This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections). 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; you can copy the modules to create more than one genus within a new family, for example.

MODULE 1: **TITLE, AUTHORS, etc**

Code assigned:	***2010.001aP***	(to be completed by ICTV officers)

Short title: Establishment of Ugandan cassava brown streak virus as a new species in genus Ipomovirus
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 9 are required)	**1** ☒	**2** ☐	**3** ☐	**4** ☐	**5** ☐
	6 ☐	**7** ☐	**8** ☐	**9** ☒	

Author(s) with e-mail address(es) of the proposer:

Jari Valkonen (jari.Valkonen@helsinki.fi) on behalf of Potyviridae SG

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 (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	Potyviridae

ICTV-EC or Study Group comments and response of the proposer:

Date first submitted to ICTV:	27/05/2010
Date of this revision (if different to above):	03/07/2010

MODULE 2: **NEW SPECIES**

creating and naming one or more new species.

If more than one, they should be a group of related species belonging to the same genus. All new species must be placed in a higher taxon. This is usually a genus although it is also permissible for species to be "unassigned" within a subfamily or family. Wherever possible, provide sequence accession number(s) for one isolate of each new species proposed.

Code	***2010.001aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Ipomovirus***
Subfamily:	
Family:	***Potyviridae***
Order:	

Fill in all that apply.

- If the higher taxon has yet to be created (in a later module, below) write "**(new)**" after its proposed name.
- If no genus is specified, enter "**unassigned**" in the genus box.

And name the new species:	**GenBank sequence accession number(s) of reference isolate:**
Ugandan cassava brown streak virus	FJ039520, FN433930 (isolates MLB3 and Ke_125, respectively, i.e., the two most different isolates characterized for the complete sequences to date)

Reasons to justify the creation and assignment of the new species:

Partial molecular characterization and comparison of viruses associated with cassava brown streak virus disease (CBSD) in East Africa indicated recently that there may be two viruses involved in the disease [2]. Characterization of the complete genomes of 12 virus isolates has confirmed this presumption [3, 4]. One of the two viruses is the previously described *Cassava brown streak virus* (CBSV; genus *Ipomovirus*; *Potyviridae*).The other virus [3] is a close relative to CBSV [4]. Both viruses contain a single-stranded (+)ssRNA genome that encodes a polyprotein processed to up to ten mature proteins by the viral proteinases. A unique property of these two viruses, as compared to other fully described members of *Ipomovirus* (and *Potyviridae*) is that one of the proteins (HAM1h) encoded by both viruses is homologous and shares the conserved amino acid motifs with the Maf/HAM1 superfamily of nucleoside triphosphate (NTP) pyrophosphatases known in prokaryotes and eukaryotes [3]. The gene for HAM1h is integrated in the 3'-proximal part of the viral genome between the viral replicase (NIb) and coat protein (CP) encoding sequences [3, 4]. A HAM1h-like sequence at the corresponding genomic position is found also in *Euphorbia ringspot virus* that is placed to genus *Potyvirus* based on the phylogeny of CP encoding sequences. Another unique feature of the two CBSD-associated viruses is that they contain a single P1 proteinase and are lacking the helper component proteinase (HCpro) at the N-proximal part of the polyprotein [3, 4]. Other ipomoviruses described to date contain HCpro (*Sweet potato mild mottle virus*, the type species of *Ipomovirus*), or are lacking HCpro but contain two P1 proteinases (*Cucumber vein yellowing virus* and *Squash vein yellowing virus*).

The genome and polyprotein structures of UCBSV and CBSV are basically similar, but consistent differences are also found by comparison of the eight and four isolates, respectively, whose complete sequences have been analyzed to date [3, 4; D. Mbanzibwa et al.,

unpublished]. The genome size of UCBSV is 9069-9070 nt and encodes a polyprotein of 2901-2902 aa, whereas the genome of CBSV is 8995-9008 nt and encodes a polyprotein of 2912-2916 aa. The differences in genome and polyprotein sizes are mainly due to a longer 3'UTR (227 nt) in UCBSV as compared to CBSV (131 nt), and a larger CP in CBSV (378 aa) than in UCBSV (367 aa), respectively [4]. The overall nucleotide sequence identities and polyprotein amino acid sequence identities between the two viruses are ~69-70% and 74 %, respectively, which corresponds well with the species demarcation in *Potyviridae* [1].

