

## 2003.032-036V

Note from Mike Adams: The history of this proposal is not well documented. The available information is collected here:

### 1. EC 33 paperwork

This set of proposals was first seen at EC33 (2-4 May 2003). The documents supplied in printed form to EC members for the meeting contain the proposal that appears in Appendix 1. This specifies creation of a new genus in the family *Reoviridae* (2003.032), naming the genus *Mycoreovirus* (2003.033), designating *Mycoreovirus 1* as the type species (2003.034) and designating *Mycoreovirus 1* as a species in the new genus (2003.035). The new species is based on a report of a virus isolated from the fungus *Rosellinia necatrix*. There is also a separate 'fast track' proposal FT2003.036 that, curiously, uses the same information to propose the species *Mycoreovirus 1* as unassigned in the family *Reoviridae*.

### 2. EC33 minutes

The minutes of EC33 session 2(3). Proposals from the Vertebrate Virus Subcommittee read:

- 2003.032V.01.** Create a new genus in the family *Reoviridae*, to contain viruses infecting fungi and having all characteristics of reoviruses.
- 2003.033V.01.** To name the new genus created in 2003.032V.01, *Mycoreovirus*
- 2003.034V.01.** To designate as '*Rosellinia necatrix reovirus* ', the type species of the new genus created in 2003.032V.01
- 2003.035V.01.** To designate as '*Rosellinia necatrix reovirus* ', as a new species of the new genus created in 2003.032V.01
- FT2003.036V.01.** To designate as '*Rosellinia necatrix reovirus* ', as a new unassigned species in the family *Reoviridae*.

Taking these five proposals together: It was agreed that there is a strong case for the new genus. However, as this is a fungal virus, and fungal virologists have been working on other, related fungal reoviruses, the SG are advised to liaise with the fungus virus SC Chair before resubmitting the proposal. It was pointed out that consultation in these circumstances is a statutory duty.

It is not clear why the minutes have a different name for the species to that in the paperwork. It appears that the redundancy of FT2003.036 was not noticed.

### 3. The published taxonomic changes (2004)

A list of taxonomic changes approved in 2004 was published in VDN by Mike Mayo [Arch Virol 150: 189–198 (2005)]. This includes the following

#### Family *Reoviridae*

...

- Create a new genus (*Mycoreovirus*) with *Mycoreovirus 1* as type species

...

- Rename *Rosellinia necatrix reovirus* as *Mycoreovirus 3* and assign it to genus *Mycoreovirus*

#### 4. The ICTV 8<sup>th</sup> Report (2005)

The list of species published in the ICTV 8<sup>th</sup> Report is as follows:

##### SPECIES IN THE GENUS

##### Group 1 (11 genome segments)

##### *Mycoreovirus 1* ‡

*Cryphonectria parasitica* mycoreovirus 1 (9B21) (CpMYRV-1/9B21)

##### *Mycoreovirus 2* ‡

*Cryphonectria parasitica* mycoreovirus 2 (C18) (CpMYRV-2/C18)

##### Group 2 (12 genome segments)

##### *Mycoreovirus 3* ‡

*Rosellinia necatrix* mycoreovirus 3 (W370) (RnMYRV-3/W370)  
(*Rosellinia* anti-rot virus)

#### 5. A suggested synthesis

Although no paperwork has been traced, it appears that some modification of the proposal occurred after EC33 and before ratification in 2004, presumably as a result of the consultation required by the EC33 minutes.

We have to assume that these changes included the use of a different virus (*Cryphonectria parasitica* mycoreovirus 1) as the basis for the type species *Mycoreovirus 1*. Two different viruses from *Cryphonectria* had been reported by this time and clearly belonged to the same genus. The virus from *Rosellinia necatrix* was then therefore assigned to *Mycoreovirus 3*.

This justifies the published taxonomic changes (2004) and is consistent with the listing in the 8<sup>th</sup> Report (although there is no evidence that *Mycoreovirus 2* was formally proposed as a species).

