sont principalement associés aux zones non chlorotiques, mais occasionnellement, il a été remarqué des amas dans des zones non chlorotiques bordant les stries ; ces zones étaient probablement à un stade précoce d'infection.

La densité des inclusions virales a pu être évaluée en microscopie optique sur des coupes semi-fines après marquage à l'or colloïdal et amplification avec un sel d'argent. On détecte au plus, par plan de coupe de feuille de la lignée résistante, une inclusion par faisceau vasculaire (y compris le mésophyle et l'épiderme voisins), alors que l'on en détecte jusqu'à 6 chez une plante sensible. Cette différence suggère une résistance à la multiplication du virus.

Complexity in evaluating resistance of barley (*Hordeum vulgare* L) to 2 pathotypes of BYDV-PAV: allelic variability at the *Yd2* gene locus. BA Chalhoub [1*], A Sarrafi [3], HD Lapierre [2] *([1] INRA, unité de génétique et amélioration des plantes; [2] INRA, unité de pathologie végétale, INRA, route de Saint-Cyr, F-78026 Versailles cedex; [3] ENSA, laboratoire de biotechnologie et amélioration des plantes, 145, avenue de Muret, F-31076 Toulouse cedex, France)*

The inheritance of resistance in barley (*Hordeum vulgare* L) to 2 pathotypes of the PAV-serotype of barley yellow dwarf virus (BYDV) was investigated. Six barley lines, which differ in their response to pathotypes RG and 2t of BYDV-PAV, were utilised in this study. Vixen, carrying the *Yd2* gene of resistance and 80-81BQCB10 are partially resistance to both pathotypes in growth chamber and field tests. Chikurin Ibaraki 1 and Carré d'hiver are susceptible to isolates 2t only in field conditions, whereas Plaisant and Ea52 (which is an induced mutant of Chikurin Ibaraki 1) are susceptible to both isolates.

Crosses were made among these cultivars and the F1 and F2 plants were tested against the 2 BYDV-PAV pathotypes in both growth chamber and field conditions.

Segregations against the pathotype RG

All F2 plants from crosses between the genotypes Vixen, 80-81BQCB10, Chikurin Ibaraki 1 and Carré d'hiver were resistant to isolate RG in growth chamber and field conditions. The F2 plants from crosses between the susceptible genotypes (Plaisant and Ea52) and the resistant ones (Vixen, 80-81BQCB10, Chikurin Ibaraki 1 and Carré d'hiver) segregate at a ratio of 1 resistant to 3 susceptible to the pathotype RG. This suggests that the resistance of each of these cultivars is controlled by single recessive gene.

Segregations against the pathotype 2t

Segregations against isolate 2t in the growth chamber tests were similar to those observed against isolate RG. In field conditions, only Vixen and 80-81BQCB10 were resistant to isolate 2t, and F2 plants from their cross were always resistant. The F2 plants of crosses between these 2 lines and the other lines segregate in a ratio of 1 resistant to 3 susceptible. All the other F2 plants were susceptible to isolate 2t in field conditions.

These results indicate that 80-81BQCB10 contains the same gene of resistance as that of Vixen *(Yd2)*. On the other hand, Chikurin Ibaraki 1 and Carré d'hiver contain the same gene of resistance, which is also allelic to the *Yd2* gene in Vixen and 80-81BQCB10. However, it differs from the *Yd2* gene in Vixen and 80-81BQCB10 by being overcome by isolate 2t in field conditions.

The nucleotide sequence and proposed genome organisation of oat chlorotic stunt, a new soil-borne virus of cereals. N Boonham [1], CM Henry [2], KR Wood [1] *([1] School of Biological Sciences, The University of Birmingham, Edgbaston, Birmingham, B15 2TT; [2] Central Science Laboratory MAFF, Hatching Green, Harpenden, Herts, AL5 2BD, UK)*

