Taxonomic proposal from the Furovirus SG, Plant Virus SC
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FT2003.002P.01.	to change the name of the virus which has been listed as Soil-borne rye mosaic virus (SBRMV) to *Soil-borne cereal mosaic virus* (SBCMV)
FT2003.003P.01.	to change the taxonomic position of *Soil-borne rye mosaic virus* (SBRMV) from the status of a Tentative Species in the Genus *Furovirus* to that of a Species in the Genus *Furovirus*.
FT2003.004P.01.	to list Soil-borne rye mosaic virus and European wheat mosaic virus as synonyms of SBCMV
FT2003.005P.01.	to add *Chinese wheat mosaic virus* (CWMV) as a Species in the Genus *Furovirus*
FT2003.006P.01.	to add *Oat golden stripe virus* (OGSV) as a Species in the Genus *Furovirus* and remove it from being a synonym/strain of *Soil-borne wheat mosaic virus*
FT2003.007P.01.	to change the taxonomic position of *Sorghum chlorotic spot virus* (SgCSV) from the status of a Tentative Species in the Genus *Furovirus* to that of a Species in the Genus *Furovirus*.

These suggested changes all arise from sequence data obtained since 1998

Proposals 1-3: wheat and rye infecting furovirus from Europe

The genome sequence of this virus has independently and simultaneously been analysed by Diao *et al.* (1999) and Koenig *et al.* (1999) (see attachments). Koenig *et al.* (1999) had proposed the name '*Soil-borne rye mosaic virus*' whereas Diao *et al.* (1999) had proposed the name '*European wheat mosaic virus'*. The sequences of three isolates analysed by Koenig *et al.* and of one isolate analysed by Diao *et al.* and further analyses made by Koenig and Huth (2000), Yang *et al.* (2001)* and Clover *et al.* (2001)* indicate that the various sources of this virus which have been obtained from wheat-growing areas in southern and western parts of Europe and from rye-growing areas in the more north-eastern parts of Europe (Germany, Poland and Denmark) share a high degree of sequence identity among each other amounting to more than 95% for most virus sources (with the only exception of RNA 2 of the German isolate G which is somewhat more different). All these very closely related European virus sources are clearly distinct from SBWMV and all other Furoviruses. The percentages of nucleotide sequence identity with SBWMV amount to c. 70% and 66% for RNAs 1 and 2, respectively (see attachments). Because Diao *et al.* (1999) and Koenig *et al.* (1999) had proposed different names (*Soil-borne rye mosaic virus* and *European wheat mosaic virus*) for what is obviously the same virus, both groups of researchers have later agreed that a new name, i.e. *Soil-borne cereal mosaic virus* (SBCMV) which does not imply restriction to a particular geographical region (Europe) or specificity for a particular host (rye) (Koenig and Huth, 2000; Yang *et al.*, 2001a*) should replace the originally proposed names. SBCMV differs from SBWMV also in some biologically properties, e.g. its ability to infect *N. benthamaina* and its inability to cause local lesions on *Ch. quinoa*.

Because SBCMV has the typical genome organisation of a Furovirus, it should be classified as a definitive species in the Genus Furovirus.

Proposal 4: wheat infecting furovirus from China

Sequences of two isolates of this virus (Diao *et al.,* 1999b*; Yang *et al.,* 2001b*) show it to be a typical Furovirus in genome organisation but differing from SBCMV, SBWMV and OGSV to a similar extent (see proposal 5).

Proposal 5: Oat golden stripe virus

At the time of the 7th ICTV report, the coat protein of OGSV had been sequenced and appeared similar to SBWMV (Chen et al., 1996). OGSV was therefore listed as a strain of SBWMV. Now that the complete sequence of the OGSV isolate has been determined (Diao *et al.*,1999) it seems that the earlier results were mistaken and have been retracted by the authors. OGSV, CWMV (proposal 4) and SBCMV (proposals 1-3) are approximately equidistant from one another and from SBWMV in molecular terms (60-70% nucleotide identity over the entire genome). OGSV infects oats and not wheat, so it is clear that there are biological differences between the viruses.

Proposal 6: Sorghum chlorotic spot virus

The genome sequence of this virus (Shirako *et al.*, 2000) clearly shows it to have the organisation of a furovirus but it differs substantially in sequence from the other viruses in the genus.

General comments

Proposal 6 is unlikely to be controversial. We believe that when 1-5 are considered together, they also make a logical and compelling case. Several European isolates of SBCMV have now been sequenced and they differ very little from one another compared to the differences between the proposed viruses. Likewise, two independent isolates of CWMV are also very similar to one another. Different isolates of SBWMV from the USA also show very high similarities, especially in their amino acid sequences (Koenig et al., 2002*). There is no evidence of a continuum between these sequences and this is strengthened by the recent discovery in Europe of a virus isolate that is highly similar (>98% nucleotides) to the SBWMV (USA) isolates (Koenig and Huth, 2003*). We therefore disagree with Y. Shirako *et al.* (2000) (also attached) who feels that the wheat-infecting viruses found in different parts of the world should all be regarded as strains of the same virus (see attachments Furoclass1.doc and Furoclass2.doc which Renate had sent to the members of the ICTV Furovirus study group).

*References in addition to those given in the attachments:

Clover GRG, Ratti C and Henry CM (2001) Molecular characterization and detection of European isolates of Soil-borne wheat mosaic virus. Plant Pathology 50: 761-7

Diao, A., Chen, J., Ye, R., Zheng, T., Yu, S., Antoniw, J.F. & Adams, M.J. (1999b). Complete sequence and genome properties of Chinese wheat mosaic virus, a new furovirus from China. Journal of General Virology 80: 1141-5

Koenig R, Bergstrom GC, Gray SM, Loss S (2002) A New York isolate of Soil-borne wheat mosaic virus differs considerably from the Nebraska type strain in the nucleotide sequences of various coding regions but not in the deduced amino acid sequences. Archives of Virology 147: 617-25

Koenig R and Huth W (2003) Natural infection of wheat by the type strain of *Soil-Borne Wheat Mosaic Virus* in a field in Southern Germany. European Journal of Plant Pathology (in press)

Yang J, Chen J, Cheng Y and Adams MJ (2001a) Sequence analysis of a soil-borne wheat mosaic virus isolate from Italy shows that it is the same virus as European wheat mosaic virus and Soil-borne rye mosaic virus. Science in China 44: 216-24

Yang, J., Chen, J., Chen, J., Jiang. H., Zhao, Q. & Adams, M.J. (2001b). Sequence of a second isolate of Chinese wheat mosaic furovirus. Journal of Phytopathology 149: 135-40

Ye, R., Zheng, T. Chen, J., Diao, A., Adams, M.J., Yu, S. & Antoniw, J.F. (1999). Characterization and partial sequence of a new furovirus of wheat in China. Plant Pathology 48: 379-87