**Appendix 1: 2003 EC33 proposal**

**Template for Taxonomic Proposal to the ICTV Executive Committee  
To create a new Genus in an existing Family**

Code<sup>†</sup>  To create a new genus in the family\*

Code<sup>†</sup>  To name the new genus\*

Code<sup>†</sup>  To designate the species   
As the type species of the new genus\*

Code<sup>†</sup>  To designate the following viruses as species of the new genus\*:

Code<sup>†</sup>  To designate the following viruses as tentative species in the new  
genus\*:

<sup>†</sup> Assigned by ICTV officers  
\* repeat these lines and the corresponding arguments for each genus created in the family

**Author(s) with email address(es) of the Taxonomic Proposal**

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**New Taxonomic Order**

Order	
Family	<i>Reoviridae</i>
Genus	<i>Mycoreovirus</i>
Type Species	<i>Mycoreovirus-1</i>
List of Species in the genus	<i>Mycoreovirus-1</i>
List of Tentative Species in the Genus	

### Argumentation to choose the type species in the genus

The *Mycoreovirus-1* isolated from *Rosallinia necatrix*, is the only member of the genus that has so far been identified. Most of its genome has now been sequenced. It is the only member of the family *Reoviridae* to have been isolated from a fungus

### Species demarcation criteria in the genus

Like other members of the family *Reoviridae*, the prime determinant for inclusion of mycoreovirus isolates within a single virus species will be an ability to exchange (reassort) genome segments during co-infection, thereby exchanging genetic information and generating viable and novel progeny virus strains. However this data is frequently unavailable and other methods can be used to detect similarities and in effect predict the compatibility of isolates for reassortment.

Data which in effect allow a prediction of the Acompatibility@ of strains for reassortment, include:

- Identification of vector and/or host species and clinical signs;
- Serological comparisons (identification of serogroups);
- Comparisons of RNA/protein sequences;
- Cross-hybridization analysis of RNA or cDNA;
- Analysis of conserved RNA terminal regions;
- Identification of the virus >serotype= (neutralization type) with one that is already classified within a species;
- Analysis of the electrophoretic migration patterns of the genome segments (electropherotype) by agarose gel electrophoresis;
- Amplification of conserved genome segments or regions by (PCR ; can be coupled with cross-hybridisation, sequence analysis or restriction fragment analysis of the products).

### List of Species in the created genus

*Mycoreovirus-1*

### List of Tentative Species in the created genus

None identified

### Argumentation to create a new genus:

A 12-segmented dsRNA virus that infects the plant pathogen *Rosellina necatrix* has been discovered and partially characterised. The estimated molecular weights of the genome segments range from  $0.41 \times 10^6$  to  $2.95 \times 10^6$ . Full length cDNA clones for eight genome segments have been analysed. One long open reading frame was found in each segment and conserved terminal sequences were identified at the 5'-end (5'-ACAAUUU-3') and at the 3'-end (5'-UGCAGAC-3') of all eight segments. This genome structure and the presence of the conserved sequences is typical of members of the *Reoviridae*, although the terminal sequences are different from those of those established species within the family for which data is available, indicating that it belongs to a different virus species (which we have named *Mycoreovirus-1*).

*Rosellina necatrix* mycoreovirus-1 has a double-shelled icosahedral capsid approximately 80 nm in diameter, with an internal (or core) particle containing 12 surface projections or spikes at the vertices of the icosahedron. This structure is similar to that of viruses within several other genera of the family *Reoviridae*, but it is not identical to members of the other genera containing 12 segmented viruses (*Coltivirus*, *Seadornavirus* or *Phytoreovirus*), which do not have surface spikes on their core particles. This suggests that the new virus belongs to a different genus.

Comparative analysis of the predicted translation products showed partial matches of specific motifs, to those of proteins from *Reoviridae* family members *Colorado tick fever virus*, *Nilaparvata lugens reovirus*, and *Rice black streaked dwarf virus*. However, the level of similarity calculated for the whole predicted protein sequence was relatively low (approximately 25-30% for amino acid sequences derived from genome segment 6 and below significant levels for other proteins). This is consistent with *Mycoreovirus-1* belonging to a distinct genus.

This is the first member of the *Reoviridae* known to infect fungi and its host range is therefore also consistent with its classification within a distinct new genus.

