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:	***2015.018aP***	(to be completed by ICTV officers)

Short title: One new species in the genus *Emaravirus*
(e.g. 6 new species in the genus *Zetavirus*)

Modules attached (modules 1 and 10 are required)	**1** ☒	**2** ☐	**3** ☐	**4** ☐	**5** ☐
	6 ☐	**7** ☐	**8** ☐	**9** ☐	**10** ☒

Author(s):

Tatineni S., McMechan A.J., Wosula E.N., Wegulo S.N., Graybosch R.A., French R. and G.L. Hein

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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)	**Emaravirus study group**

ICTV Study Group comments (if any) and response of the proposer:

Date first submitted to ICTV: June 2015
Date of this revision (if different to above):

ICTV-EC comments and response of the proposer:

EC Comments: There had been disagreements about the species name. The EC supported the suggestion from Helene Sanfacon to use the name *High Plains wheat mosaic virus* for the new species. Please also verify if Figure 2a is correct (EMARaV and PPSMV appear identical in the figure).

Author response: the proposed species name High Plains wheat mosaic virus is acceptable. This has been corrected throughout the proposal. Fig. 2a has been corrected.

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	***2015.018aP***	(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.

Name of new species:	**Representative isolate: (only 1 per species please)**	**GenBank sequence accession number(s)**
High Plains wheat mosaic virus	Wheat mosaic virus - Nebraska	KJ939623 to KJ939631

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* are:

1. Differences in relevant gene product sequences of more than 25%
2. Differences in host ranges
3. Differences in vector specificities

(i) High Plains disease (HPD), an economically important disease of wheat (*Triticum aestivum* L.) and maize (*Zea mays* L.), was first described in the Great Plains region of the United States in 1993-1994 (Jensen *et al*. 1996). The causal agent of HPD is transmitted by the wheat curl mite (*Aceria tosichella* Keifer) (Seifers *et al*., 1997) and was identified as High Plains virus based on double-membrane virus-like particles and a 32-kDa NC protein from partially purified virion preparations (Jensen *et al*., 1996). However, subsequent studies renamed the causal agent of HPD as Wheat mosaic virus (Skare *et al*., 2006). The proposed name for the new species, *High Plains wheat mosaic virus*, is an amalgamation of two names previously used to describe the causal agent of this disease. The combination of relatively pure virion RNA and high-throughput RNA sequencing technology determined that the viral genome is composed of eight RNA segments, the most found in any known negative-strand RNA plant virus. The RNA-dependent RNA polymerase (RdRp), glycoprotein precursor (GP), nucleocapsid (NC) and P4 proteins exhibited relatively low sequence identity with the ortholog proteins of other emaraviruses (Table 1), *i.e. European mountain ash ringspot-associated virus* (EMARaV), *Fig mosaic virus* (FMV), *Rose rosette virus* (RRV), *Raspberry leaf blotch virus* (RLBV) and *Pigeonpea sterility mosaic virus* (PPSMV), suggesting that the new virus is a distinct species of the genus *Emaravirus* (Tatineni *et al*., 2014), with the

proposed name *High Plains wheat mosaic virus* (HPWMoV). Furthermore, genomic-length virus- and virus complementary (vc)-sense strands of all genomic RNAs accumulated asymmetrically in infected wheat, with 10- to 20-fold more virus-sense genomic RNAs compared to vc-sense RNAs (Tatineni *et al*., 2014). These data further confirm the octapartite negative-sense polarity nature of the genome.

Virus properties

(ii) Virus particles: Double-membrane virus-like particles were observed under EM (Jensen *et al*., 1996; Louie *et al*., 2006).

(iii) ssRNA: RNA isolated from partially purified virions resolved into five distinct bands in formaldehyde-formamide agarose gels with two of these bands possibly containing multiple species of RNAs (Skare *et al*., 2006; Tatineni *et al*., 2014).

(iv) Virus-encoded proteins: RNA-dependent RNA-polymerase: 266 kDa; glycoprotein precursor: 77 kDa; Nucleocapsid protein: 33 kDa; P4 putative movement protein: 42 kDa; P5 (function unknown): 56 kDa; P6 (function unknown): 58 kDa; P7 (function unknown): 36 kDa; P8 (function unknown): 21 kDa; (see Figure 1) (proteins molecular weights were determined from deduced sequence data; Tatineni *et al*., 2014).

(v)Nucleic acid: eight segments of negative sense ssRNA. RNA1: 6981nt, RNA 2: 2211 nt, RNA3a: 1439 nt, RNA3b:1441 nt (RNA 3a and 3b found in 5 to 1 ration in a partially purified virion RNA. However, the biological significance of these two proteins are not known, except that they are nucleocapsid proteins), RNA4:1682 nt, RNA5:1715 nt, RNA6: 1752 nt, RNA7: 1434 nt, RNA8: 1339 nt (Figure 1) (Accession numbers KJ939623 to KJ 939631, respectively, for RNA1, RNA 2, RNA 3a, RNA 3b and RNA 4 to 8) (Tatineni et al., 2014).

