

Sources of resistance to septoria tritici blotch and implications for wheat breeding

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Twenty-four wheat cultivars and breeding lines were screened for isolate-specific resistance to septoria tritici blotch (STB) caused by 12 isolates of *Mycosphaerella graminicola*. New isolate-specific resistances that could be used in wheat breeding were identified. Major sources of resistance to STB used in world breeding programmes for decades, such as Kavkaz-K4500, Veranopolis, Catbird and TE9111, have several isolate-specific resistances. This suggests that 'pyramiding' several resistance genes in one cultivar may be an effective and durable strategy for breeding for resistance to STB in wheat. Several cultivars, including Arina, Milan and Senat, had high levels of partial resistance to most isolates tested as well as isolate-specific resistances. Resistance to isolate IPO323 was common, present in all but one of the major sources of resistance tested. This suggests that resistance to IPO323 may be an indicator of varietal resistance to STB in the field.

Keywords: isolate-specific resistance, *Mycosphaerella graminicola*, resistance gene pyramids, septoria tritici blotch, wheat

Introduction

Septoria tritici blotch (STB), caused by the ascomycete fungus *Mycosphaerella graminicola*, is currently the most important foliar disease of wheat in many regions of the world, including Europe (Eyal & Levy, 1987; Polley & Thomas, 1991; van Ginkel & Rajaram, 1993; Cowger *et al.*, 2000; Hardwick *et al.*, 2001). The use of fungicides to control STB is expensive and not entirely reliable. Recently, isolates of *M. graminicola* resistant to strobilurin (Qo inhibitor, QoI) fungicides have become common in Europe and there has been widespread failure of QoI fungicides to control STB (Anonymous, 2003). Resistant cultivars provide an effective and economical way to control the disease, but until recently little was known about the genetics of resistance to STB in wheat and breeders had to rely on unknown genes when breeding for resistance (Eyal, 1999).

Resistance to STB may be isolate-specific or quantitative. Isolate-specific resistance is near-complete, oligogenic (Somasco *et al.*, 1996; Arraiano *et al.*, 2001b; McCartney *et al.*, 2002) and follows a gene-for-gene relationship

(Brading *et al.*, 2002), whereas quantitative or partial resistance is incomplete, polygenic (Jlibene *et al.*, 1994; Simon & Cordo, 1998; Zhang *et al.*, 2001) and isolate nonspecific (Chartrain *et al.*, 2004). Eight genes (*Stb1*–*8*) for resistance to STB have been identified so far. *Stb1*, *Stb2* and *Stb3*, in varieties Bulgaria 88, Veranopolis and Israel 493, respectively (Wilson, 1985), were identified using natural infection probably caused by a mixture of pathogen genotypes. *Stb4*–*8* in varieties Tadinia, Synthetic 6x, Flame, Estanzuela Federal and the synthetic hexaploid wheat W7984, respectively, were identified using defined isolates of *M. graminicola* and have been mapped: *Stb4* (T.B. Adhikari and S.B. Goodwin, Purdue University, IL, USA, unpublished data, 2004); *Stb5* (Arraiano *et al.*, 2001b); *Stb6* (Brading *et al.*, 2002); *Stb7* (McCartney *et al.*, 2003); *Stb8* (Adhikari *et al.*, 2003).

As for other diseases, resistance to STB may not be durable. The population of *M. graminicola* is highly diverse genetically (McDonald *et al.*, 1999) and the fungus may reproduce sexually several times during the wheat-growing season (Kema *et al.*, 1996c). This increases the risk of adaptation of the pathogen to resistance genes deployed in the host population. An example is the breakdown of resistance of Gene in Oregon 5 years after its release due to evolution of virulent pathogen genotypes (Cowger *et al.*, 2000). However, other breeding lines and cultivars, including Kavkaz-K4500 (KK), Veranopolis and Bulgaria 88, have maintained their resistance for many years (Dubin & Rajaram, 1996; Eyal, 1999). The mechanism underlying durability of resistance in STB is unknown.

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