

## 2002.122-126V

Note from Mike Adams: The history of this proposal is complex and it seems likely that some of the changes were unintentional. These changes are documented here:

### 1. EC29 (2001)

The proposal was first seen at EC29 (2001) where the vertebrate virus SC report (5.2) has:

From the *Reoviridae* Study Group

.....

- 3 to create a genus typified by *Hyposoter exiguae reovirus*
- 4 to name the genus created in 3, *Entomoreovirus*
- 5 to nominate *Hyposoter exiguae reovirus* as type species of the genus created in 3

This proposal has been identified from the EC29 papers and appears in Appendix 1 below.

The minutes do not record any discussion or comments but there must have been some from what appears later. Nothing about this proposal appears in the minutes until EC31 (2002) where is it reported that “No modified [Reoviridae] proposals have been received following the EC request for modification to the proposals made to the Washington meeting. The EC asked that the Study Group be reminded of this and that there is a deadline for receipt of taxonomic changes that could appear in the 8th Report.”

### 2. EC33 (2003) paper version

The proposal was then seen for a second time at EC33 (2-4 May 2003). The printed documents supplied to EC members contain the proposal that appears in Appendix 2 below, which is clearly identical to the proposal from EC29 but with code numbers added. The table of species is interpreted to mean the creation of 5 new species in addition to the type species: *Dacus oleae reovirus*, *Drosophila F virus*, *Drosophila S virus*, *Ceratitis capitata reovirus*, and *Musca domestica reovirus*, together with *Diadromus pulchellus reovirus* as a tentative species.

### 3. EC33 (2003) electronic version

Documents supplied to EC members for the meeting include a different version of the proposal on the new proposal form that appears in Appendix 3 below. This lists two species to be created at V125: *Hyposoter exiguae entomoreovirus* and *Diadromus pulchellus entomoreovirus*. The first of these is proposed as the type species at V124. The following 5 tentative species are proposed at V126 : *Drosophila F Virus*, *Drosophila S Virus*, *Dacus oleae reovirus*, *Musca domestica reovirus* and *Ceratitis I virus*. It seems likely that this is a later version prepared by the Study Group but subsequent minutes suggest that it may have been overlooked.

#### 4. The EC33 minutes

The following minute appears under session 3 of the minutes of EC33:

##### 1. Proposals from the Vertebrate Virus Subcommittee ....

- 2002.V122.02** To create a new genus to contain the currently unclassified, non-occluded ten segmented insect reoviruses.
- 2002.V123.02.** To name this newly created genus *Entomoreovirus*
- 2002.V124.02** To designate the species *Hyposoter exiguae reovirus* (HeRV), as type species of the genus *Entomoreovirus*
- 2002.V125.02** To include *Dacus oleae reovirus* (DoRV), *Drosophila F virus*, (DFV), *Drosophila S virus* (DSV), *Ceratitis capitata reovirus* (CcRV), and *Musca domestica reovirus* (MdRV), as species members of the new genus.
- 2002.V126.02** To include *Diadromus pulchellus reovirus* (DpRV), as tentative species in the new genus.

The EC accepted the scientific case for these proposals. However, members disapproved of a genus name, *Entomoreovirus*, as it implies that replication in insects is a peculiarity of the members of this taxon, whereas there are many reoviruses, in a variety of other Reovirus genera, which are already known to infect insects. The SG are therefore asked to devise another genus name, e.g. a name derived from the type species name (*Hypexovirus?* *Hexareovirus?*). The proposals are approved except for 123.

The listing suggests that the electronic version of the proposal had been overlooked and the original proposal approved, except for the question of the genus name.

#### 5. 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 (*Idnoreovirus*) with *Idnoreovirus 1* as type species
- Assign *Dacus oleae reovirus*, *Drosophila F virus*, *Drosophila S virus*, *Ceratitis capitata reovirus*, and *Musca domestica reovirus*, as species in genus *Idnoreovirus*

This largely follows the EC33 minutes (omitting the tentative species) but a new genus name has been adopted and the type species *Hyposoter exiguae entomoreovirus* appears to have been renamed *Idnoreovirus 1*. The name changes were presumably done on the recommendation of the Study Group, but no paperwork has been traced.