(vi) Genome: octapartite genome of single-stranded negative sense RNAs with 8 ORFs, one in each complementary strand of the genomic RNA (Figure 1). The first 14 nt of all genomic RNAs were conserved (5'-AGU AGU GAU CUC CC) and are complementary with the the 3' end, with the exception of 2 nt, as observed in other emaraviruses. Genome structure resembling that of members of the genus Emaravirus.

(vii) Phylogenetic relationships: Phylogenetic trees with RdRp, GP and NC proteins resulted in similar topologies, with all emaraviruses clustered into two distinct clades (Figure 2). HPWMoV and RLBV formed as sister taxa in a separate clade from other emaraviruses. These two emaraviral clades share a most recent common ancestor with members of the genera *Orthobunyavirus* and *Tospovirus* (for RdRp and GP) and *Tospovirus, Nairovirus,* and *Orthobunyavirus* (for NC protein) (Tatineni et al., 2014). Though HPWMoV and RLBV formed as sister taxa in a clade, these two viruses are distinct from each other with only 42%, 35%, and 31% amino acid identity between the RdRp, GP, and NC proteins, respectively (Table 1). (meets species demarcation criterion 1).

(viii) Mechanical transmission: The virus is not mechanically transmissible, but limited success was observed with puncturing of maize embryos.

(ix) The virus is transmitted by eriophyid mites, similarly to other emaraviruses: HPWMoV (*Aceria tosichella* Keifer) (Tatineni et al., 2014; Seifers et al.,1997); FMV (*Aceria ficus*), PPSMV (*Aceria cajani*), EMARaV (*Phtoptus pyri*), RRV (*Phyllocoptes fructiphilus*),

RLBV (*Phyllocoptes gracilis*).

(x) Host range: the virus infects wheat, maize, oat, and rye.
The above data support the notion that High Plains wheat mosaic virus is a distinct species in the genus *Emaravirus*.

MODULE 10: **APPENDIX**: supporting material

additional material in support of this proposal

References:

Jensen SG, Lane LC, Seifers DL. 1996. A new disease of maize and wheat in the high plains. Plant Dis. 80: 1387-1390.

Louie R, Seifers DL, Bradfute OE. 2006. Isolation, transmission and purification of the High Plains virus. J. Virol. Methods 135: 214-222.

Seifers DL, Harvey TL, Martin TJ, Jensen SG. 1997. Identification of the wheat curl mite as the vector of the High Plains virus of corn and wheat. Plant Dis. 81: 1161–1166.

Skare JM, Wijkamp I, Denham I, Rezende JAM, Kitajima EW, Park JW, Desvoyes B, Rush CM, Michels G, Scholthof KBG, Scholthof HB. 2006. A new eriophyid mite-borne membrane-enveloped virus-like complex isolated from plants. Virology 347: 343–353.

Tatineni S, McMechan AJ, Wosula EN, Wegulo SN, Graybosch RA, French R, Hein GL. (2014). An eriophyid mite-transmitted plant virus contains eight genomic RNA segments with unusual heterogeneity in the nucleocapsid protein. Journal of Virology 88: 11834-11845.

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.

FIG 1 Genome organization of HPWMoV. The presented schematic representations are genomic RNA segments with an encoded ORF (open rectangles) in each of the genomic RNAs. The genomic RNAs are numbered from the 5' to 3' end. The columns at the right show the length of the 5' nontranslated region (NTR), coding region of an ORF, and 3' NTR. Genomic RNAs 1 to 5 were named based on sequence homology with orthologous proteins of reported emaraviruses, and RNAs 6 to 8 were designated in order of decreasing RNA size.

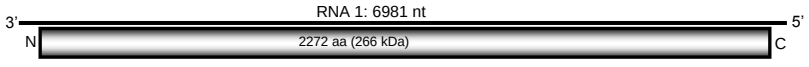
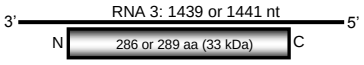
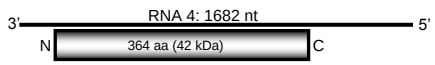
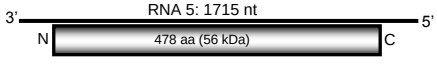
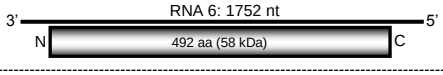
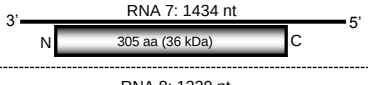
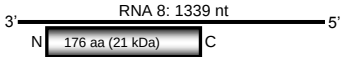
Genomic organization of HPWMoV RNAs	5'-NTR	Coding region	3'-NTR
	94 nt	nt 6913 to 98	68 nt
	128 nt	nt 2132 to 132	79 nt
	351/352 nt	nt 1215/1222 to 358/356	224/219 nt
	475 nt	nt 1570 to 479	112 nt
	158 nt	nt 1595 to 162	120 nt
	155 nt	nt 1634 to 159	118 nt
	399 nt	nt 1317 to 403	117 nt
	715 nt	nt 1246 to 719	93 nt

