Template for Taxonomic Proposal to the ICTV Executive Committee
To create a new Unassigned Genus

Code[†] | **2003.117P.01** | To create a new genus*

Code[†] | **2003.118P.01** | To name the new genus* | *Mandarivirus*

Code[†] | **2003.119P.01** | To designate the species | *Indian citrus ringspot virus (ICRSV)*
As the type species of the new genus*

Code[†] | **2003.120P.01** | To designate the following viruses as species of the new genus*:

Indian citrus ringspot virus (ICRSV)

Code[†] | To designate the following viruses as tentative species in the new genus*:

[†] Assigned by ICTV officers
* repeat these lines and the corresponding arguments for each genus created in the family

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New Taxonomic Order

Order
Family
Genus   *Mandarivirus*
Type Species   *Indian citrus ringspot virus*
List of Species in the genus *Indian citrus ringspot virus*
List of Tentative Species in the Genus

Argumentation to choose the type species in the genus

Only one virus species in the genus

Species demarcation criteria in the genus

Not applicable

List of Species in the created genus

Indian citrus ringspot virus (ICRSV)

List of Tentative Species in the created genus

Argumentation to create a new genus:

A virus unofficially named "Indian citrus ringspot virus" has been described (Byadgi et al 1993; Rustici et al 2000, 2002). This virus, found in India infecting mandarin, cv. Kinnow, and other citrus varieties, causes ringspots on the leaves. It is mechanically transmissible to herbaceous hosts; it has no known vector. The particles are flexuous filaments of 650 nm modal length, with clearly visible cross-banding. The undivided ssRNA positive-sense genome consists of 7560 nt excluding the poly(A) tail, and there is one coat protein of 34 kDa. Comparisons of the full nucleotide sequence with viruses in the genera *Allexivirus*, *Capillovirus*, *Carlavirus*, *Foveavirus*, *Potexvirus*, *Trichovirus* and *Vitivirus* show that ICRSV clusters closest to potex- and allexiviruses but does not fall within these genera (Fig. 1).

The virus has the following combination of properties that places it in the genus *Mandarivirus*.

The genome has 6 ORFs, the CP ORF being the penultimate. This arrangement is similar to that of other filamentous viruses such as carlaviruses and allexiviruses but is unlike that of potexviruses (Fig. 2). ORF 6 however shows no homologies with the corresponding ORFs of carla- and allexiviruses.

The CP (34 kDa) is larger than that of potexviruses (18-27 kDa) but limited homology with potexviruses is present in the C-terminal part of the protein; this is reflected in a distant serological relationship between ICRSV and *Potato virus X*. The N-terminal 133 aa of the CP show no significant similarities with potexviruses or any sequence in the database.

ICRSV differs from potex- and carlaviruses in having more flexuous particles that display a clear helix. This morphology is closer to that of fovea-, allexi- and capilloviruses.

Origin of the proposed genus name

The genus is named *Mandarivirus* as the type species, *Indian citrus ringspot virus*, infects mandarin (*Citrus reticulata*).

References

Byadgi AS, Ahlawat YS, Chakraborty NK, Varma A, Srivastava M, Milne RG (1993). Characterization of a filamentous virus associated with citrus ringspot in India. In: Proc. 12th Conf. International Organization of Citrus Virologists, ed. P. Moreno et al, IOCV Riverside, CA, 155-162.

Rustici G, Accotto GP, Noris E, Masenga V, Luisoni E, Milne RG (2000). Indian citrus ringspot virus: a proposed new species with some affinities to potex-, carla-, fovea- and allexivirusers. Archives of Virology 145: 1895-1908.

Rustici G, Milne RG, Accotto GP (2002). Nucleotide sequence, genome organization and phylogenetic analysis of Indian citrus ringspot virus. Archives of Virology 147: 2215-2224.

