Effect of combining two genes for partial resistance to BYDV-PAV derived from *Thinopyrum intermedium* in wheat

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Introduction

The *Barley yellow dwarf virus*-PAV (BYDV-PAV) is the most widespread virus in Western Europe (Henry et al., 1993) and in China (Du et al., 2007). Infection with BYDV-PAV induces a reduction of root length and of the number root shoots correlated with a reduction of tiller growth (Hoffman & Kolb, 1997). No high level of resistance has been found in wheat. However, high levels of resistance were found in perennial Triticeae of Agropyron sensu lato group, including Thinopyrum and Lophopyrum. Two sources of resistances from *Thinopyrum intermedium* (2n = 42, JJ^{b}S^{t}S^{t}) were exploited in wheat breeding. Firstly, wheat lines containing *Th. intermedium* translocation and BYDV-PAV resistance were obtained by Banks et al (1995). Line TC14 had the smallest translocation, located in the distal part of the 7DL. The 7DL translocated chromosome carries the *Bdv2* gene for resistance to BYDV-PAV and was designated T7DS.7DL-7Ai#1L. Secondly, 3 disomic addition lines, called Z1, Z2 and Z6, were obtained from the amphiploid Zongh5 between *Triticum aestivum* and *Th. intermedium* (Larkin et al, 1995). These lines carried the same added group-2 chromosome, 2Ai#z which carries BYDV-PAV resistance. Both sources of resistance reduce development of the virus in the plant but the genes for resistance have different effects. Therefore, their association is postulated as a mean to achieve a higher level of resistance to BYDV -PAV than either source alone.

Materials and methods

Lines used for the development of a line carrying *Bdv2* gene on the translocated chromosome 7DS.7DL-7Ai#1L and the 2Ai#z chromosome were TC14 (*Bdv2*), Z6 (2Ai#z) and the French wheat c.v. Mission used as background. To evaluate BYDV-PAV resistance of the extracted line, lines as the ditelosomic addition line ZH derived from Z6, the Australian c.v. Sunstar (background of TC14) were added. *Genomic in situ hybridization* (GISH) was carried out using total genomic DNA of *Pseudoroegneria stipifolia* (2n = 14, S^{t}S^{t}) was used as probe to visualize alien chromatin in ZT, Z6 and TC14. To select lines carrying both introgression, the SCAR AD2, converted from RAPD AD2$_{800}$ was developed and mapped in F2/F3 population of 123 plants derived from a cross between TC14 and the susceptible variety cv. Rendezvous. Bioassays for resistance to BYDV-PAV were carried out using 5 French BYDV-PAV isolates. The efficiency of the two sources of resistance was evaluated by a semi-quantitative DAS-ELISA test at 5 time-points at 7 to 21 days after inoculation (DAI) and the area under pathogen incidence progress curve (AUPPC) was calculated to described disease progress.

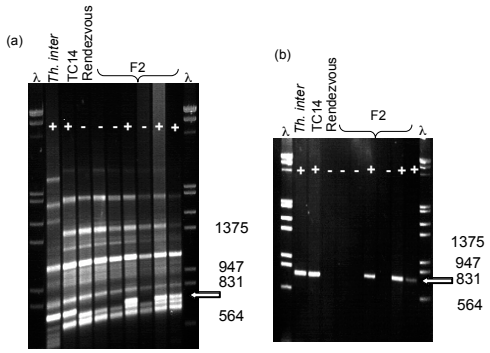

Figure. 1, Amplification patterns generated by RAPD AD2 (a) and SCAR AD2 (b) in parental lines wheat c.v. Rendezvous and *Thinopyrum intermedium*, translocation line TC14 and in the F2/F3 Rendezvous x TC14 population. Arrows indicate band used for plant screening. (Jahier *et al.*, 2009)

Results

*** Development of a line carrrying chromosomes 7DS.7DL-7Ai#1 and 2Ai#z**

The F1 hybrid between the disomic addition line Z6 and TC4 was backcrossed to Z6. In the BC1F4 generation, one plant had 44 chromosomes and the SCAR AD2 (Fig.1). A stable line designated ZT was selected in its selfed progeny. By GISH using St-genome DNA as probe, we showed that ZT line contained 2Ai#z (line Z6) and 7DS.7DL-7Ai#1L (line TC14) chromosomes which were not modified during the development of ZT (Fig. 2)

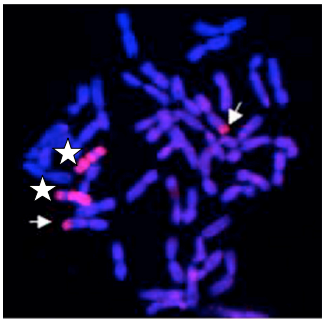

Figure. 2, Visualization by GISH of the added chromosome 2Ai#z (stars) and the translocated chromosome 7DS.7DL-7Ai#1L (arrows) in the line ZT.

*** Resistance analysis of the pyramided line ZT**

The AUPPC values for the line ZT carrying both genes for BYDV resistance were lower than ZH and TC14 lines for 4 isolates and significantly lower for one isolate (Table 1). For all isolates pooled, ZT had an AUPPC significantly lower than ZH and TC14. AT 21 DAI, virus was detected in 95% of plants of Sunstar, compared with 80, 71 and 42% of ZH, TC14 and ZT, respectively.

Table 1: Mean values of the area under pathogen incidence progression curve (AUPPC) for each Barley yellow dwarf virus (BYDV)-PAV-isolate/wheat-host combination and group means for each host and each isolate. [1]Means followed by the same letter are not significantly different (Bonferroni test, P=0.05); [2]Number of replicates of 20-plants lots.

HOST	BYDV-PAV isolate					Group means
	PAV13	PAVRG	PAV4	PAV2T	PAV6	for hosts
Sunstar	950.3 ^{a1}	879.5 ^{a}	761.1 ^{a}	980.3 ^{a}	904.0	869.9 ^{a}
ZH	263.8 ^{b}	315.8 ^{ab}	313.3 ^{b}	725.3 ^{a}	812.5	425.0 ^{b}
TC14	177.0 ^{b}	334.5 ^{ab}	316.0 ^{b}	684.5 ^{a}	565.0	383.7 ^{b}
ZT	82.0 ^{b}	135.8 ^{b}	139.5 ^{b}	157.0 ^{b}	282.5	144.6 ^{c}
Replicates[2]	2	2	4	2	1	
Mean	368.3 ^{a}	416.4 ^{ab}	382.5 ^{a}	636.8 ^{b}	641.0 ^{b}	

Conclusions - Prospects

The line ZT (2n = 44) carrying both ZH and TC14 resistances was selected. The resistance of line ZT combined a significantly lower % of infected plants and a very low virus titre than the parental lines TC14 and ZH. A SCAR AD2 cosegregates with the SSR *Xgwm37* (Ayala et al, 2001). Both became the most suitable markers for wheat breeding. The development of a wheat line with 42 chromosomes carrying both Z6 and TC14 is in progress and may be of great interest for breeding wheat genotypes with a high level of resistance.

References

Ayala L, Henry M, Gonzales de Leon D *et al* (2001). Theoretical Applied Genetics 102, 942-949.
Banks PM, Larkin PJ, Bariana HS *et al* (1995). Genome 38, 395-405.
3059.2009.02084.x
Du ZQ, Li L, Liu L, Wang XF, Zhou G (2007). Journal of Plant Pathology, 89, 251-259.
Henry M., George S, Arnold GM *et al* (1993), Annals of Applied Biology, 123, 315-329.
Hoffman TK and Kolb FL (1997). Plant Disease 81, 497-500.
Jahier J, Chain F, Barloy D, *et al* (2009), Plant Pathology, Doi:10.1111/j1365-
Larkin PJ, Banks PM, Lagudah ES *et al* (1995). Genome 38, 385-394.