**2003.001P.01** To elevate *Tobacco bushy top virus* from Tentative Species to Species in the Genus *Umbravirus* 

**Background:** Tobacco bushy top disease was first described from Zimbabwe, Zambia and Malawi by Gates in 1962 (Ann. Appl. Biol. 50:169-174). The causal agent, Tobacco bushy top virus (TBTV), was classified as a tentative species in the Genus *Umbravirus* on the basis of its biological properties, specifically the failure to detect any nucleoprotein particles, transmission mechanically and by aphids, and the loss of aphid transmissibility after mechanical transmission.

In Zimbabwe and neighbouring countries, bushy top disease seems to have supplanted the previously prevalent rosette disease of tobacco, which is caused by *Tobacco mottle virus* (TMoV), a definitive member of the Genus *Umbravirus*. Moreover, both TBTV and TMoV seem to be associated with the same helper virus, tobacco vein-distorting virus (Cole, Phytopathology 52: 1312, 1962). There was therefore a strong possibility that TBTV was a variant of TMoV, or that the two diseases were caused by the same umbravirus in association with different satellite RNAs.

**New information:** Recently, a similar bushy top disease of tobacco was reported in the Yunnan province of China (Mo *et al.*, Plant Disease 86: 74, 2002). These authors have now confirmed that a virus associated with this disease has the same biological properties that are typical of umbraviruses as has TBTV from Zimbabwe. Moreover, they have determined the nucleotide sequence of the genome of the Yunnan virus (Mo *et al.*, Archives of Virology, in press; On-line version <a href="http://dx.doi.org/10.1007/s00705-002-0919-y">http://dx.doi.org/10.1007/s00705-002-0919-y</a>; Accession number AF431890). This genome has the typical organization of an umbravirus genome, and the predicted products of the ORFs all have significant sequence similarity to the equivalent products of definitive umbraviruses.

Conclusion: TBTV from Yunnan has all the characters of a member of the genus *Umbravirus*, and its genome nucleotide sequence is distinct from that of all other species in the genus, including TMoV. It clearly merits inclusion as a species in the genus. Its relationship to TBTV from Zimbabwe is presently unclear; work to resolve this point is in progress. However, because both viruses induce distinctive symptoms in *Nicotiana* species, notably proliferation of growth from axial buds, it seems likely that they are closely related and should be regarded for the time being as isolates of the same virus species.