This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

Code(s) assigned:	*2008.016-020P*	(to be completed by ICTV officers)

Short title: Creation of genus Brambyvirus in the family Potyviridae for Blackberry virus Y
(e.g. 6 new species in the genus *Zetavirus*; re-classification of the family *Zetaviridae* etc.)

Modules attached (please check all that apply):	**1** ☐	**2** ☐	**3** ☐	**4** ☒	**5** ☒
	6 ☐	**7** ☐			

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

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

MODULE 4: **NEW GENUS** (if more than one genus is to be created, please complete additional copies of this section)

Code	*2008.016P*	(assigned by ICTV officers)

To create a new genus assigned as follows:

Subfamily:	
Family:	***Potyviridae***
Order:	

Fill in all that apply. Ideally, a genus should be placed within a higher taxon, but if not put "unassigned" here.

Code	*2008.017P*	(assigned by ICTV officers)

To name the new genus: *Brambyvirus*

Code	*2008.018P*	(assigned by ICTV officers)

To assign the following as species in the new genus:

You may list several species here. For each species, please state whether it is new or existing.

- If the species is new, please complete Module 5 to create it.
- If the species already exists, please state whether it is unassigned or is to be removed from another genus and, if the latter, complete module 6(a) to 'REMOVE' it from that genus.

***Blackberry virus Y* (new species)**

Code	***2008.019P***	(assigned by ICTV officers)

Note: every genus must have a type species

To designate the following as the type species in the new genus:
Blackberry virus Y

Argument to justify the creation of a new genus:

See below on the creation of the species

Origin of the new genus name:

From bramble, the English name of the host of the (only) species

Argument to justify the choice of type species:

It is the only species

Species demarcation criteria in the genus:

If there will be more than one species in the new genus, list the criteria being used for species demarcation and explain how the proposed members meet these criteria.

Not applicable: only one species

MODULE 5: **NEW SPECIES**

Code	***2008.020P***	(assigned by ICTV officers)

To create 1 new species assigned as follows:

Genus:	***Brambyvirus***
Subfamily:	
Family:	***Potyviridae***
Order:	

Fill in all that apply. Ideally, species should be placed within a genus, but it is acceptable to propose a species that is within a Subfamily or Family but not assigned to an existing genus (in which case put "unassigned" in the genus box)

Name(s) of proposed new species:

Blackberry virus Y

Argument to justify the creation of the new species:

If the species are to be assigned to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

Susaimuthu et al (2008) reported the complete sequence (AY994084) of a virus that they found co-infecting some blackberry plants with yellow vein disease. The putative agent of this important disease is the crinivirus *Blackberry yellow vein associated virus* (BYVaV) but some plants also contained this second virus, which has the characteristics of a member of the family *Potyviridae* but which is only distantly related to any known species. They named this virus blackberry virus Y (BVY).

Argument to justify the creation of the new species:

The complete sequence of the BVY genome was 10,851 nt long excluding the polyA tail, making it the largest monopartite member of the family. Probable polyprotein processing sites were identified, yielding the characteristic ten mature proteins of potyvirids but by comparison with other members of the family it lacked the N-terminus of the HC-Pro cistron. Another unusual feature was the presence of an AlkB domain within the P1 protein. The aa sequence of the complete polyprotein had less than 30% identity to any of the species found in the databases. These properties suggest that BVY should be placed in a new genus in the *Potyviridae* (Adams et al., 2005). Phylogenetic analyses confirm these findings. The three trees presented by Susaimuthu et al (2008) (for the helicase and polymerase conserved motifs and for the coat protein) have similar topology. The coat protein tree is shown in Fig. 1, while a tree based on the complete polyprotein sequence of fully-sequenced members of the family is shown in Fig. 2. In all cases, BVY forms a distinct branch and is not clustered with any of the existing genera.

BVY was detected in both wild and cultivated plants and was shown to spread in the field. However, attempts to transmit it by aphids or mites were unsuccessful and its vector is therefore unknown.

Susaimuthu et al. (2008) suggested the genus name *Blackyvirus* to accommodate BVY but some might find this offensive. The generic name of the host (Rubus) is not suitable for conversion to a genus names as *Rubivirus* and *Rubulavirus* are already in use. Since blackberry is a cultivated form of bramble, we are therefore proposing the genus name *Brambyvirus*.

References:

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.

Susaimuthu J., Tzanetakis I.E., Gergerich R.C., Martin R.R. (2008). A member of a new genus in the *Potyviridae* infects Rubus. Virus Res. 131:145-151

Annexes:

Include as much information as necessary to support the proposal. The use of Figures and Tables is strongly recommended.