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

The list of species published in the ICTV 8<sup>th</sup> Report differs from the version apparently ratified. Not only have all species been renamed but *Hyposoter exiguae reovirus* is listed under

*Idnoreovirus 2* and is no longer the type species, while the species *Idnoreovirus 1* embraces the virus that was listed for ratification only as a tentative species. *Drosophila S* virus now appears only as a tentative species.

*Idnoreovirus 1* (the type member)

Diadromus pulchellus idnoreovirus-1

(Diadromus pulchellus reovirus)

*Idnoreovirus 2*

Hyposoter exiguae idnoreovirus-2

(Hyposoter exiguae reovirus)

*Idnoreovirus 3*

Musca domestica idnoreovirus-3

(Musca domestica reovirus)

(housefly virus)

*Idnoreovirus 4*

Dacus oleae idnoreovirus-4

(Dacus oleae reovirus)

*Idnoreovirus 5*

Ceratitis capitata idnoreovirus-5

(Ceratitis capitata I virus)

Drosophila melanogaster idnoreovirus-5

(Drosophila F virus)

The ICTV 9th Report (2011) contains a list of species and associated viruses which is identical to that in the ICTV 8th Report. As these species have existed officially for some time, the database records indicate their creation in 2004 but it is not obvious that the list accurately reflects either the original proposal or the electronic version prepared in 2003.

## Appendix 1: 2001 EC29 proposal

### Reoviridae Proposal 2

1. Proposal To create a new genus *Entomoreovirus* to recognise and contain the currently unclassified, non occluded ten segmented insect reoviruses.  
The type species *Hyposoter exiguae reovirus* (HeRV)

2. Purpose To recognise and group the insect reoviruses that possess a genome of ten segments of dsRNA and an outer capsid layer, which do not produce polyhedra and which are therefore not cypoviruses (currently included as unclassified members of the family *Reoviridae*: see table). The relationships between these different viruses is not yet fully resolved but it seems likely that at least those that have been isolated from different host species may represent different virus species. Only further analyses will fully resolve this question. Recognition of this genus may help to stimulate further studies, particularly the generation of additional sequence analyses for phylogenetic comparisons.

Although the sequence of many of the genome segments of DpRV is already available, this virus appears to be unusual in that it can have a tenth segment, the presence of which correlates with the sex and ploidy of the host. Since this characteristic appears to be unusual and may be unique, it is considered more appropriate to use HeRV as the prototype and to recognise DpRV as a putative distinct species within the genus. The genome of HeRV is currently being analysed and sequence data will be available soon (D. Stoltz personal communication).

Virus species	source or host species	abbreviat ion	characteristics
<i>Dacus oleae reovirus</i>	<i>Dacus oleae</i> (Diptera olive fly )	(DoRV)	Non-occluded, double shelled capsid, spiked core, ten genome segments
(Drosophila F Virus) (Drosophila S Virus)	<i>Drosophila melanogaster</i> (Diptera: fruit fly) and <i>D. melanogaster</i> cell lines. <i>D.simulans</i>	(DFV)	Non-occluded, double shelled capsid, spiked core, ten genome segments.
<i>Ceratitis capitata reovirus</i> ( <i>Ceratitis I virus</i> )	<i>Ceratitis capitata</i> (Diptera)	(DSV) (CIV)	CIV has a distinct genome segment electrophoretic migration pattern (only 9 bands detected) and is serologically distinct from DFV.
<i>Musca domestica reovirus</i>	the house fly, <i>Musca domestica</i>	(MdRV)	Non-occluded, icosahedral particles ca 70 nm diameter

(housefly virus)	(Diptera: house fly)		
<i>Hyposoter exiguae reovirus</i>	<i>Hyposoter exiguae</i> (Hymenoptera: wasp)	(HeRV)	Non-occluded, buds from cell, transient envelope, non-enveloped particle is 65nm diameter, 10 segments - 4 large and 6 small, infects all wasps in colony, both ovaries and testes infected. No apparent effect caused by or on sex or ploidy of host.
<i>Diadromus pulchellus reovirus</i>	<i>Diadromus pulchellus</i> (Hymenoptera: wasp)	(DpRV)	Sequence data for seven segments [X80481; X80480; X82045; X82046; X82047; X82048; X82049] indicates no close relationships to members of established genera. Terminal sequences (5' <sup>A</sup> / <sub>G</sub> CAAUUUU <sub>n</sub> nACU.....AGUAAAAAAAU n <sup>A</sup> / <sub>G</sub> 3') are different from species in other genera. Usually ten segments, plus eleventh non-equimolar segment depending on sex and ploidy of wasp.