FIG 2 Phylogenetic trees constructed with the amino acid sequences of RdRp (A), glycoprotein precursor protein (B), and nucleocapsid protein (C) of emaraviruses. Accession numbers of sequences used are reported in Table 1. Trees were constructed by the neighbor-joining method using the JTT matrix and pairwise gap deletion with 1,000 bootstrap replicates; bootstrap support is indicated at branch points. The bar represents the number of amino acid replacements per site. Note that HPWMoV formed a separate clade with RLBV from other members of the genus *Emaravirus*.

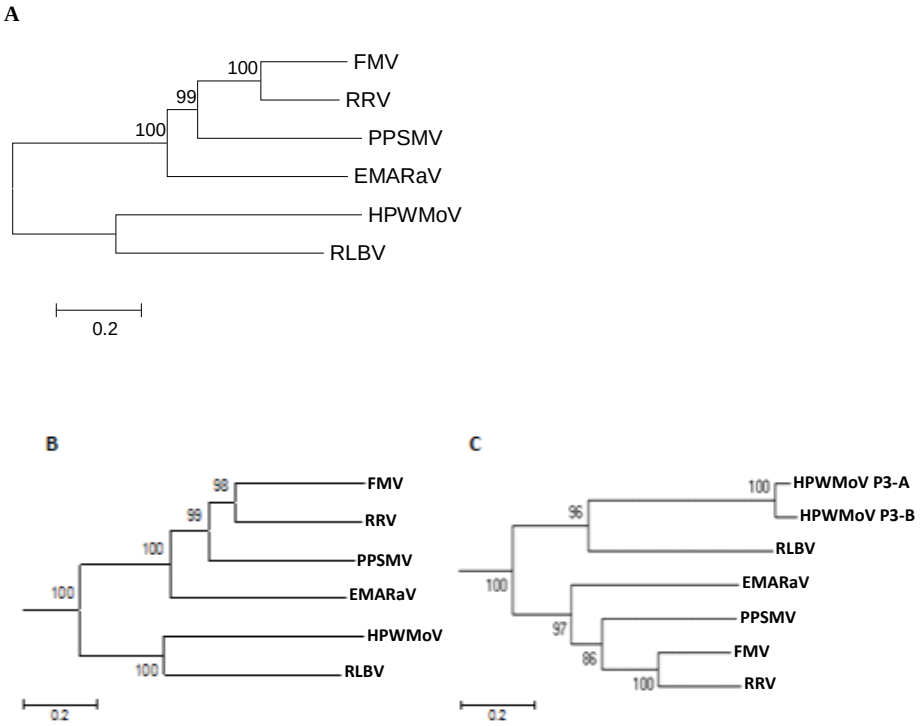


TABLE 1 Percent amino acid identities of RdRp/GP proteins (above the diagonal) and NC/P4 proteins (below the diagonal) between members of the *Emaravirus* genus.

Virus[a]	EMARaV	PPSMV	FMV	RRV	RLBV	HPWMoV
EMARaV	**100**	48.1/38.7	49.3/37.6	48.8/36.8	35.2/26.4	33.7/24.7
PPSMV	33.3/15.8	**100**	52.7/43.4	53.3/43.2	34.6/28.0	32.8/24.4
FMV	38.7/15.7	40.9/39.6	**100**	68.6/50.0	34.1/25.5	33.5/25.6
RRV	31.8/15.2	40.9/38.4	59.7/59.3	**100**	33.7/26.4	33.4/28.0
RLBV	23.8/14.1	27.7/24.1	22.2/20.3	24.8/23.7	**100**	42.2/35.1
HPWMoV	19.1(18.4)* /13.8	20.3(19.9) /20.1	21.8(20.3) /22.7	20.4(19.4) /22.3	31.0(29.6) /44.2	**100**

[a]EMARaV: *European mountain ash ringspot-associated virus* (NC_013105-08); PPSMV: *Pigeonpea sterility mosaic virus* (HF568801-04); FMV: *Fig mosaic virus* (HQ703343-46); RRV: *Rose rosette virus* (HQ871942-45); RLBV: *Raspberry leaf blotch virus* (FR823299-302); HPWMoV: High Plains wheat mosaic virus (this study).

*Identities of HPWMoV P3-A and P3-B proteins encoded by two RNA 3 sequences with the P3s of reported emaraviruses are shown outside and inside the parenthesis, respectively. The P3-A and P3-B proteins of HPWMoV are 88.9% identical to each other.

RdRp: RNA dependent RNA polymerase encoded by RNA 1; GP: glycoprotein precursor protein encoded by RNA 2; NC: nucleocapsid protein encoded by RNA 3; P4 protein encoded by RNA 4.