Recognize Rose rosette virus as a definitive species in the genus Emaravirus

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:	***2012.007aP***	(to be completed by ICTV officers)

Short title: create *Rose rosette virus* as a distinct species in the genus *Emaravirus*
(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:

I.E. Tzanetakis on behalf of the Plant virus SG; E-mail: itzaneta@uark.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 (fungal, invertebrate, plant, prokaryote or vertebrate viruses)	Emaravirus study group

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

The Emaravirus study group members have seen and discussed the proposal and fully agree with the proposal to create Rose rosette virus as new taxonomic species in the genus Emaravirus.

Date first submitted to ICTV: 25 June 2012
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	***2012.007aP***	(assigned by ICTV officers)

To create 1 new species within:

Genus:	***Emaravirus***
Subfamily:	
Family:	
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 rosette virus	HQ871942- HQ871945

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

Species demarcation criteria for the genus *Emaravirus*:
1. Amino acid sequence of relevant gene products (polymerase, nucleocapsid protein) differing by more than 25%
2. Differences in the natural host range
3. Differences in vector species

Rose rosette disease was first described in the 1940s (Conners, 1941) with symptoms that include excessive shoot growth, thorniness, witches' broom, leaf proliferation, red pigmentation, and eventually plant death. It was later determined that the disease is associated by double membrane virus-like particles (Gergerich and Kim, 1983) that are transmitted by the eriophyid mite *Phyllocoptes fructiphilus* (Amrine *et al*., 1988). Laney *et al*. (2011) used both traditional shotgun cloning as well as next generation sequencing and obtained the complete sequence of four negative strand RNAs of a tentative new virus. Molecular detection tests were developed and used in a survey of rose rosette plants. All 84 diseased plants collected from areas as far apart as 1000 km apart were infected with the new virus; whereas the agent was not detected in any symptomless plants. The 100% association between virus and disease indicated that the virus is the causal agent of the disease and the name Rose rosette virus (RRV) is proposed.

RRV properties

Virus particles: double membrane particles with a diameter of ~ 80-200nm (Gergerich and Kim, 1983)

(i) dsRNAs: observed (Di *et al*., 1990; Laney *et al*., 2011)
(ii) RNA-dependent RNA-polymerase: 264.8 kDa, glycoprotein precursor: 73.8 kDa, Nucleocapsid protein: 35.6 kDa (determined from deduced sequence data; Laney *et al*., 2011)
(iii) Nucleic acid: four molecules of negative sense ssRNA. RNA 1- 7026nt, RNA 2 – 2245nt, RNA 3-1544nt, RNA4-1541nt (HQ871942- HQ871945 respectively)
(iv) Genome: quadripartite, possibly larger, 4 ORFs, one in each of the characterized RNAs Genome structure resembling that of members of the genus *Emaravirus*
(v) Phylogenetic relationships: RRV groups with members of the genus *Emaravirus* in trees constructed with RdRp sequences. The closest species is *Fig mosaic virus* (FMV) with which RRV clusters in a distinct clade (see Annex; Laney *et al.,* 2011)
At the amino acid level, the two viruses did not show amino acid identities higher than 68% (RdRp; Laney *et al.,* 2011). This meets species demarcation criteria No. 1.
(vii) Mechanical transmission: Undetermined
(viii) Possible transmission with *Phyllocoptes fructiphilus* (Amrine *et al*., 1988), which meets species demarcation criteria No. 3.
(ix) Natural host range: *Rosa spp*., which meets species demarcation criteria No. 2.

The above data support the notion that RRV is a distinct species in the unassigned genus *Emaravirus*.

MODULE 9: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Amrine, J., Hindal, D., Stany, T., Williams, R. and Coffman, C. 1988. Transmission of the rose rosette disease agent to *Rosa multiflora* Thunb. by *Phyllocoptes fructiphilus* Keifer (Acari: Eriophyidae). Entomol News 99:239-252.

Conners, L. 1941. Twentieth Ann. Rep. Canad. Plant Dis Survey 1940 p 98.

Di, R., Hill, J. and Epstein, A. 1990. Double-stranded RNA associated with the rose rosette disease of multiflora rose. Plant Dis 74: 56-58.