#### REFERENCES

1. AnagnouVeroniki, M., Veyrunes, J.C., Kuhl, G., Bergoin, M. (1997). A nonoccluded reovirus of the olive fly, *Dacus oleae*. *Journal of General Virology*, **78**, 259-263
2. Bigot, Y., Drezen, J.M., Sizaret, P.Y., Rabouille, A., Hamelin, M.H., Periquet, G. (1995). The genome segments of DpRV, a commensal reovirus of the wasp *Diadromus pulchellus* (Hymenoptera). *Virology*, **210**, 109-119.
3. Haars, R., Zentgraf, H., Gateff, E., Bautz, F.A. (1980). Evidence for endogenous reovirus-like particles in a tissue culture cell line from *drosophila melanogaster*. *Virology*, **101**, 124-130.
4. Lopez-Ferber, M., Veyrunes, J.C., Croizier, L. (1989). *Drosophila S virus* is a member of the Reoviridae family. *Journal of Virology*, **63**, 1007-1009.
5. Moussa, A.Y. (1978) A new virus disease in the House fly *Musca domestica* (diptera). *Journal of Invertebrate Pathology*, **31**, 204- 216.

6. Plus, N., Gissman, L., Veyrunes, J.C., Pfister, H., Gateff, E. (1981). Reoviruses of *Drosophila* and *Ceratitis* populations and of drosophila cell lines ; a new genus of the Reoviridae family. *Annales de Virologie (Institut Pasteur)* **132E**, 261-270.
7. Plus, N.; Croizier, G. (1982). Further studies on the genome of *Ceratitis capitata* I virus (Reoviridae). *Annales de Virologie (Institut Pasteur)*, **133E**, 489-492.
8. Rabouille, A., Bigot, Y., Drezen, J.M., Sizaret, P.Y., Hamelin, M.H., Periquet, G. (1994). A member of the reoviridae (DpRV) has a ploidy-specific genomic segment in the wasp *Diadromus pulchellus* (Hymenoptera). *Virology*, **205**, 228-237

## Appendix 2: 2003 EC33 paper proposal

### Reoviridae Study-Group

- 2002.V122.02** To create a new genus *to* contain the currently unclassified, non occluded ten segmented insect reoviruses.
- 2002.V123.02.** To name this newly created genus *Entomoreovirus*
- 2002.V124.02** To designate the species *Hyposoter exiguae reovirus* (HeRV), as type species of the genus *Entomoreovirus*
- 2002.V125.02** To include *Dacus oleae reovirus* (DoRV), *Drosophila F virus*, (DFV), *Drosophila S virus* (DSV), *Ceratitis capitata reovirus* (CcRV), and *Musca domestica reovirus* (MdRV), as species members of the new genus.
- 2002.V126.02** To include *Diadromus pulchellus reovirus* (DpRV), as tentative species in the new genus.

- 2. Purpose** To recognise and group the insect reoviruses that possess a genome of ten segments of dsRNA and an outer capsid layer, which do not produce polyhedra and which are therefore not cypoviruses (currently included as unclassified members of the family *Reoviridae*: see table). The relationships between these different viruses is not yet fully resolved but it seems likely that at least those that have been isolated from different host species may represent different virus species. Only further analyses will fully resolve this question. Recognition of this genus may help to stimulate further studies, particularly the generation of additional sequence analyses for phylogenetic comparisons.

Although the sequence of many of the genome segments of DpRV is already available, this virus appears to be unusual in that it can have a tenth segment, the presence of which correlates with the sex and ploidy of the host. Since this characteristic appears to be unusual and may be unique, it is considered more appropriate to use HeRV as the prototype and to recognise DpRV as a putative distinct species within the genus. The genome of HeRV is currently being analysed and sequence data will be available soon (D. Stoltz personal communication).

