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Barley genotype interaction with three virulent scald (*Rhynchosporium secalis*) pathotypes from western Canada

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Introduction

Scald, incited by *Rhychosporium secalis* (Oudem.) J. J. Davis, is a major foliar disease of barley (*Hordeum vulgare* L.) in the cooler, moister regions of western Canada. High pathogenic variability (Tekauz, 1991; Xi et al. 2003) combined with limited rotational intervals between barley crops increases the risk of breakdown of cultivar resistance. Previous molecular genetic investigations demonstrated that resistance in western Canadian barley cultivars is predominantly derived from the *Rrs1* locus (*Rh/Rh3/Rh4* complex) on chromosome 3 (3H) or the *Rrs2* locus (*Rh2*) on chromosome 1 (7H) (Penner et al. 1996). The objective of the current study was to evaluate the resistance response of a diverse set of 57 barley genotypes under growth chamber and field conditions, using three pathotypes originally isolated from three cultivars with differing resistance sources.

Materials and Methods

Single-spore isolations were produced from infected leaf tissue of resistant cultivars: CDC Earl (*Rrs1*), Kasota (*Rrs2*) and Seebe (undefined resistance; different from the former two [Zantinge et al. 2005]).

Growth Chamber

Three growth chamber experiments were conducted between Feb., 2007 and Jan., 2008. Genotypes were grown in plastic pots (14 cm diameter) containing a soil-less potting mix. R. secalis was cultured on lima bean agar at 15-20°C and a 12 hr photoperiod for 2 wks before conidia were harvested. Using compressed air, a spore suspension (1×10^6 conidia/ mL) was applied to seedlings 14 days following seeding and then incubated at 100% RH for 48 hrs. Inoculated plants were grown for a further two weeks before rating. A score of percent leaf area diseased was recorded on the 2nd and 3rd leaves for all plants (0 = no infection, 1 < 10%, 2 = 10-40%, 3 >40-90%, 4 = total leaf collapse).

Field Nursery

Field experiments were conducted in 2007 and 2008 at Lacombe, AB. Genotypes were planted in hill plots (8-10 seeds) on 0.5 m centres. Inoculum was prepared from 2-3 week old cultures grown on lima bean agar, adjusted to 10^5 conidia /mL and applied as a fine mist using a compressed air sprayer. Hills were rated twice in each season, using a 0-9 scale (0 = no disease in the lower, middle and upper canopy, 9 = >50% leaf area diseased in lower, middle and upper canopy).

Experimental Design and Statistical Analysis

To prevent cross-contamination separate inoculations and experiments were conducted for each pathotype. In the field each isolate experiment was separated by at least a 5 m wheat border. Each experiment was set up as a randomized complete block design (RCBD). For growth chamber experiments, replications were inoculated together within separate chambers for each pathotype. Response variables for both growth chamber and field studies involved ordinal data. For both studies, analysis was performed using mixed-effects logistic regression in SAS (SAS Institute Inc. release 9.2.0.3) with the GLIMMIX procedure. A multinomial distribution of errors was assumed and a cumulative probit link function was applied to the disease scores.

Results

Growth Chamber

Susceptible cultivars included as controls, indicated a moderately high level of infection in all experiments and individual pathotype tests therein. The effect of genotype was significant (P<0.0001), with substantial variation observed in genotype response (Fig. 1a). The Seebe pathotype produced the highest average disease severity (2.4 ±0.1), and none of the 57 genotypes exhibited highly resistant responses (0 class). While CDC Earl and Kasota pathotypes demonstrated similar overall disease severities (1.4±0.1 and 1.4±0.2 respectively), highly resistant response was more common within the Kasota pathotype.

Field Nursery

A moderately high level of infection was observed in both years with similar infection levels in individual pathotype nurseries, as indicated by susceptible check cultivars. A wide range of disease reactions were observed (Fig. 1b), with genotype having significant influence (P<0.0001). The Seebe pathotype displayed the highest mean disease severity (6.5±1.2), followed by similar mean values for the Kasota and CDC Earl pathotypes (4.5±1.7 and 4.0±1.7 respectively).

Discussion

Differential responses were observed in the set of genotypes to the three virulent pathotypes. Seebe demonstrated a resistant reaction to both Kasota and CDC Earl pathotypes. Kasota and genotypes with similar resistance, exhibited a moderate level of resistance against the CDC Earl pathotype under both field and growth chamber conditions. CDC Earl and like genotypes exhibited resistant reactions against the Kasota pathotype in growth cabinets but exhibited susceptible-type reactions under field conditions, although infection by wildtype strains cannot be excluded. Results suggest that alternative use of cultivars carrying different types of resistance could be employed to help extend resistance over time.

The high disease levels and virulence patterns of the Seebe pathotype in the study represents a potential threat to barley production in Alberta should it increase in frequency, as resistances similar to those in cultivars CDC Earl and Kasota appear to be ineffective when challenged by it. Some genotypes with multi-gene based resistance e.g. PC11 (ICARDA/CIMMYT line) and BM0141D lines with resistance derived from it using molecular marker assisted selection (MMAS), showed an improved reaction to the Seebe pathotype. Resistance to the Seebe isolate appeared to be more effective at seedling vs. adult plant growth stages.

Several genotypes with differing resistance sources showed potential for use as parents for developing resistance to the virulent Seebe pathotype: BM0147D-94, bred using resistance source MEH#151-1 previously documented with isolate specific response (defined Rh_T; Penner et al. 1998); ND22086 (unknown resistance source); SB01634 and SB01675, bred using 145L2 and 4176/10/n/3/2/6 *H. vulgare* ssp. spontaneum interspecific crosses; Singh et al. 2003); VB0420 bred using Chieftain (resistant to pathotypes virulent on *Rh2*, *Rh3* and *Rrs13* (Wallwork and Grcic, 2011) and CIho 2208 (CN267, accession previously undocumented).

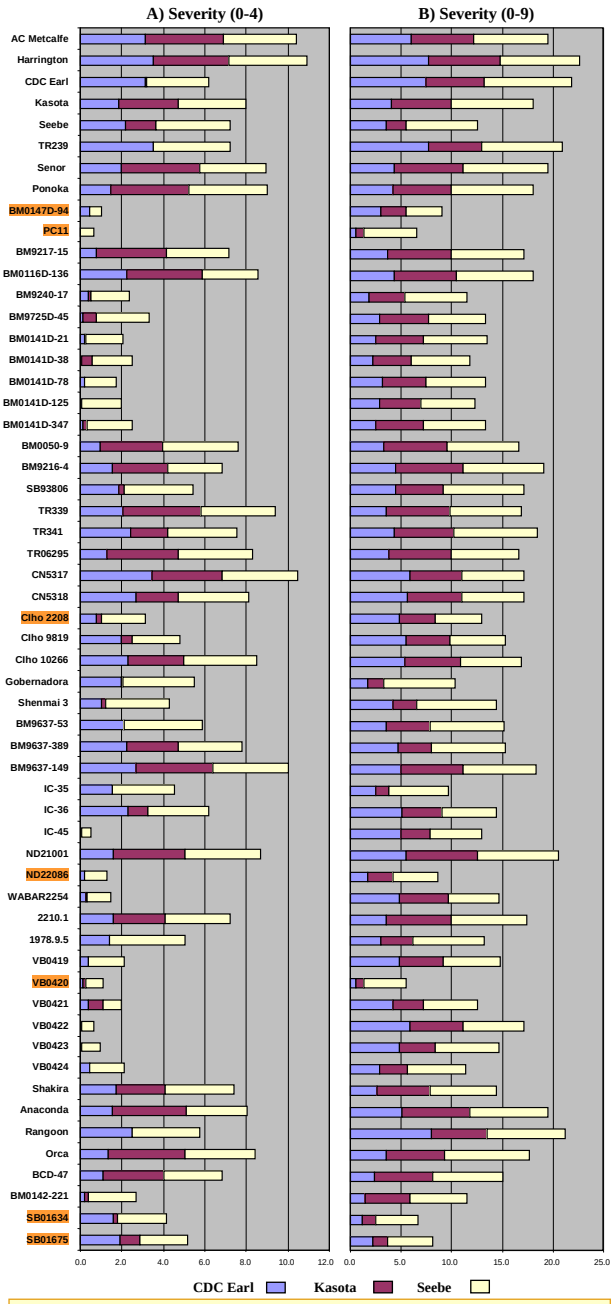

Fig 1. Scald severity response of fifty-seven barley genotypes to three virulent pathotypes under a) growth chamber and b) field nursery conditions.

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