



This form should be used for all taxonomic proposals. Please complete all those modules that are applicable (and then delete the unwanted sections).

<b>Code(s) assigned:</b>	<b>2008.007P</b>	<small>(to be completed by ICTV officers)</small>
<b>Short title:</b> 2 new species in the genus <i>Aureusvirus</i> <small>(e.g. 6 new species in the genus <i>Zetavirus</i>; re-classification of the family <i>Zetaviridae</i> etc.)</small>		
<b>Modules attached</b> <small>(please check all that apply):</small>	1 <input type="checkbox"/>	2 <input type="checkbox"/>
	3 <input type="checkbox"/>	4 <input type="checkbox"/>
	5 <input checked="" type="checkbox"/>	6 <input type="checkbox"/>
	7 <input type="checkbox"/>	

**Author(s) with e-mail address(es) of the proposer:**

G.P. Martelli and L. Rubino with approval of Tombusviridae SG martelli@agr.uniba.it
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**ICTV-EC or Study Group comments and response of the proposer:**

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MODULE 5: **NEW SPECIES**

Code	<b>2008.007P</b>	<small>(assigned by ICTV officers)</small>
<b>To create 2 new species assigned as follows:</b>		
Genus:	<i>Aureusvirus</i>	<small>Fill in all that apply. Ideally, species should be placed within a genus, but it is acceptable to propose a species that is within a Subfamily or Family but not assigned to an existing genus (in which case put "unassigned" in the genus box)</small>
Subfamily:		
Family:	<i>Tombusviridae</i>	
Order:		

**Name(s) of proposed new species:**

<i>Johnsongrass chlorotic stripe mosaic virus</i> <i>Maize white line mosaic virus</i>
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**Argument to justify the creation of the new species:**

If the species are to be assigned to an existing genus, list the criteria for species demarcation and explain how the proposed members meet these criteria.

Species demarcation criteria published in the 8 <sup>th</sup> report are:  Serological specificity (known species are serologically unrelated) Extent of sequence identity between relevant gene products Less than 45% aa sequence identity of the CP Less than 90% aa sequence identity of the polymerase Differential cytopathological features
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**Argument to justify the creation of the new species:**

Different vector  
Natural host range  
Artificial host range reactions

**Johnsongrass chlorotic stripe mosaic virus**

Johnsongrass chlorotic stripe mosaic is a soil-borne disease endemic in Iran (Izadpanah, 1982). Disease agent is Johnsongrass chlorotic stripe mosaic virus (JCSMV), which has been investigated biologically, physicochemically and at the ultrastructural level (Izadpanah, 1988; Izadpanah *et al.*, 1993, 2002; Koochi Abib *et al.*, 2001). This virus has properties resembling those of members of the genus *Aureusvirus* in the family *Tombusviridae* but the lack of molecular information has not allowed its taxonomic allocation. Following genome sequencing, JCSMV was recognized as an aureusvirus of good standing (Winter *et al.*, 2002), but a taxonomic proposal was not formalized.

**JCSMV properties**

1. Virus particles: isometric with a mean diameter of about 30 nm, rounded contour and knobby surface
2. CP: 40 kDa (determined from sequence data)
3. Nucleic acid: single molecule of ssRNA 4421 nt in size
4. Genome: monopartite, totally sequenced (accession no. AJ557804) comprising 5 ORFs. Genome structure comparable to that of members of the genera *Aureusvirus* and *Tombusvirus*
5. Phylogenetic relationships: in trees constructed with whole genome sequences JCSMV clusters with members of the genus *Aureusvirus* in a distinct clade, together with Maize white line mosaic virus (MWLMV) which is the closest viral species. Identity at the amino acid level of CP and polymerase with comparable sequences of all aureusviruses is below the 45% and 90% thresholds (see below).
6. Serological relationships: no relation detected with MWLMV
7. Cytopathology: relevant features are the peripheral vesiculation of the nuclear envelope, the presence of virus particles within chloroplasts and the accumulation of fibrillar material in inflated endoplasmic reticulum cisternae. No comparable cytological modifications occur in cells infected by other aureusviruses except for the nuclear vesiculation induced by PoLV.
8. Mechanical transmission: positive only by embryo injection of infectious sap
9. Transmission by vectors: the virus is soil-borne but no vector has been identified
10. Seed transmission: negative
11. Natural host range: *Sorghum halepense*, *Zea mais*, *Setaria* sp., *Digitaria* sp.