Gergerich, R. and Kim, K. 1983. A description of the causal agent of rose rosette disease. Arkansas Farm Res 3:7.

Laney, A.G., Keller, K.E., Martin, R.R. and Tzanetakis I.E. 2011. A discovery 70 years in the making: Characterization of the Rose rosette virus. J. Gen. Virol. 92: 1727–1732.

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.

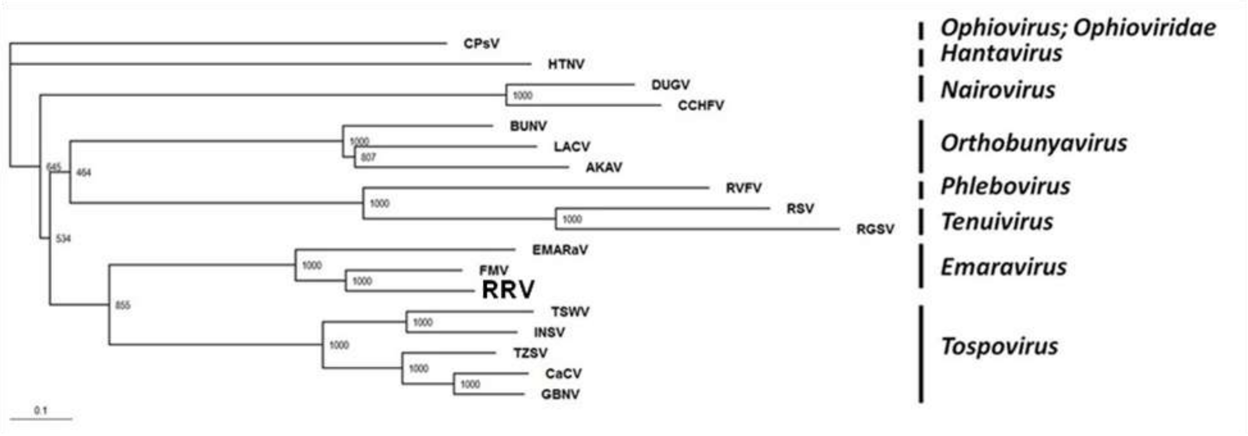

Figure: Phylogram for members of the family *Bunyaviridae (including the genera Hantavirus, Nairovirus, Orthobunyavirus, Phlebovirus and Tospovirus) and the genera Tenuivirus and Emaravirus* using the RdRp nucleotide coding region. *Citrus psorosis virus* (CPsV; NC_006314), genus *Ophiovirus,* is used as an outgroup. Recognized species and related viruses analyzed include *Tomato spotted wilt virus* (TSWV; NC_002052), capsicum chlorosis virus (CaCV; NC_008302, a virus related to the genus *Tospovirus* but that has not been approved as a species), *Impatiens necrotic spot virus*, (INSV; NC_003625), *Groundnut bud necrosis virus* (GBNV; NC_003614), tomato zonate spot virus (TZSV; NC_010491, a virus related to the genus *Tospovirus* but that has not been approved as a species), *Rice stripe virus* (RSV; NC_003755), *Rice grassy stunt virus* (RGSV; NC_002323), *Dugbe virus, Nairovirus* (DUGV; NC_004159), *Crimean-Congo hemorrhagic fever virus* (CCHFV; NC_005301), *Bunyamwera virus* (BUNV; NC_001925), *Akabane virus* (AKAV; NC_009894), *California encephalitis virus*, *Orthobunyavirus* (isolate La Crosse virus, LACV; NC_004108), *Rift valley fever virus* (RVFV; NC_014397), *Fig mosaic virus* (FMV; AM941711), *European mountain ash ringspot-associated virus* (EMARaV; NC_013105), Rose rosette virus, (RRV- HQ871942), and *Hantaan virus* (HTNV; NC_005222). Analysis was performed with ClustalW (Thompson *et al.*, 1994) using the neighbor-joining algorithm, Kimura's correction and bootstrapping consisting of 1000 pseudoreplicates. The bar represents 0.1 changes/site.