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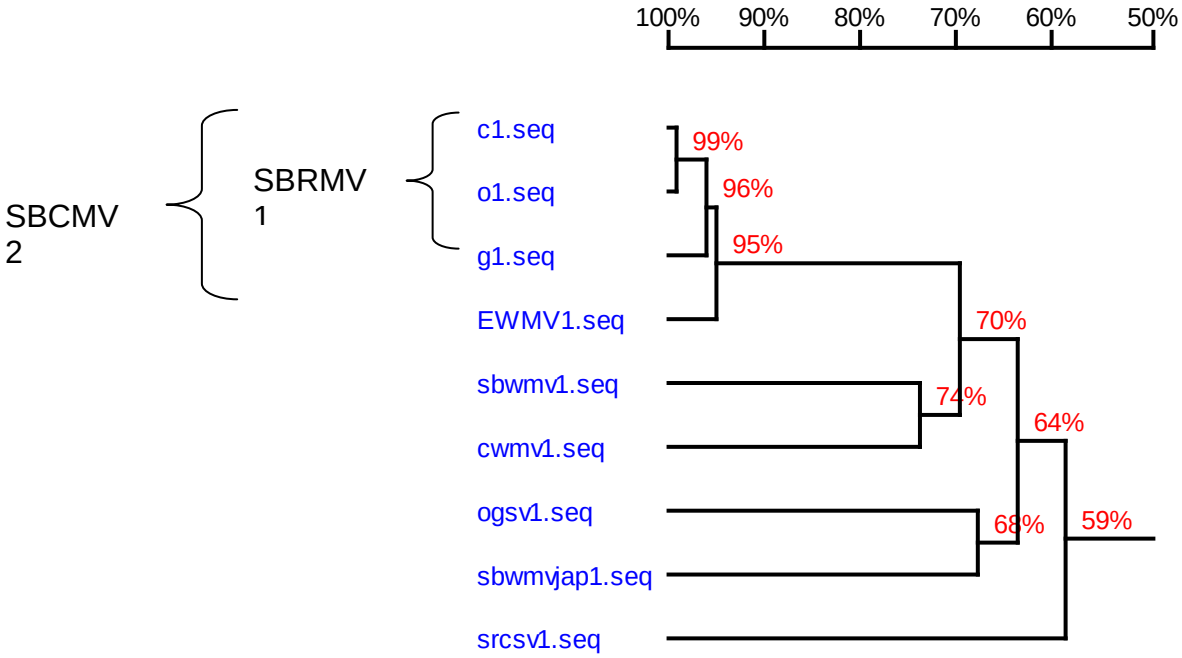
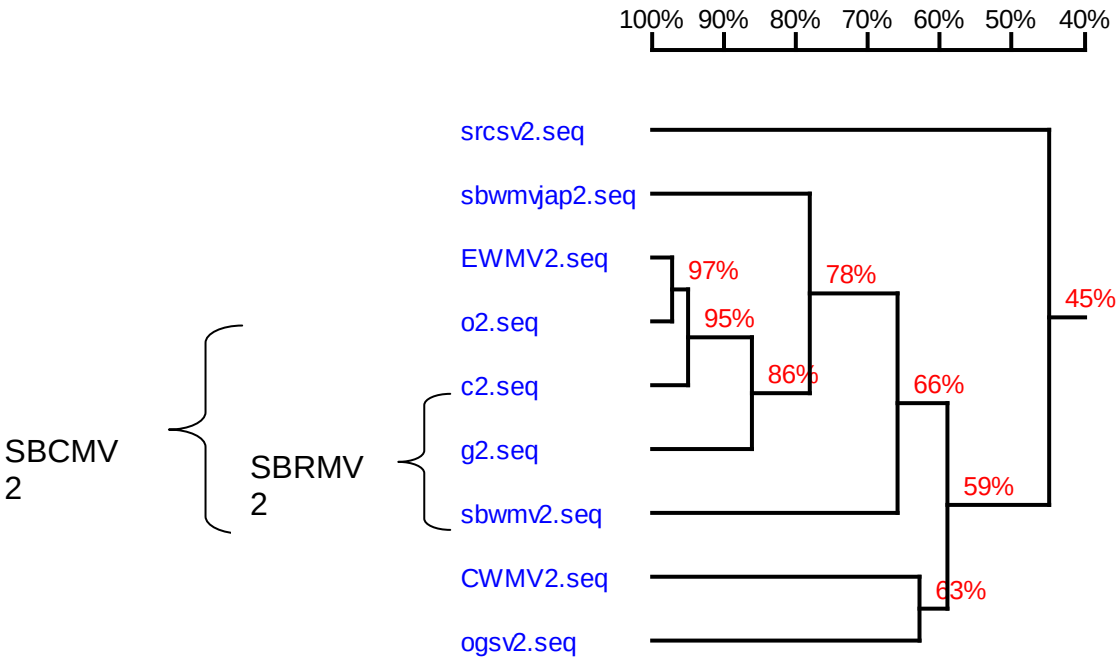
Percentage of Sequence Identities of Total RNAs of Furoviruses

RNAs 1



RNAs 2



Furovirus classification: the Shirako proposal versus the 'Koenig/Adams' proposal

The main difference between the 'Shirako' and the 'Koenig/Adams' proposals on Furovirus classification is that the former is mainly based on the exchangeability of RNAs for producing viable virus progenies whereas the latter is mainly based on pronounced sequence differences.

