

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:	2016.029aM	(to be completed by ICTV officers)
Short title: Implementation of <i>Tenuivirus</i> (e.g. 6 new species in the genus A Modules attached (modules 1 and 11 are required)	Taxon-wide non-Latinized binon Zetavirus) $ \begin{array}{c} 2 \\ 6 \\ 7 \\ 3 \end{array} $	a $5 \square$ $8 \square$ $9 \boxtimes$ $10 \square$

Author(s):

The ICTV Tenuivirus Study Group:			
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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 Tenuivirus Study Group, ICTV Bunyaviridae 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:

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	2016.029aM	(assigned by ICTV officers)
To rename the following taxon (or taxa):		
Current	name	Proposed name
Echinoc	hloa hoja blanca virus	Echinochloa hoja blanca tenuivirus
Iranian	wheat stripe virus	Iranian wheat stripe tenuivirus
Maize stripe virus		Maize stripe tenuivirus
Rice grassy stunt virus		Rice grassy stunt tenuivirus
Rice hoj	a blanca virus	Rice hoja blanca tenuivirus
Rice stri	pe virus	Rice stripe tenuivirus
Urochlo	a hoja blanca virus	Urochloa hoja blanca tenuivirus

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 means to differentiate better between species and virus names. This implementation is now extended to all viruses of the proposed order *Bunyavirales*, which is proposed to include the genus Tenuivirus (TP 2016.030). Importantly, virus names are not affected by the change above (i.e., the name maize stripe virus will remain, but maize stripe virus will become a member of the species *Maize stripe tenuivirus*).

MODULE 11: APPENDIX: supporting material

additional material in support of this proposal

References:

- Reguera J, Weber F, Cusack S (2010) Bunyaviridae RNA Polymerases (L-Protein) Have an N-Terminal, Influenza-Like Endonuclease Domain, Essential for Viral Cap-Dependent Transcription. PLoS Pathog 6(9): e1001101. doi:10.1371/journal.ppat.1001101
- Li, C.X., Shi, M., Tian, J.H., Lin, X.D., Kang, Y.J., Chen, L.J., Qin, X.C., Xu, J., Holmes, E.C., Zhang, Y.Z. (2015). Unprecedented genomic diversity of RNA viruses in arthropods reveals the ancestry of negative-strand RNA viruses. eLife 4:e05378.

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.