

June 2002

From the *Luteoviridae* Study Group

2002.P081.03: Reclassify current *Barley yellow dwarf virus*-PAV strains in two different virus species. Strains with coat proteins similar to PAV-Aus would remain in *Barley yellow dwarf virus*-PAV, while those with coat proteins similar to PAV-129 would become *Barley yellow dwarf virus*-PAS.

2. Purpose:

- a. The coat protein sequences of virus strains previously called BYDV-PAV fall into two groups, with >90% amino acid sequence identity within groups and <90% between groups. This difference has now been found in studies of a range of isolates from five continents done in France (Mastari *et al.*, 1988) Morocco (Bencharcki *et al.*, 1999) and the U.S.A. (Chay *et al.*, 1996). Amino acid sequence identities of <90% have also been found in ORFs 1 and 2 (replicase) between the two groups (Miller, unpublished; see Genbank sequences).
- b. Differences in both host range and symptom severity have been reported for the two groups of strains. Chay *et al.* (1996) reported that symptoms of PAV-129 (proposed BYDV-PAS) infection on oats were more severe than those induced by PAV- NY. Mastari *et al.* reported a strong correlation between virus genotype and host plant species. Forty-nine of 50 isolates found in ryegrass belonged to one group of strains, whereas 50 of 60 French isolates in barley belonged to the other group. Bencharcki *et al.* reported that symptoms on barley and oats infected with one group of strains were much more severe (proposed BYDV-PAS) than those that developed after infection by strains in the other group.

3. A summary of the new taxonomic situation within the family, group or genus.

The genus *Luteovirus* would now have the following viruses: BYDV-MAV, BYDV-PAV and BYDV-PAS.

4. Derivation of any names proposed.

BYDV-PAS indicates both the nonspecific nature of the aphid transmission of these strains (by *Rhopalosiphum padi* and *Sitobion avenae*) and the severity of the symptoms they induce.

5. New literature references, if appropriate.

Bencharcki, B., J. Mutterer, M. El Yamani, V. Ziegler-Graff, D. Zoiu and G. Jonard (1999). Severity of infection of Moroccan barley yellow dwarf virus PAV isolates correlates with variability in their coat protein sequences. *Annals of Applied Biology* 134:89-99.

Chay, C.A., D.M. Smith, R. Vaughan and S.M. Gray (1996). Diversity among isolates within the PAV serotype of barley yellow dwarf virus. *Phytopathology* 86:370-377.

Mastari, J., H. Lapierre and J.T. Dessens (1998). Asymmetrical distribution of barley yellow dwarf virus PAV variants between host plant species. *Phytopathology* 88:818-821.

Also, see Genbank accession numbers:

PAV-Aus	X07653
Pav-129	NC_002160

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From the *Luteoviridae* Study Group

2002.P082.03: Classify the non-beet-infecting strains of *Beet western yellows virus* as a separate species in the *Polerovirus* genus, to be renamed *Turnip yellows virus*.

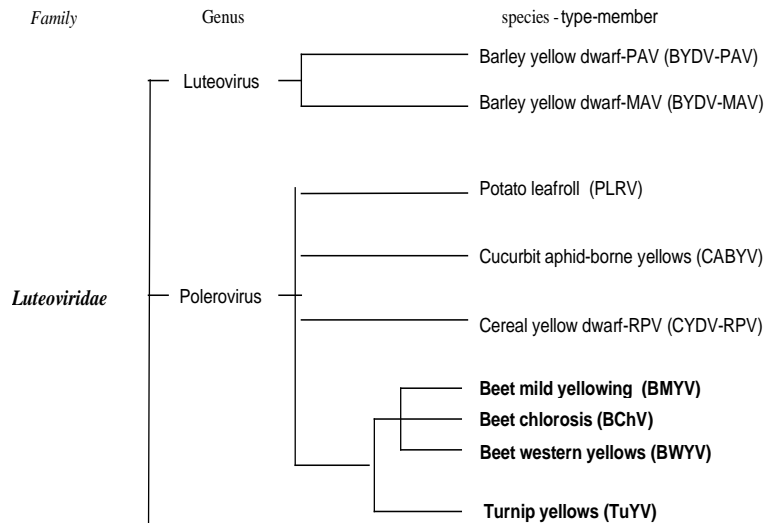
2002.P083.03: Include a new species in the *Polerovirus* genus: *Beet chlorosis virus*.

