Taxonomic proposal to the ICTV Executive Committee

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

Code(s) assigned:	***2008.013P***	(to be completed by ICTV officers)

Short title: 1 new species in the genus Crinivirus
(e.g. 6 new species in the genus *Zetavirus*; re-classification of the family *Zetaviridae* etc.)

Modules attached (please check all that apply):	**1** ☐	**2** ☐	**3** ☐	**4** ☐	**5** ☐
	6 ☐	**7** ☐			

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

G.P. Martelli (martelli@agr.uniba.it) on behalf of the Closteroviridae SG

ICTV-EC or Study Group comments and response of the proposer:

MODULE 5: **NEW SPECIES**

Code	***2008.013P***	(assigned by ICTV officers)

To create one new species assigned as follows:

Genus:	***Crinivirus***
Subfamily:	
Family:	***Closteroviridae***
Order:	

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)

Name(s) of proposed new species:

Bean yellow disorder virus

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.

The criteria demarcating species in the genus in the 8th Report are:

- Particle size,
- Size of CP, as determined by deduced amino acid sequence data,
- Serological specificity using discriminatory monoclonal or polyclonal antibodies,
- Genome structure and organization (number and relative location of the ORFs),
- Amino acid sequence of relevant gene products (CP, CPm, HSP70h) differing

Argument to justify the creation of the new species:

by more than 10%,

- Vector species and specificity,
- Magnitude and specificity of natural and experimental host range,
- Cytopathological features (i.e., aspect of inclusion bodies and origin of cytoplasmic vesicles),

Bean yellow disorder is a disease of French bean (*Phaseolous vulgaris*) reported form Spain (Segundo *et al*., 2004). The causal agent, Bean yellow disorder virus (BnYDV), has properties similar to those of members of the genus *Crinivirus.* Criniviruses have never been reported previously from species of the family *Leguminosae*. BnYDV genome has recently been completely sequenced (Martin *et al*., 2008)

BnYDV properties

Virus particles: no information (expected to be filamentous)

(i) dsRNAs: observed but the size has not been reported (the lagest likely to be c. 9kbp and 8.5 kbp)

(ii) CP: 28.9 kDa (determined from deduced sequence data)

(iii)Nucleic acid: two molecules of ssRNA. RNA-1 8,965 nt in size and RNA-2 8,530 nt in size, respectively

(iv)Genome: bipartite made up of a total of 12 ORFs, three of which comprised in RNA-1 (accession No. EU191904) and 9 in RNA-2 (accession No. EU191905). Genome structure resembling that of members of the genus *Crinivirus* but with differences in the relative position of some ORFs.

(v) Phylogenetic relationships: BnYDV groups with members of the genus *Crinivirus* in trees constructed with RdRp sequences. The closest crinivirus species is *Cucumber yellow stunting disorder virus*, (CYSDV) with which BnYDV clusters in a distinct clade (see Annex)
At the amino acid level, these two viruses do not have similarity higher than 88% in CP, HSP70h, Hel and RdRp genes.

(vi) Serological relationships: no information.

(vii) Mechanical transmission: negative

(viii) Transmission by vectors: transmitted by *Bemisia tabaci*

(ix) Cytopathology: no information

(x) Natural host range: French bean

Although more biological information would be desirable, the above data support the notion that BnYDV is a crinivirus species of good standing.

References:

Martin G., Velasco L., Segundo E., Cuadrado I.M. and Janssen D., 12008. The complete nucelotide sequence and genome organization of bean yellow disorder virus, a new member of the genus *Crinivirus*. *Archives of Virology* **153**: 999-1001.

Segundo E., Martin G., Cuadrado I.M. and Janssen D., 2004. A new yellowing disease of *Phaseolus vulgaris* associated with a whitefly-transmitted virus. *Plant Pathology* **53**: 517

Annex:

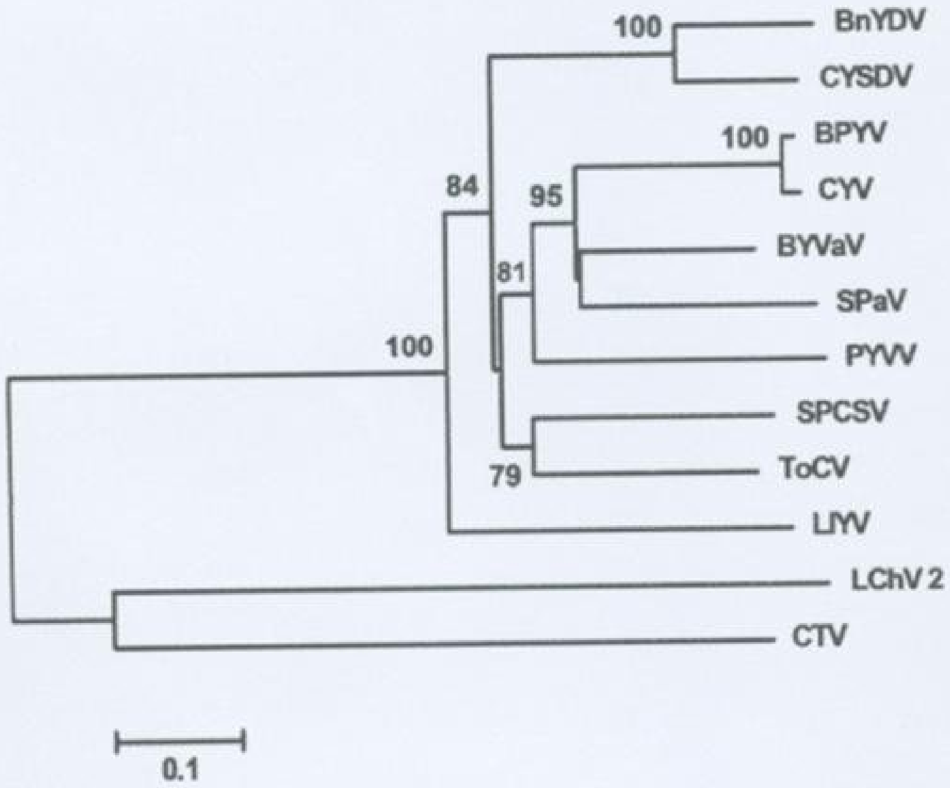

Fig. 2 Phylogenetic tree showing the relationship between BnYDV and other members of the family *Closteroviridae* based on their RdRp amino acid sequences. Virus abbreviations and GenBank accession numbers are: ampelovirus little cherry virus 2 (LChV-2, AAP87784); closterovirus citrus tristeza virus (CTV, NP733947); and criniviruses bean yellow disorder virus (BnYDV, ABY66960); beet pseudo-yellows virus (BPYV, NP940796); blackberry yellow vein associated virus (BYVaV, AAV40963); cucurbit yellow stunting disorder virus (CYS-DV, AAM73639); cucumber yellows virus (CYV, BAC66371); lettuce infectious yellows virus (LIYV, AAA61798); potato yellow vein virus (PYVV, CAD89680); strawberry pallidosis associated virus (SPaV, AY488137); sweet potato chlorotic stunt virus (SPCSV, NP733939); and tomato chlorosis virus (ToCV, AY903447). ClustalW was applied for phylogenetic analysis (neighbor-joining algorithm, Kimura's correction and bootstrap analysis consisting of 1,000 pseudoreplicates) in MEGA version 3.0. The values at the nodes indicate the percentage of trees in which this grouping occurred after bootstrapping (shown only when >50%). The *bar* represents 0.1 amino acid changes per site