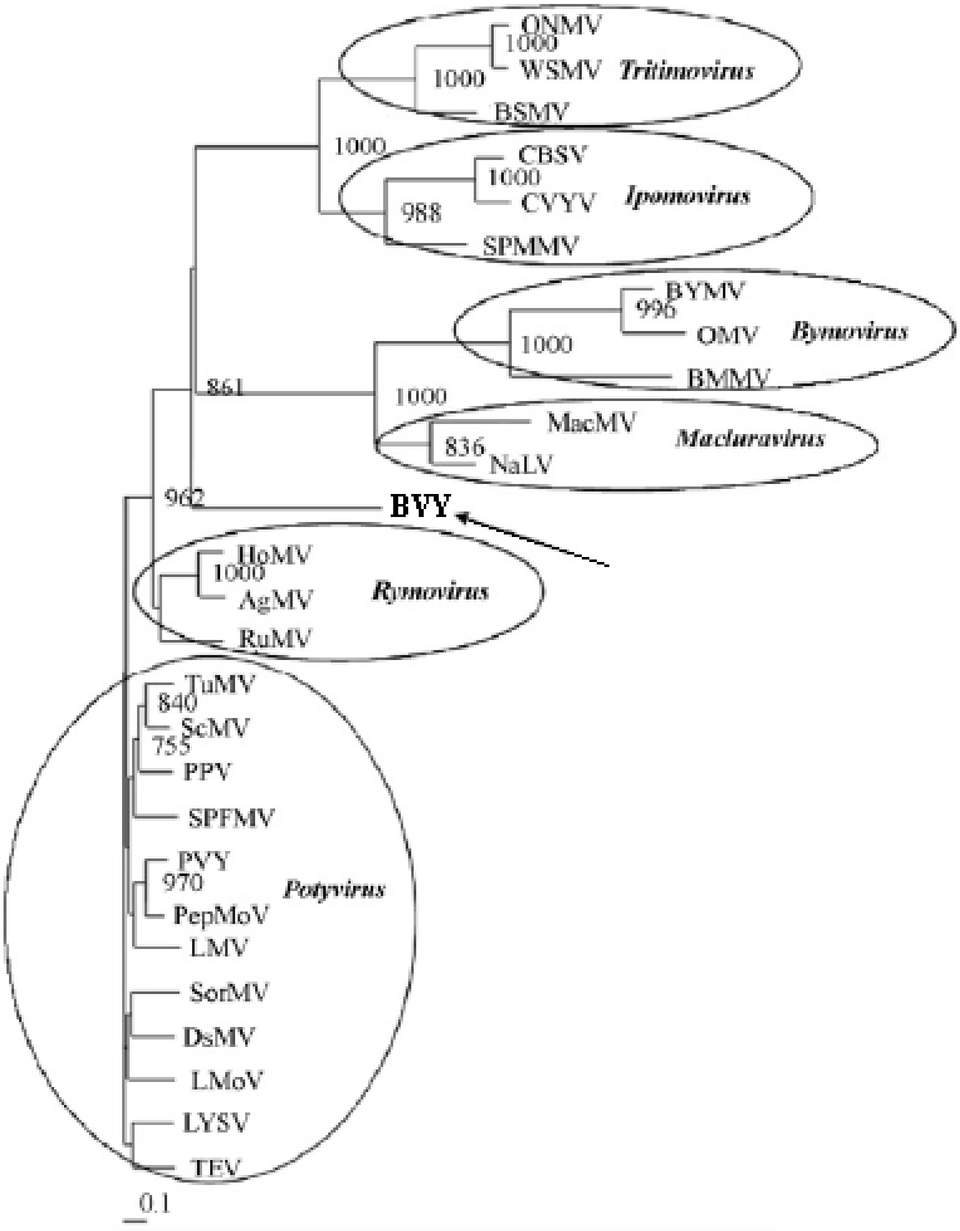

Fig. 1. Phylogenetic analysis of the coat protein amino acid sequence of potyvirids obtained using ClustalW and the neighbor-joining algorithm [from Susaimuthu et al (2008)]. The values at the forks indicate the percentage of trees in which this grouping occurred after bootstrapping (1,000 replicates; shown only when >70%). The scale bar shows the number of substitutions per base.

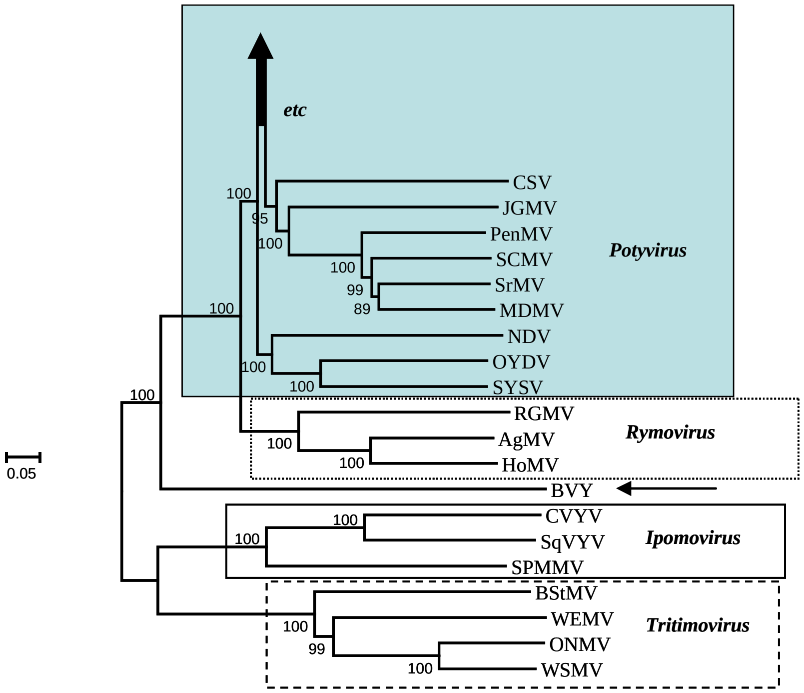

Fig. 2. Phylogenetic analysis of the complete nucleotide sequence of potyvirids obtained using MEGA 4 (maximum composite likelihood method). The values at the forks indicate the percentage of trees in which this grouping occurred after bootstrapping (10,000 replicates; shown only when >70%). The scale bar shows the number of substitutions per base.