Tillage System and Cropping Sequence Effects on Common Root Rot of Barley in Eastern Saskatchewan

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Abstract

Fusarium head blight (FHB) in barley has been spreading on the Canadian Prairies for the last decade. *Fusarium* spp. causing FHB can also cause crown/root rot of cereal crops. It is therefore of interest to determine the impact of agronomic practices on fungal populations associated with root rot of barley. From 1999 to 2001, 137 barley crops were sampled in eastern Saskatchewan for severity of subcrown internode discoloration and percent isolation of fungi. *Cochliobolus sativus* was the most commonly isolated fungus, whereas the most commonly isolated *Fusarium* spp. included the FHB pathogens *F. avenaceum*, *F. culmorum* and *F. graminearum*. Discoloration caused by *C. sativus* was favored by conventional-till, whereas *Fusarium* spp. increased in reduced tillage systems. Barley grown after a cereal-summerfallow (or summefallow-cereal) sequence under conventional- or minimum-till had increased levels of *C. sativus*. *Fusarium* spp. were most affected by the previously-grown crop(s); they were more common in barley grown after a noncereal than a cereal, and after two noncereals, or a noncereal alternated with summerfallow. Previous glyphosate applications were associated with lower *C. sativus*, and higher *Fusarium* spp., levels in barley grown under minimum-till. This suggests changes in fungal communities; however, the mechanism(s) responsible for these changes in fungal levels are not known. Increased infection of ground/underground tissue by FHB pathogens might contribute to its development in succeeding cereal crops, therefore measures aimed at reducing root/crown infections by *Fusarium* spp. might also help reduce FHB development.

Introduction

Common root rot (CRR) is an important and widespread disease of cereal crops in the Canadian Prairies (Fernandez and Jefferson, 2004) that can cause significant yield losses (Tinline and Ledingham, 1979). In general, barley is considered to be more susceptible to CRR caused by *Cochliobolus sativus* (anamorph *Bipolaris sorokiniana*) than wheat (Piening et al., 1976). However, root/crown rot of barley can also be caused by *Fusarium* spp. (Piening and Orr, 1988; Sturz and Carter, 1995; Sturz and Johnston, 1985; Windels and Wiersma, 1992).

Fusarium head blight (FHB) in barley has been established in the eastern Prairies for the last decade (Tekauz et al., 2000). *Fusarium graminearum* and *F. avenaceum* were the most common FHB

pathogens of barley grown in 2005 in Manitoba (Tekauz et al., 2006), whereas *F. avenaceum* has consistently been one of the most commonly isolated species from FHB-affected barley in Saskatchewan where this disease has occurred at lower levels than in eastern regions of the Prairies (Pearse et al., 2006). Because of concerns regarding increasing FHB development on the eastern Prairies and its apparent spread westward, it is essential to put in place a comprehensive strategy to stop or reduce the rate of spread of this disease, and to decrease the damage it has been causing to the barley industry in areas where it is already well established. To this end, there is a need for more information on the epidemiology of FHB in Saskatchewan so that the risk factors associated with its spread and development can be better understood. A comprehensive approach needs to include an examination of crown/root rot caused by *Fusarium* spp. in this region. *Fusarium* infection of ground and underground barley tissue could result in higher fungal levels in crop residues and thus be a source of inoculum for spike infection and fungal carryover from one season to the next. A better understanding of all factors affecting *Fusarium* inoculum and infection of barley tissue would help in devising a more effective strategy aimed at reducing inoculum levels and disease development and preventing the further spread of important cereal diseases caused by *Fusarium* spp.

There have been few studies conducted on the impact of agronomic practices, such as tillage system and crop rotation, on CRR of barley and associated fungal populations (Conner et al., 1996; Pienning and Orr, 1988*;* Piening et al., 1976; Sturz and Johnston, 1985; Windels and Wiersma, 1992). In recent years, Prairie producers have become more reliant on noncereal crops, including oilseeds and pulses, and have increasingly adopted more continuous cropping and greater use of conservation tillage practices. It is therefore of interest to determine the impact of currently popular cropping sequences and tillage systems on fungal populations in underground tissue of barley crops.

The objective of the present study was to determine CRR levels in barley crops grown in eastern Saskatchewan, identify and quantify fungal species from infected tissue, and determine the association between disease/fungal levels and crop production systems, with the aim of determining what crop production factors might reduce *Fusarium* infections in barley crops.

Materials and Methods

A total of 137 barley crops were sampled from 1999 to 2001 for severity of SI discoloration and percent isolation of fungi. There were 26 crops in 1999, 61 in 2000, and 50 in 2001. Of these, 63% were six-rowed and the rest were two-rowed cultivars. In late July to early August, a total of 35 to 50 plants at approximately the mid-milk to dough stage were carefully pulled randomly from each field. Samples were washed under tap water and thoroughly dried. Subcrown internodes (SI) were carefully removed and rated for extent of brown to black discoloration on a 0 to 3 scale (Fernandez and Jefferson, 2004). A SI discoloration index (CRRI) was calculated for each field based on the incidence and severity of the discoloration = ((3category value X plants in category)/total number of plants sampled)*100. The most discolored segment (about 1 cm^2) of each SI was then excised, surface-disinfested, and plated on modified PDA (Fernandez and Chen, 2005) and incubated for about 7 d. Fungi growing out of the tissue pieces were identified, and percent isolation of each fungus was calculated based on the total number of isolates in each field.

Categorization of Barley Crops/Fields into Crop Production Factors

Producers supplied information regarding agronomic practices related to the crop(s) sampled. This information was used to categorize the crops/fields according to crop production factors. For tillage system, fields were categorized based on the total number of tillage operations performed in the

previous three years. Fields under conventional-till (CT) had a total of seven or more tillage operations, those under minimum-till (MT) had one to six operations, whereas there were no tillage operations in fields under zero-till (ZT) management. Herbicide applications were categorized according to whether the fields had received any of the Group 1, 2, 4, or 9 herbicides (Saskatchewan Agriculture and Food, 2006) in the previous 18 months. For previously-grown crop(s), fields were categorized according to the crop, if any, grown the previous year: cereal, oilseed, pulse, or summerfallow. Fields were also categorized according to the crops, if any, grown the previous two years, regardless of the order in the sequence: two cereal (C) crops (C-C), two noncereal (NC) crops (NC-NC), a cereal and a noncereal crop (C-NC), or summerfallow (F) and a crop (C-F or NC-F).

Statistical Analyses

Disease- and fungal-related responses were compared with the SURVEYREG procedure of SAS and means were estimated with the SURVEYMEANS procedure of SAS (SAS Institute, Inc. 1999). Data collected for each year were assumed to be stratum for the analysis. Contrasts were performed among cropping sequences and tillage systems for total disease level (CRRI) and percentage of the most commonly isolated fungi. Effects were declared significant at $P \leq 0.10$.

Results

In all three years, the fungus with the highest percent occurrence and mean percent isolation in SI of barley was *C. sativus* (mean of 99% for percent occurrence, and 51% for percent isolation) followed by *Microdochium bolleyi* (73% and 11%). *Fusarium* spp. constituted the second most common genus; among these, the most common species were *F. equiseti* (65%, 9%) and *F. avenaceum* (54%, 5%). These were followed by *F. culmorum* (27%, 3%), *F. graminearum* (18%, 2%) and *F. acuminatum* (14%, 1%). *F. poae* and *F. sporotrichioides* were found in <10% of the fields at a mean percent isolation of <1%. Other *Fusarium* spp. isolated only occasionally included *F. pseudograminearum* and *F. oxysporum*.

Effects of Crop Production Factors on CRR and Fungal Isolations

There was not much effect of previous crop or two-year cropping sequence on the overall CRRI (Table 1). The type of crop(s) grown the previous year appeared to affect isolations of *C. sativus* more than a previous year of summerfallow, with barley grown after a cereal crop having higher levels of *C. sativus* than when grown after an oilseed, but not when grown after a pulse crop. However, a year of summerfallow alternated with a cereal crop (C-F) resulted in significantly higher levels of this fungus than when grown after other sequences, except for C-NC.

Overall, growing a noncereal crop the previous year resulted in higher relative levels of *Fusarium* spp. in barley SI than growing a cereal crop, with barley grown after a pulse having the highest levels (Table 1). *Fusarium* spp. were also most frequently isolated when no cereal was present in neither of the previous two years (i.e., NC-NC or NC-F). In regards to the individual *Fusarium* spp., there was also a tendency for isolation of *F. avenaceum* from SI to be the lowest in barley grown after a cereal than a noncereal, whereas the highest percent isolation of *F. culmorum* occurred when barley was grown after a pulse. The latter fungus was the only *Fusarium* species present at significantly lower levels when barley was grown after summerfallow than after any crop, especially pulses, and was also lowest after C-F. In contrast, *F. equiseti* tended to be more commonly isolated after summerfallow than after a crop, and its percent isolation was lowest for cropping sequences that included a cereal and a noncereal (C-NC). *Fusarium graminearum* was also present at higher levels in barley crops grown after a noncereal than a cereal. Furthermore, when the two-year cropping sequence C-NC was

further classified by the first crop in the sequence (i.e. C*-NC versus O*-C), total *Fusarium* spp. and *F. graminearum* were significantly higher when the previous crop was an oilseed (O*-C) than when it was a cereal (C*-NC). There were few differences for *M. bolleyi* related to previous cropping sequence; this fungus was present at significantly lower levels only after the NC-F sequence.

Analysis of tillage system effects was done for all barley crops regardless of cropping sequence, and also separately for barley preceded by a cereal or an oilseed crop (Table 2). The CRRI was higher under CT than reduced tillage for all crops combined. In most cases, *C. sativus* was more common, and *Fusarium* spp. less common, in SI of barley grown under CT than reduced tillage. This appeared to be attributed mostly to higher levels of *F. avenaceum* and *F. graminearum* under reduced tillage. For barley grown after a cereal crop, *F. graminearum* was also found at the highest levels under MT. *F. culmorum* was isolated at lower levels when barley was grown under ZT than MT and/or CT when barley was grown after a cereal or an oilseed. *F. equiseti* was also present at lower levels under CT when barley was grown after a cereal, whereas *M. bolleyi* was lowest under CT when barley was grown after a cereal or an oilseed crop.

Herbicide Effects on CRRI and Fungal Isolations

Herbicide analysis (yes/no) was done by tillage system, although sample size was larger for MT- than for CT- or ZT-managed fields (Table 3). There was no significant effect of herbicide group on CRRI under MT, with significant effects of Group 4 on CRRI for barley under CT and ZT not being consistent. For all herbicide groups, there were significant negative and positive effects of herbicide applications in the previous 18 months on the most common fungal isolates. For barley grown under MT, Group 1 herbicides were associated with significantly lower levels of total *Fusarium* spp. and *F. culmorum*, whereas Group 9 herbicides were associated with higher levels of total *Fusarium* spp., *F. culmorum* and *F. graminearum*, but lower levels of *C. sativus*. There was also a tendency for levels of *F. avenaceum* to be higher in sprayed than unsprayed fields for Group 9, but lower for sprayed than unsprayed fields for Group 1 herbicides. The same effects of Group 9 herbicides on fungal isolations observed under MT were in most cases also observed under CT and/or ZT; although, in most cases these were not significant ($P > 0.10$), except for *F. avenaceum* for barley under ZT which was present at higher levels in sprayed than unsprayed fields. In contrast, for Group 2 and 4 herbicides, there were generally lower levels of *Fusarium* spp. in sprayed than unsprayed fields under CT and/or ZT management.

Discussion

Cropping sequence had less impact on the extent of SI discoloration (CRRI) than tillage system. In general, tillage effects on SI discoloration or percent fungal isolations did not seem to depend on the previously-grown crop. While CRRI and *C. sativus* isolations from SI were favored by CT management, colonization by *Fusarium* spp., especially *F. avenaceum* and *F. graminearum*, increased under reduced tillage. Our observations on tillage effects on the relative prevalence of these fungi agree with previous studies (Fernandez, unpublished; Windels and Wiersma, 1992).

C. sativus also occurred at higher levels in barley grown in production systems of cereals alternated with summerfallow under CT or MT than in most other sequences. However, levels of this fungus in barley grown immediately after summerfallow were not significantly different than when grown after a crop. Piening and Orr (1988) found that CRR in barley was lower after summerfallow than after another susceptible crop. For the most part, *Fusarium* spp. were not significantly affected by

summerfallow versus a crop either, except for *F. culmorum* which was significantly reduced when barley was grown after summerfallow, or a cereal crop and summerfallow.

Although an oilseed grown in the previous year was associated with lower levels of *C. sativus* than a cereal crop, barley grown after two years of noncereals had lower levels of this fungus than when grown after a cereal alternated with a noncereal, though its levels were not significantly different than after two cereals.

Growing a noncereal crop in the previous one or two years was in turn associated with higher levels of *Fusarium* spp. in the succeeding barley crop compared to a cereal or other continuous sequences that included a cereal. This could be attributed to higher levels of *F. avenaceum, F. culmorum*, *F. equiseti,* and *F. graminearum* observed after an oilseed and/or pulse crop, or two years of noncereals. Most of the barley crops grown after one or two noncereals were under reduced tillage (MT and ZT), which may have confounded these results considering the positive effect of reduced tillage on *Fusarium* isolations. However, barley grown after NC-F (mostly under CT and MT) had similar levels of *Fusarium* spp. than when grown after NC-NC, suggesting that the previously-grown crop had a greater impact on these fungi than the method of tillage management.

