



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:	2016.020aM	(to be completed by ICTV officers)
Short title: Implementation of taxon-wide non-Latinized binomial species names in the genus <i>Emaravirus</i> (e.g. 6 new species in the genus <i>Zetavirus</i>)		
Modules attached (modules 1 and 11 are required)	6 <input type="checkbox"/> 2 <input type="checkbox"/> 3 <input type="checkbox"/> 4 <input type="checkbox"/> 5 <input type="checkbox"/> 7 <input type="checkbox"/> 8 <input type="checkbox"/> 9 <input checked="" type="checkbox"/> 10 <input type="checkbox"/>	

Author(s):

The ICTV <i>Emaravirus</i> Study Group:			
Elbeaino, Toufic	Chair	Italy	elbeaino@iamb.it
Digiario, Michele	Member	Italy	digiario@iamb.it
Martelli, Giovanni P.	Member	Italy	martelli@agr.uniba.it
Muehlbach, Hans-Peter	Member	Germany	muehlbach@botanik.uni-hamburg.de
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Elbeaino, Toufic Chair Italy elbeaino@iamb.it

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 <i>Emaravirus</i> Study Group, ICTV <i>Bunyaviridae</i> Study Group
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ICTV Study Group comments (if any) and response of the proposer:

The ICTV *Bunyaviridae* Study Group has seen and discussed this proposal, and agreed to its submission to the ICTV Executive Committee based on votes of support by individual Study Group members or the absence of dissenting votes.

Date first submitted to ICTV: July 18, 2016
Date of this revision (if different to above): September 21, 2016

ICTV-EC comments and response of the proposer:

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MODULE 9: **RENAME**

Use this module to change the name of one or more existing taxa (but note that stability of nomenclature is encouraged wherever possible). Insert extra lines in the table if needed.

Renaming one or more taxa

Code	2016.020aM	(assigned by ICTV officers)
To rename the following taxon (or taxa):		
Current species name		Proposed species name
<i>European mountain ash ringspot-associated virus</i>		<i>European mountain ash ringspot-associated emaravirus</i>
<i>Fig mosaic virus</i>		<i>Fig mosaic emaravirus</i>
<i>High Plains wheat mosaic virus</i>		<i>High Plains wheat mosaic emaravirus</i>
<i>Pigeonpea sterility mosaic virus</i>		<i>Pigeonpea sterility mosaic emaravirus 1</i>
<i>Raspberry leaf blotch virus</i>		<i>Raspberry leaf blotch emaravirus</i>
<i>Rose rosette virus</i>		<i>Rose rosette emaravirus</i>

Reasons to justify the renaming:

Explain why the taxon (or taxa) should be renamed

The ICTV *Bunyaviridae* Study Group implemented non-Latinized binomial species names last year throughout the entire family (approved by the ICTV and ratified by the IUMS) as a mean to differentiate better between species and virus names. This implementation is now extended to all viruses of the proposed order *Bunyavirales*, which are proposed to include the genus *Emaravirus* in a new family *Fimoviridae* (TP 2016.030). Importantly, virus names are not affected by the change above (i.e., the name fig mosaic virus will remain, but fig mosaic virus will become a member of the species *Fig mosaic emaravirus*).

MODULE 11: **APPENDIX**: supporting material

additional material in support of this proposal

References:

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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.

