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MULTIPLE RESISTANCE TO POWDERY MILDEW, LEAF RUST AND STEM RUST IN WHEAT CONFERRED BY GENES ON CHROMOSOME 6V INTROGRESSED FROM *DASYPYRUM VILLOSUM*

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Stem rust caused by *Puccinia graminis* f.sp. *tritici* (*Pgt*) was effectively controlled worldwide, for the past half century, by systematically introducing stem rust resistance (*Sr*) genes in wheat cultivars. However, a new stem rust race, known as Ug99 or TTKSK is becoming a new potential threat to wheat production because it has broad virulence to currently deployed *Sr* genes. It has been shown that introgression of 6V chromosome into wheat genome bestow slow rusting type resistance to TTKSK isolate. Leaf rust and powdery mildew due to *Puccinia triticina* (*Pt*) and *Blumeria graminis* f.sp. *tritici* (*Bgt*) fungal infections, are also important diseases affecting wheat worldwide. The incorporation of effective resistance genes to these diseases into wheat is a breeding strategy for can be achieved using gene introgression from wild related species.

We report that chromosome 6V#4 from a *Dv* ecotype collected in Latium, when introgressed in *T. aestivum* cv. Chinese Spring (CS), determines multiple and simple inherited resistance to virulent races of *Bgt*, *Pt* and *Pgt*. Two wheat introgression inbred lines (IBL*s*), the 6V#4 disomic addition line CS-DA6V#4 and the monosomic 6V#4 substitution line CS-MS6V#4(6B) were studied. The former line was completely resistant to *Bgt* at seedling and adult plant stage, to *Pt* at adult plant stage (APR), and to *Pgt* at seedling stage. The latter line showed the same pattern of resistance as CS-DA6V#4, although its selfed progenies segregated due to the monosomic condition of the 6V#4.

The CS-DA6V#4 line was crossed to the susceptible CS-DA6V#1 line, obtained by Sears by utilizing a different *Dv* ecotype. An F_2 mapping population, segregating for response to *Bgt* infection, was obtained. The segregation fitted a 3:1 monogenic inheritance. These data suggest the presence of one dominant gene for resistance to powdery mildew (indicated *"PmVt*" and probably allelic to *Pm21* known gene). Molecular analysis using both the marker $OPH17_{1900}$ and $NAU/Xibao15_{902}$ (reported as linked to *Pm21*) were carried out to confirm the location of *"PmVt*"on the 6VS. In our 6V materials, $OPH17_{1900}$ was not linked to *PmVt*. $NAU/Xibao15_{902}$ was detected by PCR in both parental lines, amplicons displayed the same molecular weight but with significant difference in band intensity between the two parental lines, the CS-DA6V#1 expressing the fainter band. $NAU/Xibao15_{902}$ primers targeted a DNA sequence encoding for a serine-threonine kinase enzyme that might be involved in the resistance response. The amplified $NAU/Xibao15_{902}$ DNA fragments showed differences in the nucleotide sequences at the exons 3 and 4 which include the regions complementary to the primers. A nucleotide mutation in one of the primer pairing site in CS-DA6V#1 might explain the fainter band. Further molecular analyses are in progress. The F_3

progeny, from the F_2 mapping population, was naturally infected by *Pt* in the field. The APR response implied that resistance was not due to genes already present in CS, which was susceptible, but it was encoded at a locus on the 6V#4. Resistance to *Pgt* was observed in CS-DA6V#4 line by controlled infection at the seedling stage at CRA-QCE, and at the adult stage of CS-MS6V#4(6B) at ARI-HAS, using a total of four different isolates. Therefore 6V#4 is extremely important to deploy genes for multiple resistance to new virulent races of fungal pathogens in wheat germplasm.