Transfer of the *Aegilops ventricosa* gene *Yr17* to wheat chromosome 2D

Jahier J., Verplancke G., Paillard S., Dedryver F.

INRA, UMR 118, Amélioration des Plantes et Biotechnologies Végétales, BP 35327, 35653 Le Rheu, France

Introduction

The tetraploid species *Aegilops ventricosa* is closely related to bread wheat (2n = 42, AABBDD) since its genomic constitution is $D^vD^vN^vN^v$ with D^v and N^v genomes partially homologous to the D genome of *Ae. tauschii* and to the N genome of *Ae. uniaristata* respectively. As demonstrated by the isolation of the wheat parent VPM1 in the progeny of *Ae. ventricosa* / *Triticum persicum* // 3* *T. aestivum*, *Ae. ventricosa* is the donor of valuable agronomic genes to bread wheat (Maia 1967). These include *Pch1*, the only major gene for resistance to eyespot (Jahier *et al* 1978) and the *Yr17*, *Lr37*, *Sr38*, *Cre5* gene cluster conferring resistance to yellow, leaf, and stem rusts and cereal cyst nematode (Bariana and McIntosh 1993; Jahier et al 1996). The genes *Yr17*, *Lr37*, *Sr38*, *Cre5* are carried by a translocated chromosome in *Ae. ventricosa*. The structure of this chromosome, designated $6N^v$ was defined as being $6N^v$Sdel.$6N^v$L-$2N^v$S with $2N^v$S carrying the four genes (Tanguy *et al* 2005). Any spontaneous transfer from N^v would be expected to occur into D genome. However the genes *Yr17+Lr37+Sr38+Cre5* initially carried by the translocated chromosome $6N^v$ were transferred to chromosome 2AS of the parent VPM1 and of derived varieties as cv. Renan. An experiment was carried out to check whether the introgression systematically occurs on the A genome.

Fig. 1- Ears of *Ae. ventricosa*

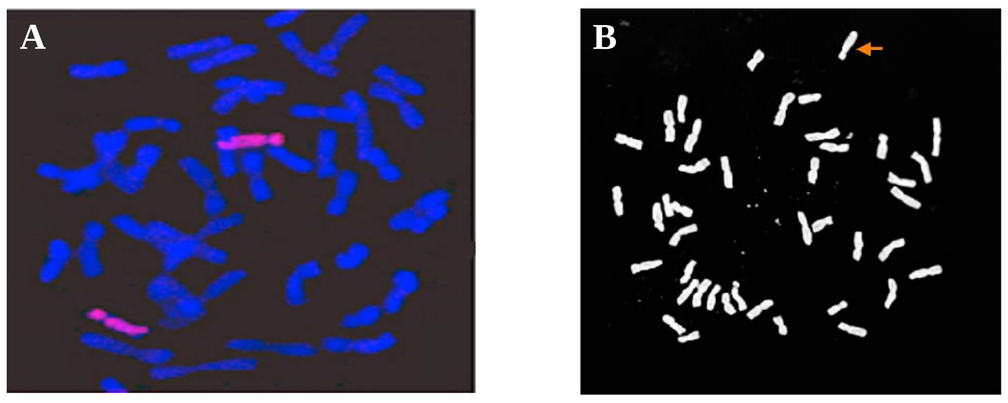

Fig. 2-A, Visualization (GISH) of the $6N^v$ pair in the addition line, **B**, Root-tip cell of a double monosomic 2B -$6N^v$ plant ($6N^v$ arrow)

Materials and methods

Chromosome $6N^v$ was added to the wheat complement in the rust susceptible background cv. Fidel. That addition line was crossed to monosomics 2A, 2B and 2D of cv. Courtot. Within the F1 plants, double monosomic 2A-$6N^v$, 2B-$6N^v$ and 2D-$6N^v$ plants were selected using chromosome counting and backcrossed to cv. Fidel.

The three BC progenies composed each of 1500 plants were grown in the field and inoculated at the adult plant stage with the yellow rust pathotype 237E141 AV17. Plants resistant at two node stage and not obviously possessing distinctive traits conferred by $6N^v$ (height, pale-green leaf, long peduncle) were selected.

Results

Selection of putative recombinant

61, 65 and 97 putative recombinants were selected in the families 2A-$6N^v$, 2B-$6N^v$ and 2D-$6N^v$ before the meiosis stage. Anthers at the MI stage of meiosis were collected on each plant. Meiotic analysis revealed that most selected plants were double monosomics or addition plants. Only two plants in the 2D-$6N^v$ family were considered as putative recombinants. The first one was with 43 chromosomes, but a careful examination of the added chromosome showed that it was a deleted $6N^v$. If the deletion concerned the region carrying the genes for resistance, then the plant could be a recombinant. The second plant was with 42 chromosomes forming 21 bivalents at meiosis.

The progenies of these two plants were sown in pots and their chromosomes counted from root tips. They were transplanted in the field and evaluated again for resistance. The 43-chromosome progeny had plants with different number of chromosomes (42, 43, 44) and only plants with 43 and 44 chromosomes were resistant. That demonstrated that the first selected plant was not a recombinant. The recombinant status of the second selected plant was confirmed since its progeny was euploid (42 chromosomes) and segregated for resistance. In the following year, a line fixed for resistance was selected.

Evidence of a 2D-$6N^v$ recombinant

Molecular markers of the introgression in VPM1 as well as group 2S wheat specific markers were used in order to localize the novel introgressed segment. It was found that the distal part of chromosome 2DS had been replaced by a *Yr17*-carrying *Ae. ventricosa* chromosome segment of same or similar size as that in VPM1. Physical mapping is still in progress.

Table 1: Detection of the *Ae. ventricosa Yr17*-carrying segment into the wheat chromosome 2D using group 2 microsatellite markers.

microsatellites	*Aegilops ventricosa* allele	2AS wheat alleles	2DS wheat alleles
gpw7617	**present**	+	
cfd36	**present**	+	-
gwm455			-
gwm210	**null allele**	+	
barc212	**null allele**	+	
gdm5	**null allele**	+	-

+ presence of Courtot or/and Fidel alleles; - absence of Courtot and Fidel alleles

The resistance of the recombinant line was not effective at the seedling stage, when the 237E141 V17 pathotype possessing the virulence to *Yr17* was used. That demonstrated that the *Yr17* gene was present in the recombinant line.

Conclusions - Prospects

Our experiment showed that spontaneous recombination between $6N^v$ and wheat group 2 chromosomes is a rare event and that *Yr17* may be introduced either in 2A or in 2D. Further characterization is needed to know whether the translocation point on chromosome $6N^v$ is identical in both transfers (2A and 2D). In case the length of the introgressed segment is shorter than that of VPM1, it will be a useful tool to more precisely locate the gene(s) for resistance. The introgressions on 2A and 2D will be introduced in the same background in order to develop near isogenic lines. The objective will be to compare expression of the genes for resistance against yellow and/or leaf rusts and the agronomical value of both transfers.The novel material offers the possibility to produce and evaluate genotypes with an increased copy number of *Yr17* and/or *Lr37* . The feasibility of achieving that goal will depend on the occasional pairing between the *Yr17*-carrying chromosomes 2A and 2D.

References

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