

A gene in European wheat cultivars for resistance to an African isolate of *Mycosphaerella graminicola*

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Genes for specific resistance to European and American isolates of *Mycosphaerella graminicola*, the causal agent of septoria tritici blotch (STB) of wheat, have been identified and mapped in various cultivars and breeding lines and are distributed throughout the genome. The location of a gene for resistance to an Ethiopian isolate, IPO88004, which is currently the most widespread resistance present in European wheat cultivars, is reported. The resistance was mapped in the Swiss cultivar Arina which, besides high partial resistance to STB, also has specific resistance to IPO323, controlled by *Stb6* and to IPO88004. An F5 recombinant inbred population from a cross between Arina and the susceptible cultivar Forno was tested in whole seedling trials. Using multiple QTL mapping (MQM), a gene for resistance to *M. graminicola* isolate IPO88004 in cv. Arina was located to chromosome 6AS. The gene is named *Stb15*. Seedling tests on a double haploid population of cvs Arina × Riband indicated that the UK wheat cv. Riband also has *Stb15* or another gene for specific resistance to IPO88004 allelic or closely linked to *Stb15*.

Keywords: disease resistance gene, multiple QTL mapping, QTL analysis, septoria tritici blotch, *Stb15*

Introduction

Mycosphaerella graminicola (anamorph *Septoria tritici*), is the causal agent of septoria tritici blotch (STB) which is now the most important foliar disease of wheat worldwide, including most of western Europe (Goodwin *et al.*, 2003; Pillinger *et al.*, 2004). The recent evolution of resistance to strobilurin (QoI) fungicides (Fraaije *et al.*, 2005) together with little flexibility in the timing of the application of triazole fungicides has increased interest in breeding and growing cultivars resistant to STB as a cost-effective means of controlling the disease. Wheat breeders throughout Europe now consider it one of their major criteria for selection of new varieties. Knowledge of the genetics of a disease is essential for effective resistance breeding.

Resistance to STB may be isolate-specific or quantitative. Specific resistance to STB is near-complete, oligogenic, and follows a gene-for-gene relationship (Brading *et al.*, 2002). In recent years 12 major genes for resistance to *M. graminicola*, *Stb1* to *Stb12*, have been identified and

mapped (Somasco *et al.*, 1996; Arraiano *et al.*, 2001; Brading *et al.*, 2002; Adhikari *et al.*, 2003; McCartney *et al.*, 2003; Adhikari *et al.*, 2004a,b,c; Chartrain, 2004; Chartrain *et al.*, 2005a,b). A gene-for-gene relationship has been demonstrated for *Stb6* (Brading *et al.*, 2002), a gene which is widespread in sources of resistance to STB world-wide (Chartrain *et al.*, 2004a). Three specific resistance genes, *Stb10*, *Stb11*, *Stb12* have been mapped using quantitative trait locus (QTL) analysis because in each case, several lines in the populations could not be clearly classified as resistant or susceptible (Chartrain *et al.*, 2005a,b).

The Swiss wheat cultivar Arina is not only one of the most STB-resistant European wheat cultivars known (Brown *et al.*, 2001) but also has resistance to *Phaeosphaeria* (anamorph *Stagonospora*) *nodorum* and fusarium head blight (Paillard *et al.*, 2003). Besides being a good source of partial resistance to STB in the field, cv. Arina has specific resistances to two *M. graminicola* isolates, IPO323 controlled by *Stb6* (Chartrain *et al.*, 2005c), and to isolate IPO88004 (Chartrain *et al.*, 2004a; Arraiano & Brown, 2006).

An Ethiopian *M. graminicola* isolate, IPO88004, has been used previously to identify specific isolate × line interactions (Kema *et al.*, 1996a,b, Chartrain *et al.*, 2004a). Resistance to IPO88004 was first detected not only in sources of resistance to STB but also in highly susceptible

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