Virus species	source or host species	abbreviation	characteristics
<i>Dacus oleae reovirus</i>	<i>Dacus oleae</i> (Diptera olive fly )	(DoRV)	Non-occluded, double shelled capsid, spiked core, ten genome segments
( <i>Drosophila F Virus</i> )	<i>Drosophila melanogaster</i> (Diptera: fruit fly) and		Non-occluded, double shelled capsid, spiked core, ten

(Drosophila S Virus)	<i>D. melanogaster</i> cell lines. <i>D. simulans</i>	(DFV)  (DSV)	genome segments. CIV has a distinct genome segment electrophoretic migration pattern (only 9 bands detected) and is serologically distinct from DFV.
<i>Ceratitis capitata</i> reovirus ( <i>Ceratitis I virus</i> )	<i>Ceratitis capitata</i> (Diptera)	(CIV)	
<i>Musca domestica</i> reovirus (housefly virus)	the house fly, <i>Musca domestica</i> (Diptera: house fly)	(MdRV)	Non-occluded, icosahedral particles ca 70 nm diameter
<i>Hyposoter exiguae</i> reovirus	<i>Hyposoter exiguae</i> (Hymenoptera: wasp)	(HeRV)	Non-occluded, buds from cell, transient envelope, non-enveloped particle is 65nm diameter, 10 segments - 4 large and 6 small, infects all wasps in colony, both ovaries and testes infected. No apparent effect caused by or on sex or ploidy of host.
<i>Diadromus pulchellus</i> reovirus	<i>Diadromus pulchellus</i> (Hymenoptera: wasp)	(DpRV)	Sequence data for seven segments [X80481; X80480; X82045; X82046; X82047; X82048; X82049] indicates no close relationships to members of established genera. Terminal sequences (5 <sup>A</sup> / <sub>G</sub> CAAUUUUUn nACU.....AGUAAAAAAA Un <sup>A</sup> / <sub>G</sub> 3') are different from species in other genera. Usually ten segments, plus eleventh non-equimolar segment depending on sex and ploidy of wasp.

## REFERENCES

1. Anagnou-Veroniki, M., Veyrunes, J.C., Kuhl, G., Bergoin, M. (1997). A nonoccluded reovirus of the olive fly, *Dacus oleae*. *Journal of General Virology*, **78**, 259-263
2. Bigot, Y., Drezen, J.M., Sizaret, P.Y., Rabouille, A., Hamelin, M.H., Periquet, G. (1995). The genome segments of DpRV, a commensal reovirus of the wasp *Diadromus pulchellus* (Hymenoptera). *Virology*, **210**, 109-119.
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5. Moussa, A.Y. (1978) A new virus disease in the House fly *Musca domestica* (diptera). *Journal of Invertebrate Pathology*, **31**, 204-216.
6. Plus, N., Gissman, L., Veyrunes, J.C., Pfister, H., Gateff, E. (1981). Reoviruses of *Drosophila* and *Ceratitis* populations and of drosophila cell lines ; a new genus of the Reoviridae family. *Annales de Virologie (Institut Pasteur)* **132E**, 261-270.
7. Plus, N.; Croizier, G. (1982). Further studies on the genome of *Ceratitis capitata* I virus (Reoviridae). *Annales de Virologie (Institut Pasteur)*, **133E**, 489-492.
8. Rabouille, A., Bigot, Y., Drezen, J.M., Sizaret, P.Y., Hamelin, M.H., Periquet, G. (1994). A member of the reoviridae (DpRV) has a ploidy-specific genomic segment in the wasp *Diadromus pulchellus* (Hymenoptera). *Virology*, **205**, 228-237

**Appendix 3: 2003 EC33 electronic version of the proposal**

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

Code<sup>†</sup> **2002.122V.02** To create a new genus in the family\* *Reoviridae*

Code<sup>†</sup> **2002.123V.02** To name the new genus\* *Entomoreovirus*

Code<sup>†</sup> **2002.124V.02** To designate the species *Hyposoter exiguae entomoreovirus*  
As the type species of the new genus\*

Code<sup>†</sup> **2002.125V.02** To designate the following viruses as species of the new genus\*:

