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:	***2013.007aP***	(to be completed by ICTV officers)

Short title: Create a new species in the family *Potyviridae*

(e.g. 6 new species in the genus *Zetavirus*)

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

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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)	

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

Date first submitted to ICTV:	June 2013
Date of this revision (if different to above):	

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	***2013.007aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Unassigned***
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:**
Rose yellow mosaic virus	JF280796

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

- Explain how the proposed species differ(s) from all existing species.
    - If species demarcation criteria (see module 3) have previously been defined for the genus, **explain how the new species meet these criteria**.
    - If criteria for demarcating species need to be defined (because there will now be more than one species in the genus), please state the proposed criteria.
- Further material in support of this proposal may be presented in the Appendix, Module 9

Lockhart et al., (2011) reported the discovery of a virus with filamentous 720- to 750-nm particles associated with a disease of roses characterized by yellow mosaic, premature leaf senescence and necrotic stem lesions. The virus was found to occur naturally in New York and Minnesota in several rose cultivars. Preliminary sequence data from the 3' terminus of the genome indicated a relationship with potyviruses.

A complete sequence of the virus (JF280796= NC_019031) has now been reported by Mollov et al., 2013. This was determined from purified virions isolated from symptomatic plants. No other virus-like particles were observed in these plants and while Koch's postulates have not been fulfilled, it seems highly likely that the virus isolated is the cause of the disease. Genome organization is typical of that of a member of the family *Potyviridae*. The RoYMV genome is 9508 nucleotides long excluding the 3'-poly-(A) tail and contains a single predicted open reading frame encoding a polyprotein of 3067 amino acids. Polyprotein cleavage sites were predicted by comparisons with other members of the family. The single structural (capsid) protein approximately 35-36 kDa in size shown by SDS PAGE corresponds well with that predicted from the sequence (34.5 kDa).

Sequence comparisons and phylogenetic analyses show that RoYMV is a distinctive member of the family *Potyviridae*. Its P3 and CI cistrons appear to be shorter than those of other members of the family, and the authors suggest that the 6K1 cistron is completely absent (although the expression and function of this small gene in other members of the family is uncertain). It is only distantly related to other viruses in the family: over the complete polyprotein, there is no more than about 22% amino acid identity (38% similarity) to other sequenced members. In phylogenetic analyses using the entire polyprotein nucleotide (Annex Fig. 1) or amino acid sequence (Mollov et al., 2013), RoYMV falls within the family *Potyviridae*, but fails to cluster significantly with any other member of it, including *Blackberry virus Y* (genus *Brambyvirus*), which also infects plants in the family *Rosaceae*.

According to criteria published in the ICTV 9th Report (Adams et al., 2011), different species in the family usually have CP aa sequence identity less than ca. 80%; and nt sequence identity less than 76% either in the CP or over the whole genome. There are also differences in polyprotein cleavage sites. Polyproteins of viruses in the same genus have >40% aa identity (Adams et al., 2005). It is therefore clear that RoYMV should be classified as a species outside any of the existing genera.

Within the *Potyviridae*, genera are mostly distinguished by the type of vector (aphids, whiteflies, mites, fungal protists), a distinction that is supported by phylogenetic analysis. The vector of RoYMV is unknown but the genome lacks the characteristic protein motifs in the HC-Pro and capsid proteins that are known to be associated with aphid transmission in the genus *Potyvirus*. RoYMV deserves classification in a new genus but without any more similar viruses, it is difficult to know what characteristics this new genus might have. We are therefore proposing that it should be an unassigned species in the family for the time being.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Adams MJ, Antoniw JF, Fauquet CM (2005). Molecular criteria for genus and species discrimination within the family *Potyviridae*. Arch Virol 150:459–479

Adams MJ, Zerbini FM, French R, Rabenstein F, Stenger DC, Valkonen JPT. (2011). Family *Potyviridae*. In: Virus Taxonomy, Ninth Report of the International Committee on Taxonomy of Viruses (A.M.Q. King, M.J. Adams, E.B. Carstens & E.J. Lefkowitz, eds), pp. 1069-1089. Elsevier Academic Press, London.

Lockhart B, Zlesak D, Fetzer J (2011). Identification and partial characterization of six new viruses of cultivated roses in the USA. Acta Horticulturae 901:139–147

Mollov D, Lockhart B, Zlesak D (2013). Complete nucleotide sequence of rose yellow mosaic virus, a novel member of the family *Potyviridae*. Arch. Virol. DOI 10.1007/s00705-013-1686-7

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.

Figure 1: Maximum likelihood phylogenetic tree using the codon-aligned complete polyprotein coding sequences of fully sequenced members of the family *Potyviridae*. Only selected viruses in the genus *Potyvirus* are shown. Tree produced in MEGA5.10 with 1,000 bootstrap replicates. Rose yellow mosaic virus (RoYMV) is highlighted in red. Virus abbreviations were as listed in the *Potyviridae* chapter of the Ninth Report of the ICTV (Adams et al., 2011). Accession numbers used in this alignment were also as listed in the Ninth Report for the type isolate of each species with the caladenia virus A (CalV-A, accession number JX156425) and rose yellow mosaic virus (RoYMV, accession number JF280796).