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**Maize white line mosaic virus**

Maize white line mosaic is a soil-borne disease first reported from New York State, USA (Boothroyd and Israel, 1980). Maize white line mosaic virus (MWLMV), the agent of the disease has been extensively investigated biologically, physicochemically and at the ultrastructural level (De Zoeten *et al.*, 1980; Louie *et al.*, 1982; De Zoeten and Reddick, 1984. Zhang *et al.*, 1991a; Russo *et al.*, 2008). MWLMV is one of the four plant viruses supporting the replication of an isometric satellite virus 17 nm in diameter (Mayo *et al.*, 2005a) containing a totally sequenced ssRNA genome 1.2 kb in size (Gingery and Louie, 1985; Zhang *et al.*, 1991b). Notwithstanding the fact that the properties of MWLMV resemble very much those of members of the family *Tombusviridae*, lack of molecular information prompted its inclusion among the “Unassigned virus” section in the 8th Report of ICTV (Mayo *et al.*, 2005b). The MWLMV genome has now been completely sequenced (Russo *et al.*, 2008), thus the taxonomic allocation of the virus is feasible.

**Argument to justify the creation of the new species:**

**MWLMV properties**

1. Virus particles: isometric c. 35 nm in diameter, rounded contour and knobby surface
2. CP: 35 kDa (determined from sequence data)
3. Nucleic acid: single molecule of ssRNA 4293 nt in size
4. Genome: monopartite, totally sequenced (accession no. EF589670), comprising 5 ORFs. Genome structure comparable to that of members of the genera *Aureusvirus* and *Tombusvirus* (see Fig. 1)
5. Phylogenetic relationships: in trees constructed with whole genome sequences, MWLMV clusters with members of the genus *Aureusvirus*, in a distinct clade together with Johnsongrass chlorotic stripe mosaic virus (JCSMV) which is the closest viral species (Fig. 2). Identity at the amino acid level of CP and polymerase with comparable sequences of all aureusviruses is below the 45% and 90% threshold (see Table 1).
6. Serological relationships: no relationship with *Pothos latent virus* (PoLV), JCSMV and Maize necrotic streak virus (MNSP).
7. Cytopathology: no virus-specific cytological alterations. Cytopathology differing from that of PoLV and JCSMV infections
8. Mechanical transmission: positive only by vascular puncture of kernels
9. Transmission by vectors: suspected but not proven to be by soil fungi
10. Seed transmission: negative
11. Natural host range: restricted to *Zea mais*, *Panicum dichotomiflorum*, *Setaria faberi*, *S. viridis*, *Triticum aestivum* and *Digitaria sanguinalis*.

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**References:**

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Russo M., De Stradis A., Boscia D. Rubino L., Redinbaugh M.G., Abt J.J., Martelli G.P., 2008. Molecular and ultrastructural properties of Maize white line mosaic virus. *Journal of Plant Pathology* **90** (in press, July 2008)

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**Annexes:** From Russo *et al.*, 2008

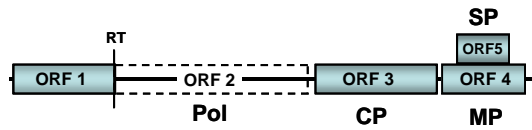
Include as much information as necessary to support the proposal. The use of Figures and Tables is strongly recommended.

**Table 1.** Pairwise amino acid sequence comparison of proteins encoded by the genome of MWLMV with corresponding gene products of aureusviruses and selected tombusviruses.

Virus	Amino acid identity (%)				
	ORF 1	ORF 2	ORF 3	ORF 4	ORF 5
<b>Aureusviruses</b>					
CLSV	24	64	31	39	35
JCSMV	57	80	34	62	62
PoLV	24	62	35	42	40
SNMV	21	61	41	41	39
<b>Tombusviruses</b>					
CIRV	16	44	36	23	19
CymRSV	19	44	36	22	16
TBSV	20	44	37	22	28
<b>Unassigned in the family <i>Tombusviridae</i></b>					
MNeSV	20	44	17	16	20

CLSV, *Cucumber leafspot virus*; JCSMV, Johnsongrass chlorotic stripe mosaic virus; PoLV, *Pothos latent virus*; SNMV, Sesame necrotic mosaic virus; CIRV, *Carnation Italian ringspot virus*; CymRSV, *Cymbidium ringspot virus*; TBSV, *Tomato bushy stunt virus*; MNeSV, Maize necrotic streak virus

**Fig. 1.** Genome structure of MWLMV



**Fig 2.** Tree constructed with whole genome sequences of members of the family *Tombusviridae*. Aureusviruses are: Maize white line mosaic virus (MWLMV), Johnsongrass chlorotic spot mosaic virus (JCSMV), Sesame necrotic mosaic virus (SNMV), *Cucumber leaf spot virus* (CLSV) and *Pothos latent virus*

