation of full geminivirus genomes from dried plant tissue. J Virol Meth 149:97-102.

Simmonds P, Adams MJ, Benko M, Breitbart M, Brister JR, Carstens EB et al. (2017) Consensus statement: Virus taxonomy in the age of metagenomics. Nat Rev Microbiol 15:161-168.

Srivastava A, Kumar S, Jaidi M, Raj SK (2015) Molecular characterization of a new begomovirus associated with leaf yellow mosaic disease of *Jatropha curcas* in India. Arch Virol 160:1359-1362.

Stamatakis A (2014) RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics 30:1312-1313.

Tang YF, He ZF, Brown JK, She XM, Lan GB (2017) Molecular characterization of a novel bipartite begomovirus isolated from *Lycianthes biflora* in China. Arch Virol doi: 10.1007/s00705-017-3333-1

Vaca-Vaca JC, Carrasco-Lozano EC, López-López K (2017) Molecular identification of a new begomovirus infecting yellow passion fruit (*Passiflora edulis*) in Colombia. Arch Virol 162:573-576.

Vaghi-Medina CG, Martin DP, López-Lambertini PM (2015) Tomato mottle wrinkle virus, a recombinant begomovirus infecting tomato in Argentina. Arch Virol 160:581-585.

Wyant PS, Gotthardt D, Schäfer B, Krenz B, Jeske H (2011) The genomes of four novel begomoviruses and a new *Sida micrantha mosaic virus* strain from Bolivian weeds. Arch Virol 156:347-352.

**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.