### Origin of the proposed genus name

Myc (indicating fungus) and reovirus to indicate its membership of the family *Reoviridae*

## References

[www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&list\\_uids=12206302&dc\\_pt=Abstract](http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&list_uids=12206302&dc_pt=Abstract)

Osaki, H., Wei, C. Z., Arakawa, M., Iwanami, T., Nomura, K., Matsumoto, N. and Ohtsu, Y. (2002) Nucleotide sequences of double-stranded RNA segments from a hypovirulent strain of the white root rot fungus *Rosellinia necatrix*: possibility of the first member of the Reoviridae from fungus. *Virus Genes* **25**(1):101-7

## Annexes:

**Template for Taxonomic Proposal to the ICTV Executive Committee  
Creating Unassigned Species in an existing Family**

Code<sup>†</sup> **FT2003.036V.01** To designate the following viruses as unassigned species in the family: ***Reoviridae***

*Mycoreovirus-1*

<sup>†</sup> Assigned by ICTV officers

<sup>°</sup> leave blank if inappropriate or in the case of an unassigned genus

**Author(s) with email address(es) of the Taxonomic Proposal**

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**New Taxonomic Order**

**Order**

**Family** *Reoviridae*

**List of Unassigned Species in the Family** *Mycoreovirus -1*

### Argumentation to justify the designation of unassigned species in the family

A 12-segmented dsRNA virus that infects the fungal plant pathogen *Rosellinia necatrix* has been discovered and partially characterised. The estimated molecular weights of the genome segments range from  $0.41 \times 10^6$  to  $2.95 \times 10^6$ . Full-length cDNA clones for eight genome segments have been analysed. One long open reading frame was found in each segment and conserved terminal sequences were identified at the 5'-end (5'-ACAAUUU-3') and 3'-end (5'-UGCAGAC-3') of all eight segments. This genome structure and organisation, including these conserved sequences, are typical of members of the *Reoviridae*. However, the conserved sequences differ from those of the other species that have (so far) been analysed, within the family, indicating that this new virus is not a member of an existing species.

No members of the family *Reoviridae* have previously been isolated from fungi. The host range alone therefore places this virus apart from other members of the family.

The new virus has a double-shelled icosahedral capsid approximately 80 nm in diameter, with an internal (or core) particle containing 12 surface projections or 'spikes' at the vertices of the icosahedron. This structure is similar to that of viruses within several other genera of the family *Reoviridae*, but it is not identical to members of the other genera containing 12 segmented viruses (*Coltivirus*, *Seadornavirus* or *Phytoreovirus*), which do not have surface spikes on their core particles.

Comparative analysis of the predicted translation products showed partial matches of specific motifs to those of proteins from *Reoviridae* family members *Colorado tick fever virus*, *Nilaparvata lugens reovirus*, and *Rice black streaked dwarf virus*. However, the overall level of similarity calculated for the whole protein was relatively low (approximately 25-30% for the amino acid sequences derived from genome segment 6 and below significant levels for the other proteins) indicating that the new virus belongs to a distinct virus species.

The new virus species will be named *Mycoreovirus-1* (MCRV-1), while *Rosellinia necatrix* mycoreovirus-1 (RnMCRV-1) will be a named isolate. In this way any potential problems associated with the identification of further isolates of the same virus species from different fungi, or isolates of different *Mycoreovirus* species from the same fungus, will be avoided. This naming style is similar to that already used for the genus *Cypovirus* and is in keeping with the new proposals for virus nomenclature.

### List of created Unassigned Species in the family

*Mycoreovirus -1*

### References

[v.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&list\\_uids=12206302&dopt=/](http://v.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&list_uids=12206302&dopt=/)

Osaki, H., Wei, C. Z., Arakawa, M., Iwanami, T., Nomura, K., Matsumoto, N. and Ohtsu, Y. (2002) Nucleotide sequences of double-stranded RNA segments from a hypovirulent strain of the white root rot fungus *Rosellinia necatrix*: possibility of the first member of the *Reoviridae* from fungus. *Virus Genes* **25**(1):101-7.

### Annexes: