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