Annexes:

Figure 1. Unrooted phylogenetic tree based on full nucleotide sequences of selected filamentous RNA viruses, using the program ClustalW with gap open penalty of 10 and gap extension penalty of 5, and 1000 bootstrap replications. Branch lengths are proportional to estimated divergence. All bootstrap values exceeded 90%, except those indicated. (From Rustici et al, 2002).
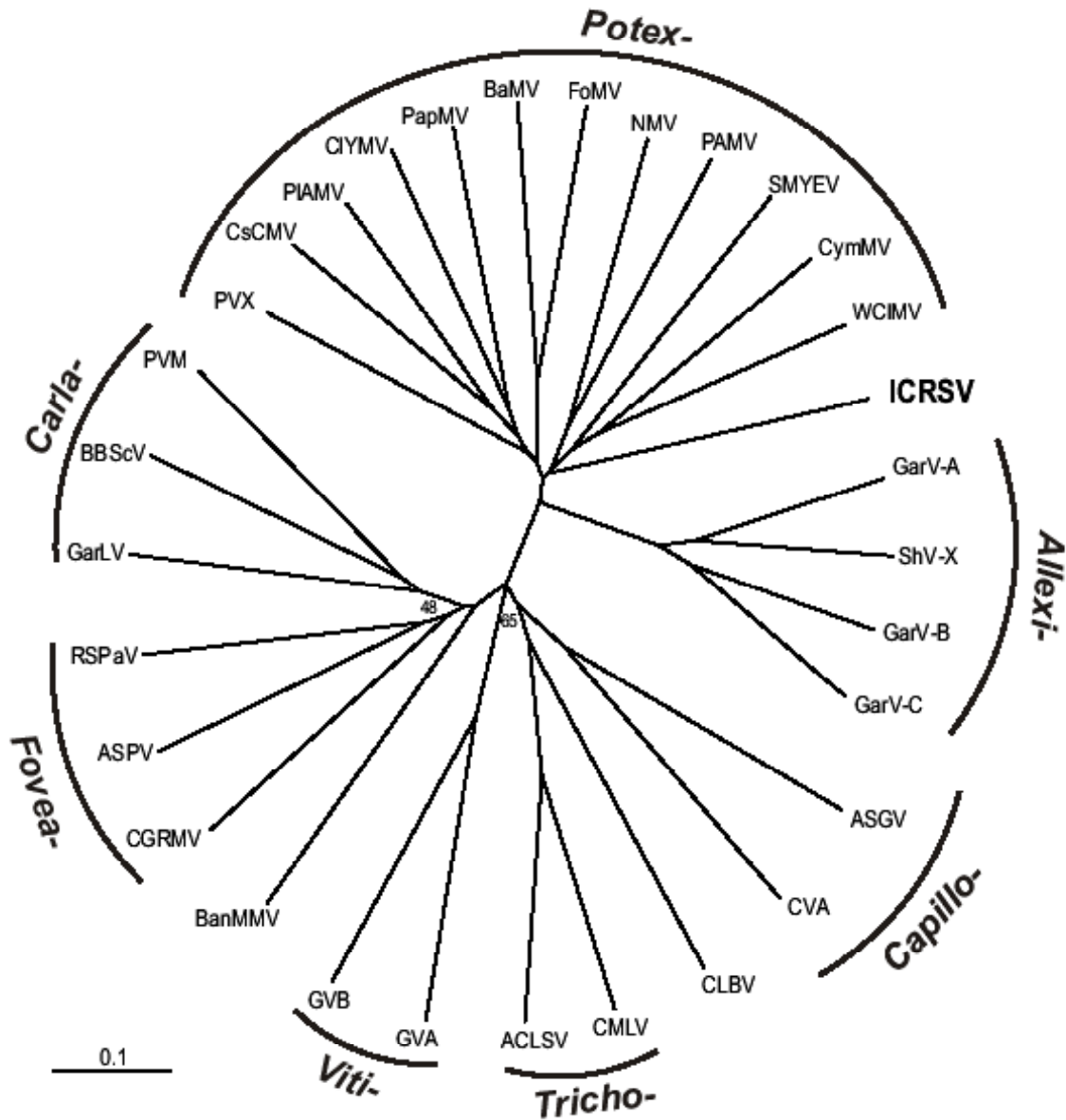
Figure 2. Comparison of the genome structures of ICRSV, CGRMV (*Cherry green ring mottle virus*, foveavirus), PVX (*Potato virus X*, potexvirus), PVM (*Potato virus M*, carlavirus) and ShV-X (*Shallot virus X*, allexivirus). Boxes with the same pattern represent comparable ORFs. (From Rustici et al, 2002).