

Major Gene and Field Resistance to Blackleg in Winter Oilseed Rape Germplasm for the U.S. Southern Great Plains

John Damicone, Felipe Cevallos, Claudia Diaz, Josh Lofton, Mark Payton, Oklahoma State University, Stillwater, OK 74078; Mike Stamm, Kansas State University, Manhattan, KS 66506 USA



Introduction

Blackleg, caused by the fungus *Leptosphaeria maculans*, is a widespread disease of winter oilseed rape in the U.S. Southern Great Plains (Fig. 1). The primary management strategy for blackleg is the use of genetic resistance.



Fig. 1. Blackleg symptoms on leaves and stems.

Objectives

- Evaluate open-pollinated (OP) cultivars, hybrids, and breeding lines for quantitative (field) and major-gene (cotyledon) resistance to blackleg.
- Assess the benefits of major-gene resistance for blackleg control in the field.

Materials and Methods

- Entries consisting of OP cultivars (n=47), hybrids (n=87), and breeding lines from the Kansas State University winter canola breeding program (n=373) were grown in field plots infested with local races of the pathogen from 2011 to 2018. Stem canker severity was assessed on stubble after swathing using a 0 to 5 scale based on the degree of internal stem decay (Fig. 2). Disease severity data were rank-transformed within trial prior to analysis over trials.



Fig. 2. Levels of stem canker severity observed in field plots.

- A subset of entries (19 OP cultivars, 19 hybrids, and 117 breeding lines) was evaluated for major-gene resistance on seedling cotyledons using a gene-for-gene interaction with prevalent local races (*AvrLm6-7* and *AvrLm1-6-7*) and race *AvrLm1-2-4-7-S* from Australia (courtesy A. Van de Wouw). Disease severity was assessed using infection classes (IC) of 1 to 6 where 1-3 are resistant and 4-6 are susceptible (Fig. 3). Mean IC scores <3.5 were considered resistant. IC scores were rank transformed prior to analysis.

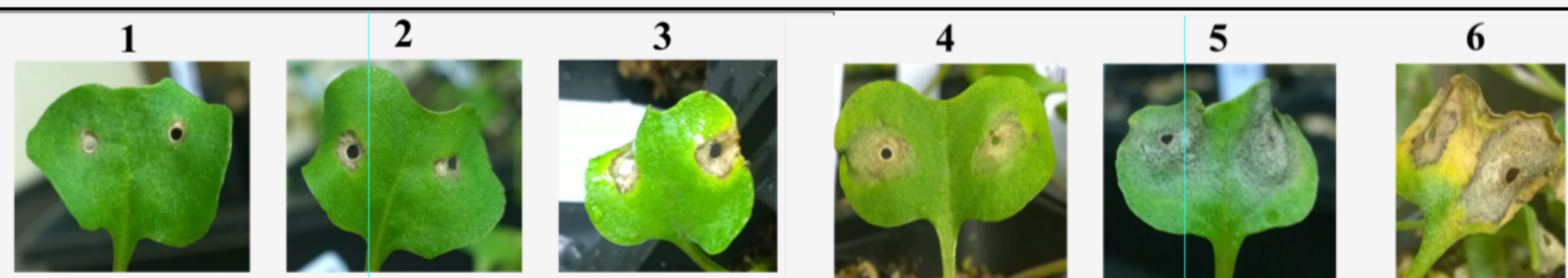


Fig. 3. IC scores from 0-6 where 1-3 are resistant and 6 are susceptible responses

Results

- Blackleg developed in all field trials, but only averaged moderate levels of disease severity (Fig. 4). Over all trials, disease severity ranks were negatively correlated with yield ($r=-0.29$, $P<0.01$).