The sequence differences between the *Furovirus* isolates that Koenig and Adams propose as 'new viruses' (65 to 70 % over the entire genomes) are much larger than those used for the differentiation of virus species in many other genera (e.g. *Potyviruses, Tombusviruses, Tymoviruses*). It is recognised of course that sequence differences alone would be an inadequate basis for taxonomy in general, but in this case the degree of sequence difference is large and there are indications of related host-range differences. In addition, unpublished observations of W. Huth and D.E. Lesemann revealed that in immunoelectron microscopical decoration tests the homologous and heterologous titres of antisera to SBCMV and SBWMV with the respective viruses may differ by several twofold dilution steps.

For several reasons we doubt whether the exchangeability of RNAs is a good means for differentiating between 'virus strains' and 'virus species'.

1) This approach can be used only for viruses with a divided genome
2) The information obtained with this approach would probably depend on the distribution of genes between the various viral RNAs. Some genes encode proteins which are presumably much more interdependent than others. If, for instance, the coding sequences for the replication-associated enzyme regions (methyltransferase, helicase, polymerase) are distributed between two RNAs, an exchange of these RNAs between different virus species might be rather problematic. An exchange of RNAs which encode proteins which are presumably less interdependent, for instance capsid proteins on the one hand and replication-associated proteins on the other, may, however, be tolerated more readily. This is seen with the Cucumoviruses and Bromoviruses cited by Miyanishi et al. (Arch. Virol. 147, 1141, 2002). The RNA3s of these viruses which encode the coat proteins can - at least to a certain degree - be exchanged between different virus species whereas a reassortment of their RNA1s (containing the coding sequences for the methyltransferase and helicase regions) and their RNA2s (containing the coding sequence for the polymerase) does not yield viable progenies. With Furoviruses, the situation of an exchange of RNA 1, which contains (among others) the coding sequences for all replication-associated enzyme regions, and RNA 2, which contains (among others) the coat protein gene, seems to be more analogous to that of an RNA 3 exchange in the case of Cucumo- and Bromoviruses. It, therefore, appears to be doubtful whether the exchangeability of RNAs 1 and 2 of Furovirus isolates would be a good criterion for the classification of isolates as 'genetically distantly related strains' rather than distinct viruses.
3) Reassortment experiments are not an easy task. Even an expert like Yukio Shirako obtained viable progeny only with the RNA 1 of one Furovirus isolate and the RNA 2 of another, but not vice versa (Miyanishi et al., Arch. Virol. 147, 1141, 2002). If it were necessary to wait for the outcome of such reassortment experiments before deciding whether a new virus isolate should be considered as a 'genetically distantly related strain' or a 'new virus species', many new isolates

would remain with only a preliminary taxonomic status for a long time, and in many cases renaming would later be necessary. This would be very confusing for scientists as well as breeders and plant protection workers. Sequence information and serological data, on the other hand, are usually obtained in much shorter times and such studies will more easily be funded, because they are very important for practical work, e.g. designing PCRs and ELISA for routine diagnosis.

4) As has been pointed out many times, there may be no clear-cut border between 'new viruses' and 'new strains of known viruses' and the decisions we make between these man-made taxonomic categories will necessarily be quite often more or less arbitrary ones. In this case, a sufficient number of different sequences have been obtained from Europe, China and USA to indicate an evident discontinuity between the different isolates/viruses. It therefore seems unlikely that large numbers of intermediary isolates will be discovered that will confuse the boundaries. The decisions made should also take into account the practical needs of the people who have to work with them.