

Contributions of disease resistance and escape to the control of septoria tritici blotch of wheat

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The contributions of disease escape and disease resistance to the responses of wheat to septoria tritici leaf blotch (STB) were analysed in a set of 226 lines, including modern cultivars, breeding lines and their progenitors dating back to the origin of scientific wheat breeding. Field trials were located in the important wheat-growing region of eastern England and were subject to natural infection by *Mycosphaerella graminicola*. STB scores were related to disease-escape traits, notably height, leaf spacing, leaf morphology and heading date, and to the presence of known *Stb* resistance genes and isolate-specific resistances. The *Stb6* resistance gene was associated with a reduction of 19% in the level of STB in the complete set of 226 lines and with a 33% reduction in a subset of 139 lines of semidwarf stature. Greater plant height was strongly associated with reduced STB in the full set of lines, but only weakly in the semidwarf lines. Shorter leaf length was also associated with reduced STB, but, in contrast to earlier reports, lines with more prostrate leaves had more STB on average, probably because they tended to have longer leaves. Several lines, notably cvs Pastiche and Exsept, had low mean levels of STB which could not be explained by either escape traits or specific resistance genes, implying that they have unknown genes for partial resistance to STB.

Keywords: disease escape, isolate-specific resistance, *Mycosphaerella graminicola*, septoria tritici blotch, *Stb6*, *Triticum aestivum*

Introduction

For the last three decades *Mycosphaerella graminicola* (anamorph *Septoria tritici*), the causal agent of septoria tritici blotch (STB), has been the most important foliar disease of winter wheat in Western Europe and many other wheat-growing areas worldwide (Goodwin *et al.*, 2003). The lack of highly resistant cultivars means that the only fully effective method of controlling this disease is by programmed application of fungicides. However, the emergence of widespread resistance to strobilurin (Fraaije *et al.*, 2005) and, more recently, triazole fungicides (Brunner *et al.*, 2008) has made selection for resistance to STB a high priority for wheat breeders.

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Thirteen major genes for resistance to STB, *Stb1* to *Stb12* and *Stb15*, have been identified and mapped (Arraiano *et al.*, 2001, 2007; Brading *et al.*, 2002; Adhikari *et al.*, 2003, 2004a,b,c; McCartney *et al.*, 2003; Chartrain *et al.*, 2005a,b, 2009). Each of these genes is effective against one or a few known isolates of *M. graminicola*. A gene-for-gene relationship was demonstrated for *Stb6* (Brading *et al.*, 2002), which is widespread in sources of resistance to STB worldwide (Chartrain *et al.*, 2005c). *Stb6* and *Stb15* are the genes most commonly present in current European wheat germplasm (Arraiano & Brown, 2006). Several other isolate-specific resistances, which have been identified but not yet analysed genetically (Chartrain *et al.*, 2004a), are present in European cultivars (Arraiano & Brown, 2006).

Stb1, which originated from wheat cv. Bulgaria 88 (Adhikari *et al.*, 2004a) is, to date, the only known STB-specific resistance gene to be considered durable in the sense of Johnson (1984). This gene has been effective for over 25 years in widely grown cultivars across the STB-prone region of Indiana and adjacent states in the USA (Adhikari *et al.*, 2004a). *Stb4*, originally from spring wheat cv. Tadinia, was effective in California for more

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