

Template for Taxonomic Proposal to the ICTV Executive Committee Creating Species in an existing genus

Code To designate the following viruses as species in the genus:

belonging to the family^o :

[†] Assigned by ICTV officers

^o leave blank if inappropriate or in the case of an unassigned genus

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

New Taxonomic Order

Order

Family

Reoviridae

Genus

Cypovirus

Type Species

List of Species in the genus

Cypovirus-1

Cypovirus-1

Cypovirus-2

Cypovirus-3

Cypovirus-4

Cypovirus-5

Cypovirus-6

Cypovirus-7

Cypovirus-8

Cypovirus-9

Cypovirus-10

Cypovirus-11

Cypovirus-12

Cypovirus-13

Cypovirus-14

List of Tentative Species in the Genus 

Cypovirus-15 (isolated From *Trichoplusia.ni*)

Christoneura fumiferana cypovirus

Heliiothis armigera cypovirus ("B strain")

List of Unassigned Species in the Family

Argumentation to justify the designation of new species in the genus Species demarcation criteria in the genus

Within the family *Reoviridae*, the prime determinant for inclusion of virus isolates within a single virus species is their ability to exchange genetic information by reassortment of their genome segments during co-infection, thereby generating viable progeny virus strains. However, there is no direct evidence concerning genome segment reassortment between different cytovirus isolates. Evidence of similarity and therefore of the genetic compatibility required for reassortment, can be provided by other methods.

Members of a single *Cypovirus* species may be identified by :

- 1) Their ability to exchange genetic material by genome segment reassortment during dual infections, thereby producing viable progeny virus strains.
- 2) Similar electrophoretic migration of at least 7 genome segments, as analysed using either an agarose, or a low percentage (3%) polyacrylamide gel system. Viruses of different species will have significant migrational differences in at least three genome segments.
- 3) High levels of serological cross-reaction by ELISA or AGID (eg. using polyclonal antisera to purified virions or polyhedrin proteins). Different but more closely related species (types) may show low levels of serological cross reaction (eg. CPV-1 and 12).
- 3) A high degree of sequence conservation (estimated >80%).
- 4) Cross-hybridization of genome segments under high stringency conditions (designed to detect >90% homology) (Northern or dot blots, with probes made from viral RNA or cDNA).
- 5) Current evidence suggests that the conserved terminal sequences are likely to be the same within a cytovirus species but different between different species. The similarity between more closely related species (eg. CPV-1, 12 and 14) is unknown.

Argumentation to justify the designation of new species in the genus

A new cytovirus has been isolated from *Trichoplusia ni*. The entire genome has been sequenced and accession numbers have been acquired for these data. [NC 002557](#), [NC 002558](#), [NC 002559](#), [NC 002567](#), [NC 002560](#), [NC 002561](#), [NC 002562](#), [NC 002563](#), [NC 002564](#), [NC 002565](#), [NC 002566](#).

Comparisons of the genome segment sizes (electrophoretic migration patterns), their nucleotide sequences and the conserved terminal regions, show significant differences to the members of the other established *Cypovirus* species and therefore that this virus should be regarded as an isolate of a new species '*Cypovirus -15*'.

There remains one complication, in that the new virus was found to contain 11 distinct genome segments. Most cytoviruses contain only 10 genome segments and the nature of this 11th segment remains unclear. It is possible, either that this is the first authentic 11 segmented cytovirus, or that the virus population contains two distinct versions of one of the genome segments.

Current species parameters (see parameter 2 above) for this genus indicate that if virus isolates are identical in at least 7 out of (normally) 10, genome segments, they will still be classified within the same virus species (or electropherotype). Even if two distinct versions of one of the segment are present within this virus population, the different viruses present, would therefore still be classified within a single species,. We anticipate that this position may be clarified by some further study.

Cypovirus-15

References

Rao S, Carner GR, Scott SW, Omura T, Hagiwara K.

Comparison of the amino acid sequences of RNA-dependent RNA polymerases of cypoviruses in the family Reoviridae. *Arch Virol.* 2003 **148**:209-19.

Annexes: