

Associations between fungal and abiotic leaf spotting and the presence of *mlo* alleles in barley

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The hypothesis that the increased use of the powdery mildew-resistance gene *mlo* has caused the increase in spotting diseases of barley over the past 20 years was tested in field trials. Near-isogenic lines with alleles of the *Mlo* gene for susceptibility or resistance to mildew in two parental backgrounds were trialled at four sites in Scotland and two in Ireland that were prone to spotting diseases, over 3 consecutive years. Mildew was controlled by sprays with quinoxifen. Disease levels were low in the trials, the two most important diseases being scald caused by *Rhynchosporium secalis* and ramularia leaf spot caused by *Ramularia collo-cygni*. There were high levels of abiotic spotting. Lines with mutant *mlo* alleles consistently developed less *Rh. secalis* and *Ra. collo-cygni*, but more abiotic spots. This study indicates that the *mlo* mildew-resistance gene has not alone been responsible for the rise in spotting diseases over the past 20 years. Possible reasons for the rise are discussed, including the interaction of the *mlo* gene with the environment.

Keywords: barley powdery mildew resistance, barley scald, *Hordeum vulgare*, *Ramularia collo-cygni*, ramularia leaf spot of barley, *Rhynchosporium secalis*

Introduction

In northern Europe in recent decades, there has been an increase in spotting diseases of spring barley caused by fungi. Data on disease trends in England and Wales have come from annual surveys by ADAS and the Central Science Laboratory (CSL), who surveyed spring barley between 1967 and 1980 and winter barley since then. Powdery mildew, caused by *Blumeria graminis*, was by far the most important disease of spring barley up to 1980 (data not shown). The subsequent decline in the importance of mildew on winter barley (Fig. 1) may be attributed to the use of *mlo* in spring barley, which acts as a source of inoculum for subsequent crops of winter barley, and to successful breeding for partial resistance to mildew in winter barley. Spotting pathogens, however, have become more significant on winter barley, particularly *Rhynchosporium secalis*, which causes scald or leaf blotch (Shipton *et al.*, 1974; Beer, 1991), and *Pyrenophora teres*, which causes net blotch (Shipton *et al.*, 1973) (Fig. 1). In a smaller dataset from Northern Ireland, powdery mildew was the major disease between 1976 and 1987, but scald became dominant by 2000 (Mercer & Ruddock, 2004).

Data for Scotland, based on disease surveillance in commercial crops, show more severe incidences of scald in the late 1990s and early 2000s than in earlier years (Anonymous, 2006c).

Ramularia collo-cygni, which causes ramularia leaf spot (RLS), has recently become a serious pathogen, but there are few quantitative reports of its importance. However, since the disease was first recognized as a threat to barley production in the late 1980s, it has spread to become an important disease in most northern European countries (Pinnschmidt & Hovmoller, 2003).

It is very widely believed among barley workers that the level of necrotic spotting not accounted for by *Rh. secalis* or *P. teres* has increased greatly in the last 20 years (Oxley *et al.*, 2002; Wu & von Tiedemann, 2002). There are few quantitative data on necrotic spotting of abiotic origin, although a high incidence (51% of surveyed fields affected) was recorded on spring barley in Northern Ireland in 2000, despite having only been recorded once before (in 1987) and even then with low mean severity (5%) (Mercer & Ruddock, 2004).

The *mlo* powdery mildew-resistance gene was discovered in 1942 in an Ethiopian barley line, Grannenlose Zweizeilige. It was named *mlo-11*, and along with other *mlo* alleles, is a non-functional allele of the *Mlo* gene (Jørgensen, 1992). The wild-type allele (*Mlo*⁺) suppresses defence functions and attenuates the cell death response

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