<i>Hyposoter exiguae entomoreovirus</i>	(HeERV)
<i>Diadromus pulchellus entomoreovirus</i>	(DpERV)

Code<sup>†</sup> **2002.126V.02** To designate the following viruses as tentative species in the new genus\*:

<i>Drosophila F Virus</i>	(DFV)
<i>Drosophila S Virus</i>	(DSV)
<i>Dacus oleae reovirus</i>	(DoRV)
<i>Musca domestica reovirus</i>	(MdRV)
<i>Ceratitis I virus</i>	(CIV)

<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**

<b>Order</b>	
<b>Family</b>	<i>Reoviridae</i>
<b>Genus</b>	<i>Entomoreovirus</i>
<b>Type Species</b>	<i>Hyposoter exiguae entomoreovirus</i> (HeERV)
<b>List of Species in the genus</b>	<i>Hyposoter exiguae entomoreovirus</i> (HeERV) <i>Diadromus pulchellus entomoreovirus</i> (DpERV)
<b>List of Tentative Species in the Genus</b>	

Drosophila F Virus	(DFV)
Drosophila S Virus	(DSV)
Dacus oleae reovirus	(DoRV)
<i>Musca domestica reovirus</i>	(MdRV)
<i>Ceratitis I virus</i>	(CIV)

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

Although the sequences of many of the genome segments of DpERV are available, this virus appears to be unusual in that it can have an 11<sup>th</sup> segment, the presence of which correlates with the gender and ploidy of the host. Since this characteristic appears to be unusual and may be unique, it is considered more appropriate to use HeERV as the prototype and to recognise DpRV as a distinct species within the genus. The genome of HeRV is currently being analysed and near complete sequences are available for four of the ten genome segments, which possess no detectable sequence similarity to existing genera (D, Stotlz personal communication).

### Species demarcation criteria in the genus

Like other members of the family *Reoviridae*, the prime determinant for inclusion of entomoreovirus 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 recognised 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

<i>Hyposoter exiguae reovirus</i>	(HeRV)
<i>Diadromus pulchellus reovirus</i>	(DpRV)

## List of Tentative Species in the created genus

Drosophila F Virus	(DFV)
Drosophila S Virus	(DSV)
Dacus oleae reovirus	(DoRV)
<i>Musca domestica reovirus</i>	(MdRV)
<i>Ceratitis I virus</i>	(CIV)

### Argumentation to create a new genus:

The family Reoviridae contains several genera of viruses that replicate in insects or arthropods. These include the 10 and 12 segmented genome plant viruses (Oryzavirus, Phytoreovirus and Fijivirus), the ten and 12 segmented genome mammalian viruses (Orbivirus, Seadornavirus and Coltivirus), which all have insect or arthropod vectors, and the ten segmented genome cypoviruses (which are only known to infect insects).

However there are several other viruses (currently classified as unassigned species within the family *Reoviridae*) that only appear to infect insects, which have a double-shelled capsid structure with 'spiked' core particles, and a ten segmented dsRNA genome. Since these viruses do not appear to have alternative plant or animal hosts it would be inappropriate to classify them within any of the existing genera except *Cypovirus*. However, the cypoviruses (**C**ytoplasmic **p**olyhedrosis **v**iruses) are distinctive in that they become occluded within large proteinaceous crystalline structures called 'polyhedra' and have only a single capsid shell. In contrast the non-occluded insect viruses, that would be classified within the genus *Entomoreovirus*, have outer capsid layers (and proteins), suggesting significantly different protein functions, genome coding organisation and transmission strategies. It therefore seems inappropriate to classify these non polyhedron-producing viruses, within a genus that was named for polyhedron production.

The sequence data that is available for HeERV and DpERV, show no significant sequence similarity with the members of the existing genera within the family for which sequence data is available, indicating that they do not belong to any of the existing genera. However, there are also only low levels of homology between HeERV and DpERV, suggesting only a distant relationship.

It is interesting to note that low levels of similarity have also been observed between the different virus species classified within the genus *Cypovirus*, which is reflected in the large differences in their genome segment migration patterns during electrophoresis. However, these cypoviruses are considered sufficiently similar in terms of their structural appearance host range and production of polyhedra, to be classified with the single genus *Cypovirus*. The high level of sequence variation observed between the insect viruses even within a single genus may be indicative of a very long relationship between these viruses and the insects that they infect. A view supported by the suggestion of a commensal relationship between DpERV and HeERV and their respective insect hosts.

