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Chromosomal location of a gene for resistance to septoria tritici blotch (*Mycosphaerella graminicola*) in the hexaploid wheat ‘Synthetic 6x’

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Abstract Septoria tritici blotch, caused by the fungus *Mycosphaerella graminicola*, is currently the major foliar disease of wheat world-wide, and new sources of resistance and knowledge about the genetics of resistance are needed to improve breeding for resistance to this disease. Sears’s ‘Synthetic 6x’ hexaploid wheat, derived from a hybrid of *Triticum dicoccoides* and *Triticum tauschii*, was resistant to 12 of 13 isolates of *M. graminicola* tested. Chromosome 7D of ‘Synthetic 6x’ was identified as carrying resistance to all 12 isolates in tests of seedlings of inter-varietal chromosome substitution lines of ‘Synthetic 6x’ into ‘Chinese Spring’ and to two isolates in tests of adult plants. A septoria tritici blotch resistance gene, named *Stb5*, was identified using the *M. graminicola* isolate IPO94269 and mapped on the short arm of chromosome 7D, near the centromere, in a population of single homozygous chromosome-recombinant lines for the 7D chromosome.

Keywords Septoria tritici blotch · *Mycosphaerella graminicola* · Synthetic hexaploid wheat · Disease resistance · Genetic mapping · *Stb5*

Introduction

Septoria tritici blotch, caused by the ascomycete fungus *Mycosphaerella graminicola* (anamorph *Septoria tritici*), is an important disease in all major wheat-growing areas. The disease has the potential to cause considerable reductions in total yield throughout the world (Scharen 1999) and is an important target for fungicide applications (Cook 1999). Owing to the rising cost of fungicides and the difficulty of controlling the disease where chemical control is expensive, farmers are increasingly inter-

ested in varieties which combine resistance to septoria tritici blotch with high agronomic value. New sources of resistance are required in order for this goal to be achieved as few varieties currently available have adequate resistance.

Compared to other diseases of wheat, there has been little progress in genetic analysis of resistance to septoria tritici blotch. Reports on the mode of inheritance of resistance to *M. graminicola* have been inconsistent with respect to the number and effects of genes involved (Kema 1996). This is partly because many experiments on progeny populations of inter-varietal crosses relied on natural infection, instead of using defined isolates (for an exception see Somasco et al. 1996), so it has not always been possible for other workers to confirm the identity of resistance genes. The use of single isolates enables geneticists and breeders to distinguish isolate-specific and non-specific resistance in the host (Parlevliet 1993). Four genes for resistance to *M. graminicola* have been identified, but they have not been mapped or located to chromosomes (Wilson 1979; Somasco et al. 1996; McIntosh et al. 1998). Only *Stb4* was identified by the use of a single pathogen isolate (Somasco et al. 1996).

The wild relatives of wheat are a valuable pool of germplasm that can be used as a source of genetic resistance to several diseases, including septoria tritici blotch (Yechilevich-Auster et al. 1983). Wheat can be hybridised with many related species, and many resistance genes have been transferred to wheat cultivars from other species and genera of the Triticeae (Cox et al. 1992). The species *Triticum tauschii* (syn. *Aegilops squarrosa*, $2n=2x=14$) is the donor of the D genome of bread wheat (Kimber and Feldman 1987). Different accessions of this grass carry a wide range of disease resistances (Appels and Lagudah 1990; Cox et al. 1992; Villareal et al. 1994). May and Lagudah (1992) tested several accessions of *T. tauschii* and synthetic hexaploid wheats in Australia. Most accessions were resistant to infection by *M. graminicola* in tests using one pathogen isolate from Australia. May and Lagudah (1992) sug-

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