The complete nucleotide sequence of a new soil-borne virus of cereals has been deduced. The genome consists of a monopartite positive-sense single-stranded RNA molecule, of 4 114 nucleotides in length. The genome contains 4 putative open reading frames (ORFs). The first ORF at the 5'-end of the genome (ORF1) encodes a protein with a predicted M_r of 23 476 kDa (p23). The second ORF is punctuated by the amber termination codon of ORF1 and encodes a protein of predicted M_r of 84 355 kDa (p84). The third ORF (ORF3) is situated at the 3'-end of the genome and encodes a protein of predicted M_r 48 231 kDa (p48). The final ORF (ORF4) is nested within ORF3 and codes for a protein with predicted M_r of 8 220 kDa (p8). The functions of ORF2 and ORF3 have been established; ORF2 contains amino acid sequence motifs characteristic of the RNA-dependent RNA polymerases of positive-strand RNA viruses. ORF3 has been identified as the coat protein both by direct peptide sequencing and also

amino acid sequence similarities. Comparisons of the peptide sequences within these regions highlight similarities with members of the carmovirus and tombusvirus groups. However, the genome size and predicted strategy seem intermediate between the 2 groups. We propose the name of oat chlorotic stunt for the new virus and suggest that although evolutionarily related to both the tombusviruses and the carmoviruses, it is distinct from both and should therefore not be classified within either group. Epidemiological studies at one of the infected sites have shown that the virus causes mainly root localised infection, and only in a small number of cases does it cause systemic infection. Infection is not limited to oats; although this seems to be the major host, infection is also detected in winter wheat and winter barley.

Some properties of *Lolium* latent virus. W Huth, DE Lesemann, R Götz, HJ Vetten *(Biological Research Center for Agriculture and Forestry, Institute for Biochemistry and Plant Virology, Messeweg 11/12, D-38104 Braunschweig, Germany)*

Lolium latent virus (LLV) was found during investigations on ryegrass mosaic virus (RMV) and hitherto it was only detected on *Lolium perenne* and *L multiflorum* collected in breeding stations in Germany and the Netherlands. From a total of 348 virus-infected plants of *L perenne* 20 (6%) plants were infected exclusively by LLV, 183 (52%) by RMV only whereas 145 (42%) plants were dually infected by both viruses, LLV and RMV.

LLV is mechanically transmissible but with crude plant extract in general a low proportion of inoculated plants becomes infected. *L multiflorum* is more susceptible than *L perenne*. Whereas infected *Lolium* spp remain symptomless, the more susceptible *Bromus* spp, *Briza maxima*, oat, barley, rye and some other Poaceae reacted with mild streaks on their leaves. On leaves of infected *L multiflorum* grown in the greenhouse yellow spots were occasionally observed. Unusually for virus diseases these spots appear on old leaves only and led to an earlier senescense of these. Plants of *Lolium* spp dually infected by LLV and RMV showed reduced growth and intensified RMV symptoms. White streaks on the youngest still rolled leaves are predominant symptoms of dually infected plants.

LLV is also easily transmissible to some dicotyledonous plants. After inoculation on leaves of *Gomphrena globosa* local lesions with red margins appear. *Chenopodium amaranticolor*, *Nicotiana benthamiana* and *Tetragonia expansa* develop systemic infections. The latter is especially useful as propagation host.

A natural vector of LLV has not yet been found although preliminary transmission studies indicate that *Rhopalosiphum padi* might very ineffectively transmit the virus to *L multiflorum* (8 of 508 plants became infected).

The flexible particles of LLV have a normal length of *ca* 640 nm. Their surface structure with cross-banding and longitudinal files resembles that of potexviruses. From foxtail mosaic virus (FMV), the only definite potexvirus of Poaceae, LLV differs in particle length (FMV *ca* 550 nm) and the molecular weights of coat protein (LLV 35 kDa, FMV 32 kDa) and nucleic acid (LLV 2.7×10^6 kDa, FMV 2.1×10^6 kDa).

LLV is not serologically related to FMV or to 25 definite or possible members of the potexivirus group as well as to 25 members of the carlavirus group.

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Paulsen AQ, Niblett CL (1977) Purification and properties of foxtail mosaic virus. *Phytopathology* 67, 1346-1351

Interaction of BYDV and *Fusarium culmorum* in winter wheat. N Koch, W Huth *(Federal biological Research Center, Institute for Biochemistry and Plant Virology, Messeweg 11/12, D-38104 Braunschweig, Germany)*

Although BYDV is one of the most common pathogens of cereals in Germany, epidemics of this virus have been very rare. Nevertheless there was a serious outbreak over 3 years from 1988–1990 and it was not barley but mainly wheat which reacted with strong symptom expression upon infection (Huth, 1990). In some regions reddening of flag leaves, the most prominent symptom of BYDV infection of wheat, was found on most of the plants; surprisingly the late-sown wheat was much more affected than the early-sown one.

During these epidemic wheat was infected at late growth stages from May to July. Nevertheless in some fields yield reductions over