In response to the previous submission of this proposal it was suggested that the name Entomoreovirus might imply that all members of the *Reoviridae* that grow in insects should be belong to this genus. However, there are sufficient differences from those viruses that also infect plants or other animals to avoid confusion. Indeed such considerations do not appear to have caused problems with the phytoreoviruses. The cypoviruses are also sufficiently distinct to avoid any significant problems.

## Origin of the proposed genus name

Entomo (indicating insect) and reovirus to indicate its membership of the family *Reoviridae*

## References

1. Anagnou Veroniki, M., Veyrunes, J.C., Kuhl, G., Bergoin, M. (1997). A nonoccluded reovirus of the olive fly, *Dacus oleae*. *Journal of General Virology*, **78**, 259-263.
2. Bigot, Y., Drezen, J.M., Sizaret, P.Y., Rabouille, A., Hamelin, M.H., Periquet, G. (1995). The genome segments of DpRV, a commensal reovirus of the wasp *Diadromus pulchellus* (Hymenoptera). *Virology*, **210**, 109-119.
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4. Lopez-Ferber, M., Veyrunes, J.C., Croizier, L. (1989). Drosophila S virus is a member of the Reoviridae family. *Journal of Virology*, **63**, 1007-1009.
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7. Plus, N.; Croizier, G. (1982). Further studies on the genome of *Ceratitis capitata* I virus (Reoviridae). *Annales de Virologie (Institut Pasteur)*, **133E**, 489-492.
8. Rabouille, A., Bigot, Y., Drezen, J.M., Sizaret, P.Y., Hamelin, M.H., Periquet, G. (1994). A member of the reoviridae (DpRV) has a ploidy-specific genomic segment in the wasp *Diadromus pulchellus* (Hymenoptera). *Virology*, **205**, 228-237.
9. Stoltz D, Makkay A Co-replication of a reovirus and a polydnavirus in the ichneumonid parasitoid *Hyposoter exiguae* *Virology* 2000 Dec 5;278(1):266-75

## Annexes:

Virus species	source or host species	abbreviation	characteristics
Dacus oleae reovirus	<i>Dacus oleae</i> (Diptera olive fly )	(DoRV)	Non-occluded, double shelled capsid, spiked core, ten genome segments
(Drosophila F Virus)  (Drosophila S Virus)  <i>Ceratitis capitata</i> reovirus ( <i>Ceratitis I virus</i> )	<i>Drosophila melanogaster</i> (Diptera: fruit fly) and <i>D. melanogaster</i> cell lines.  <i>D. simulans</i>  <i>Ceratitis capitata</i> (Diptera)	(DFV)  (DSV)  (CIV)	Non-occluded, double shelled capsid, spiked core, ten genome segments.  CIV has a distinct genome segment electrophoretic migration pattern (only 9 bands detected) and is serologically distinct from DFV.
<i>Musca domestica</i> reovirus (housefly virus)	House fly, <i>Musca domestica</i> (Diptera: house fly)	(MdRV)	Non-occluded, icosahedral particles ca 70 nm diameter
<i>Hyposoter exiguae</i> reovirus	<i>Hyposoter exiguae</i> (Hymenoptera: wasp)	(HeRV)	Non-occluded, buds from cell, transient envelope, non-enveloped particle is 65nm diameter, 10 segments - 4 large and 6 small, infects all wasps in colony, both ovaries and testes infected. No apparent effect caused by or on gender or ploidy of host.
<i>Diadromus pulchellus</i> reovirus	<i>Diadromus pulchellus</i> (Hymenoptera: wasp)	(DpRV)	Sequence data for seven segments [X80481; X80480; X82045; X82046; X82047; X82048; X82049] indicates no close relationships to members of established genera.  Terminal sequences (5' <sup>A</sup> / <sub>G</sub> CAAUUUUUn nACU.....AGUAAAAAAAUn <sup>A</sup> / <sub>G</sub> G3') are different from species in other genera. Usually ten segments, plus eleventh non-equimolar segment depending on gender and ploidy of wasp.