We wish to put forwards a proposal to establish the new CBSD-associated virus as a new species in genus *Ipomovirus*, family *Potyviridae*, and to name it **Ugandan cassava brown streak virus** (UCBSV). This name is in line with the recommendations agreed by the international CBSD research community in a conference held in Entebbe, Uganda, in May 2010. The name is also consistent with some previously established names for viruses in the family *Potyviridae*, such as *Colombian datura virus*, *East Asian passiflora virus*, *Japanese yam mosaic virus*, *Moroccan watermelon mosaic virus*, and *Peru tomato virus*.

Additional support for this proposal in included in Appendix 9.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

1. Adams, M.J., Antoniw, J.F. & Fauquet, C.M. 2005. Molecular criteria for genus and species discrimination within the family Potyviridae. Arch Virol 150:459–479
2. Mbanzibwa, D.R., Tian, Y.P., Tugume, A.K., Mukasa, S.B., Tairo, F., Kyamanywa, S., Kullaya, A. & Valkonen, J.P.T. 2009. Genetically distinct strains of Cassava brown streak virus in the Lake Victoria basin and the Indian Ocean coastal area of East Africa. Arch Virol 154:353-359.
3. Mbanzibwa, D.R., Tian, Y., Mukasa, S.B. & Valkonen, J.P.T. 2009. Cassava brown streak virus (Potyviridae) encodes a putative Maf/HAM1 pyrophosphatase implicated in reduction of mutations and a P1 proteinase that suppresses RNA silencing, but contains no HC-Pro. J Virol 83:6934–6940.
4. Winter, S., Koerbler, M., Stein, B., Pietruszka, A., Paape, M. & Butgereitt, A. 2010. The analysis of Cassava brown streak viruses reveals the presence of a distinct virus species causing cassava brown streak disease in East Africa. J Gen Virol 91:1365 -1372.

Annex:

Include as much information as necessary to support the proposal, including diagrams comparing the old and new taxonomic orders. The use of Figures and Tables is strongly recommended but direct pasting of content from publications will require permission from the copyright holder together with appropriate acknowledgement as this proposal will be placed on a public web site. For phylogenetic analysis, try to provide a tree where branch length is related to genetic distance.

Table 1 Percentage nucleotide (upper diagonal) and amino acid (lower diagonal) sequence identities between the whole genomes and polyproteins, respectively, of eight Ugandan cassava brown streak virus isolates (Ke54, Ke125, Ma43, Ma42, MLB3, Ug, Ug23 and UGNamEBW) and four *Cassava brown streak virus* isolates (KOR6, M83, Tan and Tan70).

	Ke54	Ke125	Ma43	Ma42	MLB3	Ug	Ug23	UGNamEBW	KOR6	Mo83	Tan	Tan70
Ke54	***	93.2	93.2	93.2	86.5	93.2	95.0	93.3	69.4	69.6	69.6	69.6
Ke125	96.6	***	93.4	93.3	86.3	93.5	95.4	93.5	69.0	69.8	70.0	69.6
Ma43	96.5	96.7	***	99.3	86.7	93.0	95.6	93.3	69.5	69.9	69.9	70.1
Ma42	96.5	96.6	99.4	***	86.5	92.8	95.3	93.3	69.5	69.9	69.8	70.1
MLB3	93.0	92.8	93.3	93.0	***	86.3	86.6	86.5	69.4	70.0	70.3	69.8
Ug	96.0	96.5	96.0	95.6	92.6	***	93.6	93.6	69.7	70.0	70.0	69.9
Ug23	97.6	97.7	97.5	97.3	93.3	96.5	***	94.8	69.2	69.7	69.8	69.7
UGNamEBW	96.5	96.6	96.4	96.1	92.8	96.2	97.5	***	69.4	69.7	69.8	69.6
KOR6	73.7	73.6	73.9	73.8	74.0	73.9	74.1	74.0	***	79.4	79.7	91.4
Mo83	73.8	73.7	73.9	73.7	73.9	73.7	74.1	73.9	87.3	***	95.5	79.3
Tan	74.0	74.0	74.2	74.0	74.3	74.1	74.4	74.0	87.5	97.5	***	79.9
Tan70	73.9	73.9	74.2	74.2	74.2	73.9	74.3	74.0	95.2	87.5	87.7%	***

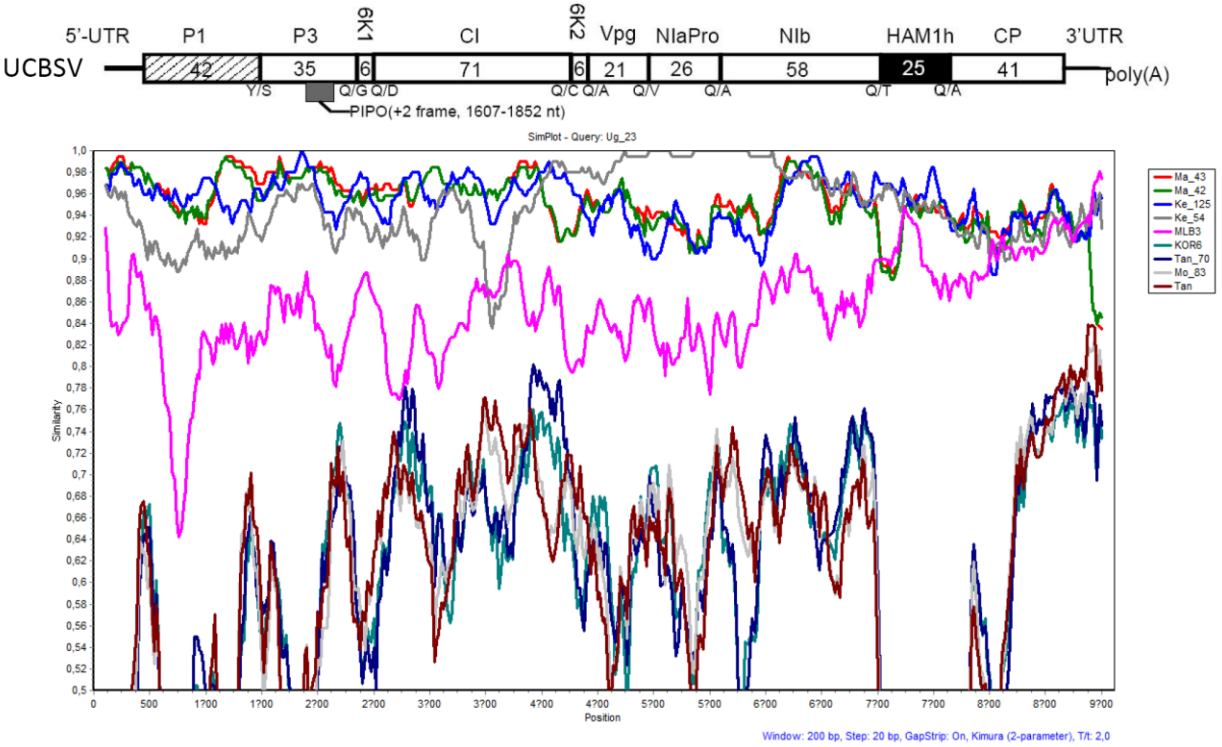

Figure 1 Plot of nucleotide identities over the entire genomes between the isolate Ug23 of Ugandan cassava brown streak virus (UCBSV) and five other isolates of UCBSV (Ma43, M42, Ke125, Ke54 and MLB3) and four isolates (KOR6, Tan70, Mo83 and Tan) of *Cassava brown streak virus* (CBSV) using a 200-nt sliding window. A schematic presentation of the genome structure of UCBSV is on the top. The box represents the viral polyprotein translated from a large open reading frame (ORF). In both viruses, the genome structure is basically similar and contains a small ORF (PIPO) created by +2 frameshifting. The 5' and 3' untranslated regions (UTR) are shown as bold lines. The amino acids at the predicted proteolytic cleavage sites of the polyprotein are shown below the polyprotein. The estimated molecular weights of the mature proteins are indicated in each protein (section of the large box) in kilodaltons. The names of proteins are above the polyprotein: P1, a serine proteinase, the first protein; P1a and P1b, two diversified serine proteinases; HC-Pro, helper component cysteine proteinase; P3, third protein; 6K1 and 6K2, 6kDa proteins; CI, cylindrical inclusion protein; VPg, viral genome-linked protein; NIa-Pro, the main viral proteinase; NIb, replicase; CP, coat protein. In addition, UCBSV and CBSV contain an insertion (678 nt) resulting in a novel polypeptide of 226 aa (HAM1h) between the replicase (NIb) and CP. HAM1h is homologous and shares the conserved amino acid motifs with the Maf/HAM1 superfamily of nucleoside triphosphate (NTP) pyrophosphatases known in prokaryotes and eukaryotes.

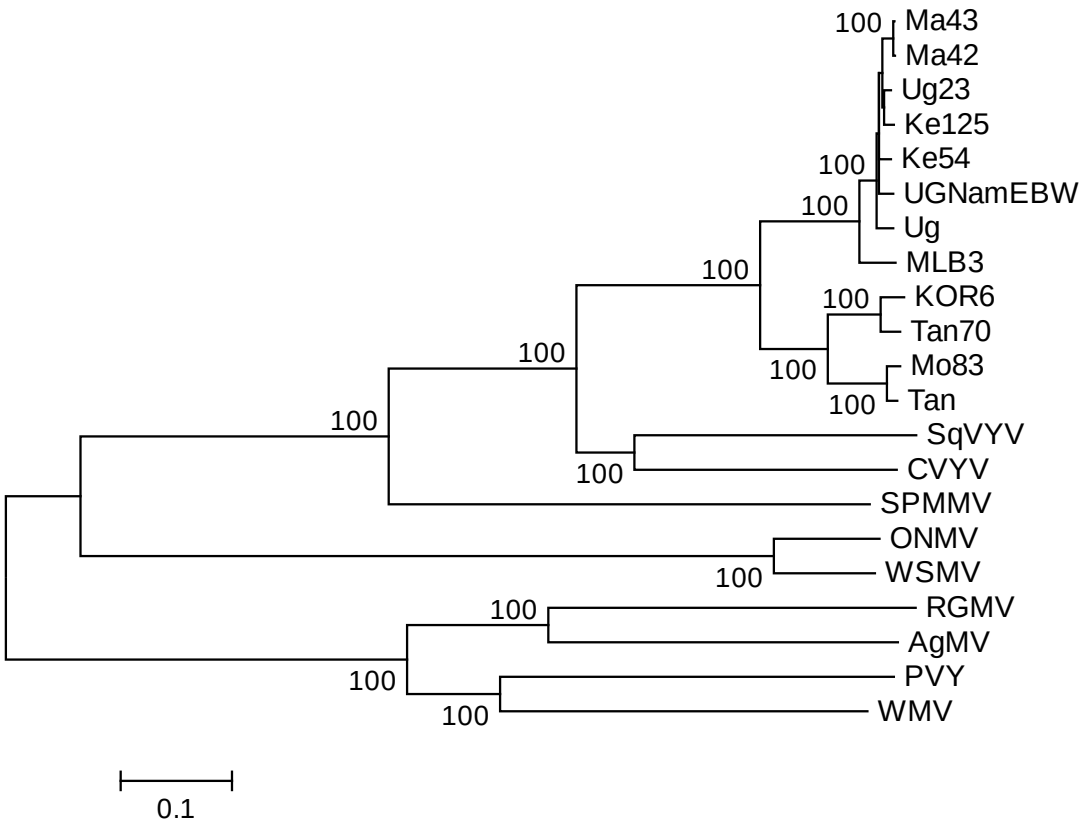

Figure 2 Phylogenetic analysis of the polyprotein amino acid sequences of four *Cassava brown streak virus* isolates (KOR6, Tan70, Mo83 and Tan) and eight Ugandan cassava brown streak virus isolates (Ma43, M42, Ug23, Ke125, Ke54, UGNamEBW, Ug and MLB3) in comparison with three other members of genus *Ipomovirus* (CVYV, *Cucumber vein yellowing virus*, AY578085; SqVYV, *Squash vein yellowing virus*, EU259611; and SPMMV *Sweet potato mild mottle virus*, Z73124) and some representative species of other genera of the family *Potyviridae*: *Tritimovirus* (ONMV, *Oat necrotic mottle virus*, AY377938; WSMV, *Wheat streak mosaic virus*, AF454454), *Rymovirus* (RGMV, *Ryegrass mosaic virus*, Y09854; AgMV, *Agropyron mosaic virus*, AY623626), and *Potyvirus*; PVY (*Potato virus Y*, GQ200836) and WMV (*Watermelon mosaic virus*, AY437609). Numbers at branches represent bootstrap values of 1000 replicates, of which only values of ≥70% are shown. Scale indicates units in amino acid substitutions per site.

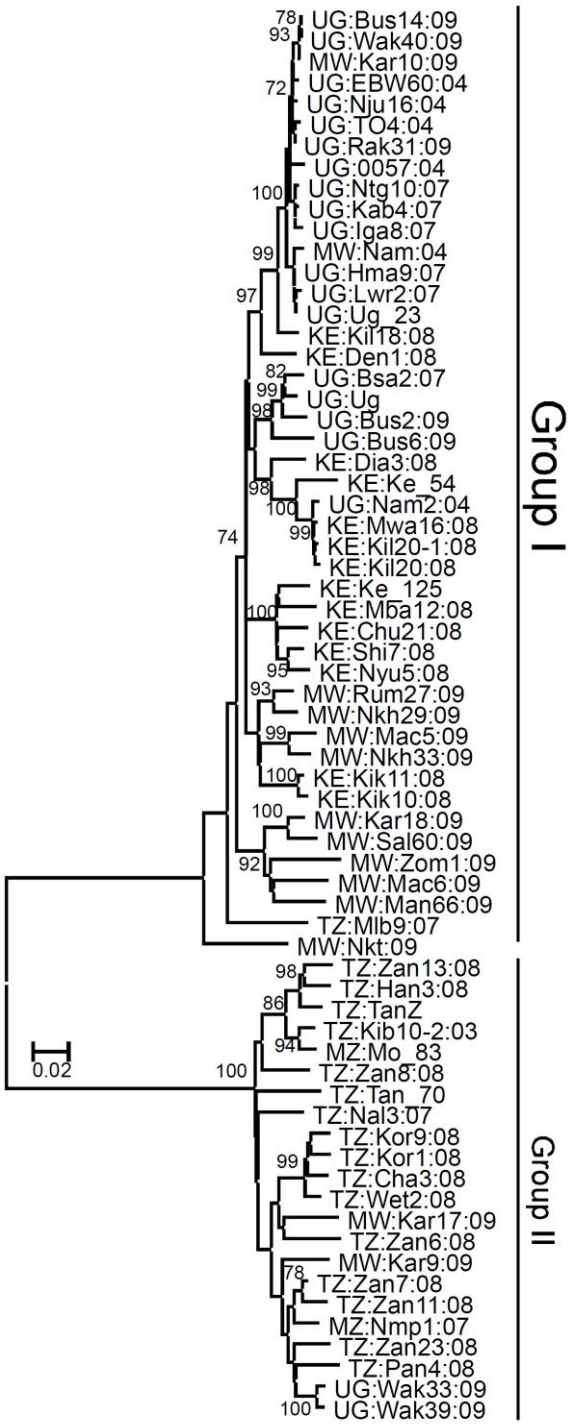

Figure 3 Phylogenetic tree (using Kimura 2 parameter distance and neighbor joining) of the coat protein encoding nucleotide sequences showing the two clusters of isolates corresponding to *Cassava brown streak virus* (Group II, 22 isolates) and Ugandan cassava brown streak virus (Group I, 45 isolates). All sequences predicted to be a result of recombination were excluded from analysis. Numbers at branches represent bootstrap values of 1000 replicates, of which only values of ≥70% are shown. The scale indicates Kimura units.