2. Purpose:

- a. American isolates of *Beet western yellows virus* (BWYV) cause stunting and chlorosis in a large number of crop plants, including sugar beet, spinach, lettuce and broccoli. European BWYV isolates also infect a broad range of commercially important crops, such as *Brassica species* (e.g. oilseed rape) and lettuce, but do not infect sugar beet.
- b. Recently, sequence data of a number of geographically distinct beet polerovirus isolates have shown that the coat protein amino acid sequences are highly conserved (>90% identity), whereas the P0 sequences (open reading frame, ORF 0) are highly variable; isolates within P0 clusters exhibit similar biological and serological properties. The complete genomic sequence of a BWYV sugar beet-infecting isolate from the U.S. has also been obtained recently, and showed that it is distinct from isolates of BWYV that do not infect sugar beet in the U.S. and Europe. The U.S. isolate shares significant sequence homology (greater than 89%) with other beet poleroviruses within the structural proteins at the 3' end, but less than 40% homology in P0, P1 and P2 at the 5' end. It is proposed that the name BWYV be retained for sugar beet-infecting isolates from the U.S., and that the name *Turnip yellows virus* be used for non-beet-infecting isolates.
- c. It is also proposed that a new species be included in the *Polerovirus* genus. Similar viruses named *Beet chlorosis virus* (BChV) that produce pale symptoms on sugar beet were identified in 1989 in England and the U.S. English BChV failed to react with the monoclonal antibody BYDV-PAV-IL-1 (hence, similar to BWYV), and did not infect the traditional indicator species *Montia perfoliata* and *Capsella bursa-pastoris*. BChV from the U.S. was found to be serologically related to BWYV, but had a narrower host range than American BWYV. Like the European BChV, the American isolate failed to infect *C. bursa-pastoris*, which is infected by American BWYV. Comparisons of the coat protein and ORF 0 sequences of BChV, BWYV and *Beet mild yellowing virus* (BMYV) showed that the three viruses were closely related in the CP (>90% amino acid sequence identity), but there was little sequence homology in the predicted P0 amino acid sequences. More recently, the complete genomic sequences of an American and a European isolate of BChV have been deduced (Hauser et al., 2002). The genomic organization of BChV identifies it as a typical *Polerovirus*.

3. A summary of the new taxonomic situation within the family, group and genus.

The genus *Polerovirus* would now have the following viruses: BChV, BMV, BWYV, CABYV, CYDV-RPS (see proposal 3), CYDV-RPV, PLRV and TuYV.



Note: The proposed *Luteovirus* BYDV-PAS (proposal 2) and the proposed *Polerovirus* CYDV-RPS (proposal 3) are not included in this figure.

4. Derivation of any names proposed.

The name *Turnip yellows virus* (TuYV) is proposed for European isolates of BWYV because this acronym has already been used in the literature (Vanderwalle, 1950; Rabenstein *et al.*, 1996), these isolates do not infect sugar beet and can produce chlorotic and/or red discoloration of brassica leaves.

The name *Beet chlorosis virus* (BChV) has been used in the literature, and was proposed due to the symptoms of interveinal chlorosis observed on infected sugar beet leaves.

5. New literature references.

Beuve, M., C. Schwartz, S. Hauser and O. Lemaire (2001). Caracterisation et repartition des Polerovirus de la betterave en Europe et aux USA; mise en evidence d'une nouvelle espece endemique aux USA. in proceedings of the 8eme Rencontres de Virologie Vegetale, held at Aussois, France, 11-15 March 2001, p. 17.

Hauser, S., M. Stevens, C. Mougel, H.G. Smith, C. Fritsch, C. E. Herrbach and O. Lemaire (2000). Biological, serological and molecular variability suggest three distinct polerovirus species infecting beet or rape. *Phytopathology* 90:460-466.

Hauser, S., M. Stevens, M. Beuve and O. Lemaire (2002). Biological properties and molecular characterisation of Beet chlorosis virus (BChV). *Archives of Virology*. 147:745-762.

Hauser, S. C. Weber, G. Vetter, M. Stevens, M. Beuve and O. Lemaire (2000). Improved detection and differentiation of poleroviruses infecting beet or rape by multiplex RT-PCR. *Journal of Virological Methods* 89:11-21.

Lemaire O., M. Beuve, M. Stevens and S. Hauser (2001). Les Polerovirus de la betterave; la fin d'une polemique? in proceedings of the 8eme Rencontres de Virologie Vegetale, held at Aussois, France, 11-15 March 2001, p. 60.

Liu, H.Y., G.C. Wisler, J.L. Sears J.E. and Duffus (1998). A new yellowing disease of sugarbeet caused by a luteovirus. *Phytopathology* 88:S54.

Liu, H.Y., G.C. Wisler, J.L. Sears and J.E. Duffus (1999). Beet chlorosis virus - a new luteovirus affecting sugarbeet. *J. Sugar Beet Research* 36:69.

Schubert, J., F. Rabenstein, K. Graichen and K. Richter (1998). Comparison of the 5'-end nucleotide sequences of luteoviruses from oilseed rape and sugar beet. *Arch. Phytopathol. Planzenschutz* 31:519-530.

Also, see Genbank accession number:  
BWYV-USA AF473561