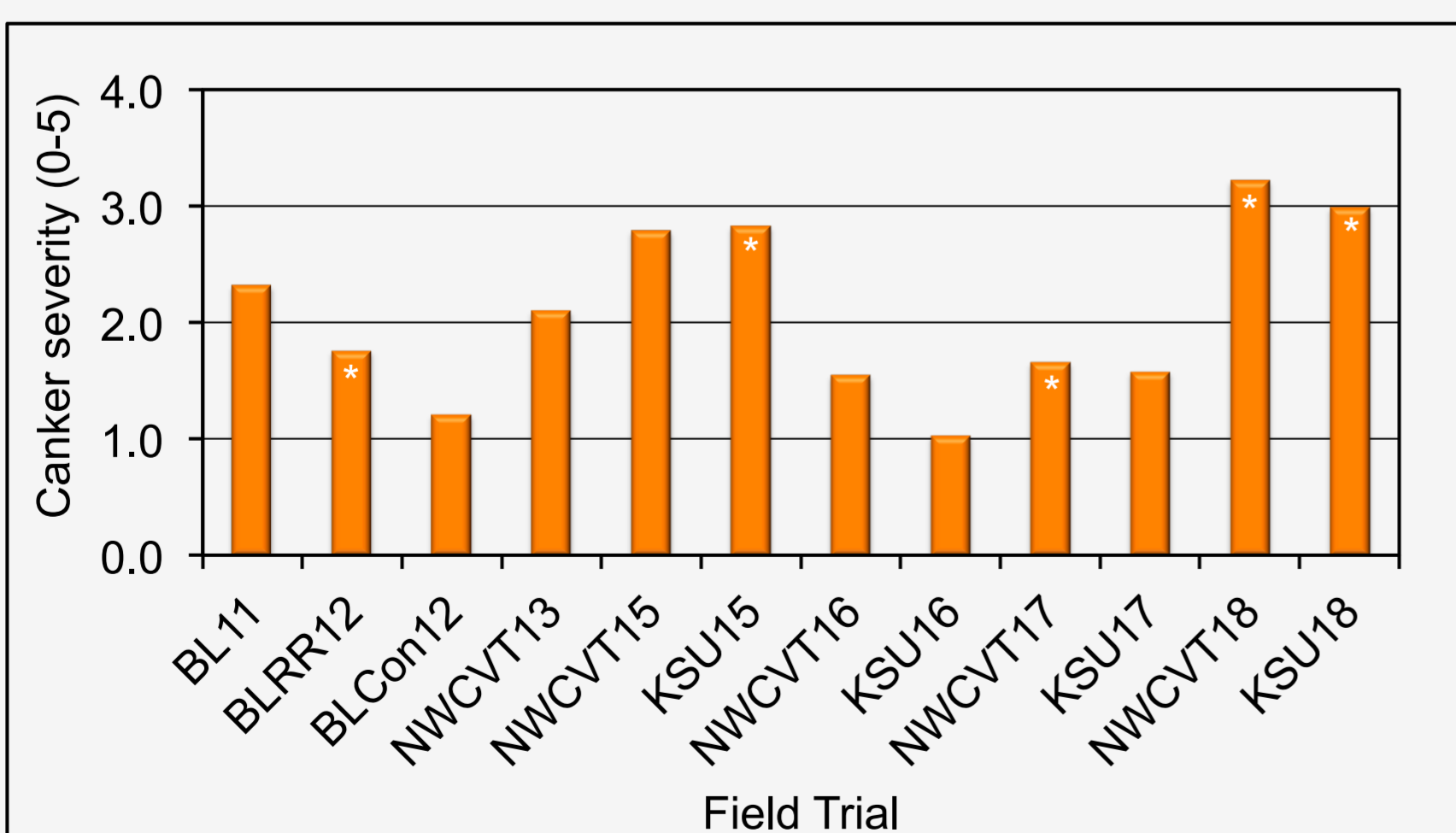


Fig. 4. Mean stem canker severity ratings for field trials from 2011 to 2018 that evaluated resistance to blackleg. * Indicates a significant ($P=0.05$) negative correlation of disease severity with yield.

- OP cultivars had the highest stem canker ratings compared to hybrids and KSU breeding lines (Fig. 5). Yields were lowest for the OP cultivars and highest for hybrids. Yields of KSU breeding lines were intermediate and did not differ from hybrids.

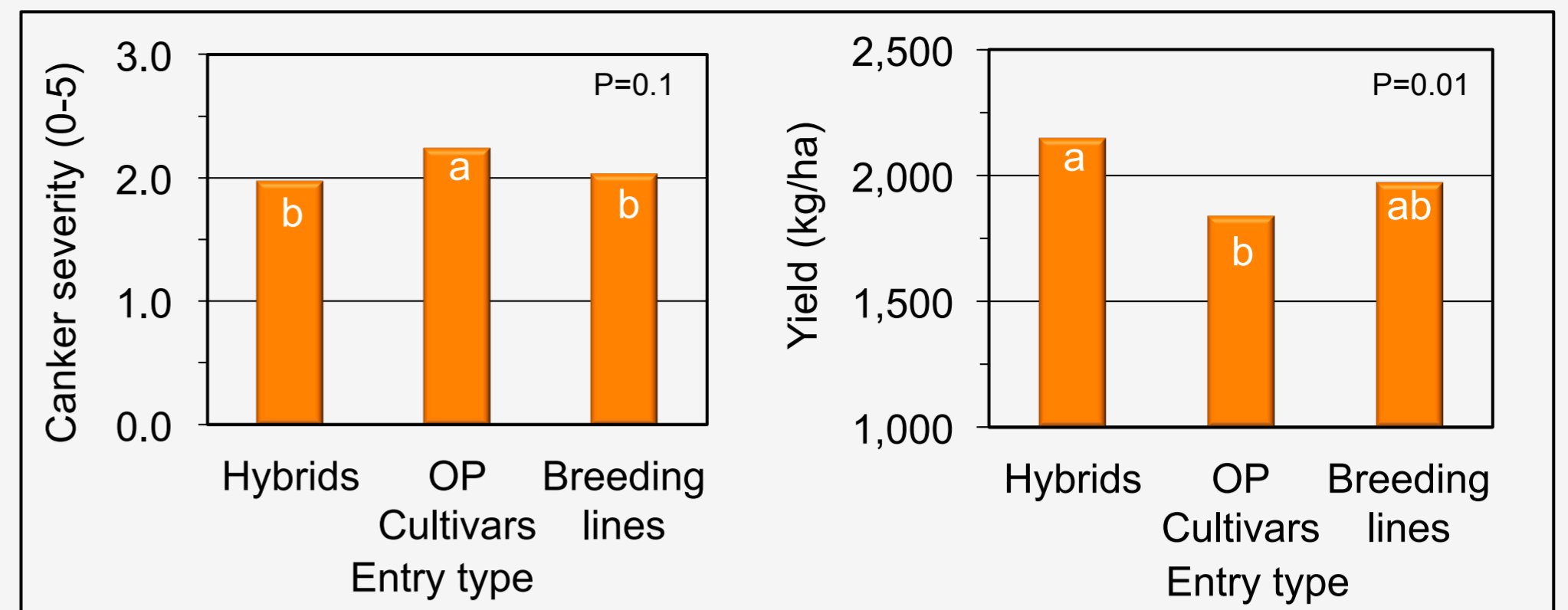


Fig. 5. Field responses of winter oilseed rape entries (hybrids n=481, OP cultivars n=454, breeding lines n=984) to blackleg in trials from 2011 to 2018.

- For entries evaluated for both major-gene and quantitative resistance (n=155), there were three main phenotypic responses (Table 1): 1) susceptible to all races and lacking major resistance genes (31% of entries), 2) susceptible to the local races *AvrLm1-6-7* and *AvrLm6-7* and resistant to *AvrLm1,2,4,7,S* possibly from *Rlm1, Rlm2, Rlm4, or RlmS* (54% of entries), 3) resistant to all races (5%) possibly from *Rlm6* or *Rlm7*. Entries (9%) with intermediate responses to one or more races could not be assigned a likely *Rlm* gene.

Table 1. Major-gene and field resistance responses of entries (breeding lines (n=117), OP cultivars (n=19), hybrids (n=19)). Entries are grouped based on mean separations of cotyledon IC scores and resistant ($IC<3.5$) or susceptible ($IC\geq 3.5$) classifications

Entries (n)	Cotyledon IC score (1-6)			possible <i>Rlm</i> genes ^z	Field responses	
	<i>AvrLm</i> 1-6-7	<i>AvrLm</i> 6-7	<i>AvrLm</i> 1-2-4-7-S		Canker severity (0-5)	Yield (kg/ha)
45	4.5 a ^y	4.3 a	4.0 a	none	2.1	2167
50	4.6 a	4.3 a	2.8 b	2,4,S	1.9	1985
18	4.2 a	4.2 a	3.2 a	2,4,S	1.9	1894
12	4.7 a	4.3 ab	3.2 b	2,4,S	2.4	1720
3	5.3 a	4.9 ab	3.9 b	none	2.3	856
4	4.1 ab	4.5 a	2.9 b	2,4,S	2.4	2690
7	2.7 a	2.8 a	2.5 a	1,2,4,6,7	1.8	2380
2	3.0 b	3.2 b	4.7 a	6	1.6	1611
14 ^x	3.6	3.5	3.4	?	2.0	1651

- ^z Based on IC scores classified as resistant ($IC<3.5$) or susceptible ($IC\geq 3.5$).
- ^y Values in a row followed by the same letter are not significantly different at $P=0.05$.
- ^x Entries with intermediate responses or that could not be assigned a *Rlm* gene.

- Entries with resistant responses on cotyledons did not always have reduced canker severity or higher yields in the field (Table 1), but IC scores averaged over the three races were positively correlated with canker severity (Table 2). Yields were negatively correlated with IC scores from the local races, and IC scores averaged over the three races (Table 2).

Table 2. Rank correlations between cotyledon IC scores and field resistance responses for entries (n=155) screened both on seedling cotyledons and in the field

Field responses	Seedling responses			
	<i>AvrLm</i> 1-6-7	<i>AvrLm</i> 6-7	<i>AvrLm</i> 1-2-4-7-S	Mean
Canker severity (1-5)	0.14	0.10	0.13	0.19**
Yield (kg/ha)	-0.23**	-0.18*	0.12	-0.16*

Correlation coefficients significant at ** $P=0.01$ and * $P=0.05$.

- Among individual entries included in multiple field trials, those with major-gene resistance generally had low disease resistance and higher yield compared to Star 915W, the most susceptible entry evaluated (Table 3).

Table 3. Major-gene and field responses of selected entries

Entry (type)	Seedling responses ^z				Field responses	
	<i>AvrLm</i> 1-6-7	<i>AvrLm</i> 6-7	<i>AvrLm</i> 1-2-4-7-S	<i>Rlm</i> ^y	Severity (0-5)	Yield (kg/ha)
Chrome (H)	V	V	V	-	2.1 a ^x	2212 bc
Star 915W (OP)	V	V	V	-	2.9 ab	1559 c
HC115W (OP)	V	V	V	-	2.4 a	1912 bc
Surefire (OP)	V	V	A	4	2.0 b	2495 ab
Wichita (OP)	V	V	A	4	2.1 a	2032 bc
Claremore (OP)	A	A	A	?	1.9 ab	2207 bc
DK Sensi (H)	A	A	A	7	1.9 b	3154 a
Safran (H)	A	V	A	1	1.9 ab	2232 b

^z V=virulent, $IC\geq 3.5$, A=avirulent, $IC<3.5$). ^yLikely *Rlm* gene. ^xValues in a column followed by the same letter are not different at $P=0.05$.

- Most entries had adequate quantitative resistance in field trials.
- Rlm4* was likely present in over 50% of entries evaluated.
- Major-gene resistance was beneficial in the field, particularly when effective against the local races.