The positive relationship of reduced tillage and previously-grown noncereal crops with *Fusarium* spp. in SI and the association of *F. graminearum* with a previously-grown oilseed were similar to that observed for spike infections of the same barley crops (Fernandez et al., 2007). The mechanism(s) by which noncereal crops, most of which were canola, contributed to the higher populations of *F. avenaceum* and *F. graminearum,* especially the latter, in SI of barley is not known. However, in both of these barley studies and a spring wheat study conducted in the same area and during the same years (Fernandez et al., 2005), there was also a positive impact of glyphosate applied mostly on fields where canola had been grown, on pathogenic *Fusarium* spp., including *F. avenaceum*, *F. culmorum* and *F. graminearum.* Glyphosate was in fact the only herbicide associated with higher levels of *Fusarium* spp. in SI of barley in the present study. Although analysis of barley grown after a crop other than canola showed similar associations of *Fusarium* isolations with previous glyphosate use, because of the nature of these studies the impact of a previously-grown canola crop from that of previous glyphosate applications could not be completely separated.

In addition to a positive association of previous glyphosate use with isolation of *Fusarium* spp. from barley SI, this study also showed a significant negative association of previous glyphosate use with *C. sativus* in fields under MT, suggesting changes in populations of the most common root rot fungi associated with the use of this herbicide. No other herbicide group seemed to consistently affect levels of this cereal pathogen. The observation that similar negative associations of previous glyphosate use with *C. sativus* were also apparent under CT and ZT suggests that changes in levels of this pathogen might be due to direct effect(s) of this herbicide and were not related to tillage management. There are no previous reports of glyphosate effects on plant tissue infection by *C. sativus*. The observation that *Fusarium* spp. in barley increased in fields previously treated with glyphosate formulations agrees with previous reports on *Fusarium* colonization of other crops being associated with glyphosate use. For example, Levesque et al. (1987) reported that glyphosate application increased root colonization of various treated weeds by *F. avenaceum* and *F. oxysporum*, and it also increased the propagule density of these *Fusarium* spp. in the soil. In addition, Levesque et al. (1993) reported that glyphosate-treated wheat seedlings were colonized to a greater extent than

untreated seedlings by *Fusarium* spp. under warm and dry conditions than under lower temperatures and moist conditions. Further, glyphosate-treated quackgrass rapidly colonized by *F. culmorum* caused damage to a subsequent barley crop (Lynch and Penn, 1980).

From our data, we could not determine if the higher *Fusarium* levels associated with previous glyphosate use was due to effects on fungal inoculum or host susceptibility, or to the absence of competition from *C. sativus*. Furthermore, how much the observed association with previous glyphosate use contributed to increased relative levels of *Fusarium* spp. in reduced tillage systems, and how much might be due to other factors such as microenvironment in these systems, could also not be determined. Separating the effects of the various agronomic practices relating to cropping sequence and tillage system would be necessary to understand the role that each of these play in disease levels and the relative frequency of the various pathogens.

Based on the results of this CRR survey of barley conducted in eastern Saskatchewan, we conclude that growing this crop under reduced tillage systems that include glyphosate applications and with noncereal crops incorporated in the rotation, will result in lower levels of *C. sativus*, the most common CRR pathogen in western Canada. However, these production systems will likely result in an increase in infection by *Fusarium* spp. Although the latter remained at lower levels than *C. sativus*, increases in populations of *F. avenaceum* and *F. graminearum*, especially in areas with higher disease pressure than where the present study was conducted, might not only cause greater development of crown/root rot but also of spike infections in subsequently-grown cereal crops. Because *Fusarium* infections in crown/roots would be less affected by environmental conditions than spike infections, they might also contribute to the maintenance of inoculum in years not conducive to FHB development and thus to the further spread of this disease in the Canadian Prairies. As suggested by Fernandez et al. (2007) for a study of FHB and *Fusarium*-damaged kernels on the same barley crops sampled in this study, the observation that similar crop production factors were associated with some of the most common pathogenic *Fusarium* spp. in SI and spikes/kernels of barley suggests that measures aimed at reducing crown/root rot caused by *Fusarium* spp. might also help to reduce FHB development in this crop on the Canadian Prairies.

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Table 1. Effect of Previous Crop(s)/Summerfallow on Common Root Rot Index (CRRI) and Percentage Isolation of the Most Common Fungi Isolated from Subcrown Internodes, Sampled in Crop Districts 1B and 5A in Eastern Saskatchewan, 1999-2001.

Effect/ Contrast	No.	CRRI	*Cs*[1]	*Fus*spp.	*Fav*	*Fc*	*Fe*	*Fg*	*Mb*
		---------- *P* value ----------							
Previous crop		0.315	0.153	0.001	0.323	0.154	0.212	0.312	0.689
cereal vs. oilseed/pulse		0.981	0.297	0.001	0.152	0.032	0.612	0.092	0.242
cereal vs. oilseed		0.395	0.076	0.008	0.208	0.979	0.249	0.124	0.357
cereal vs. pulse		0.711	0.934	0.006	0.282	0.026	0.932	0.278	0.334
oilseed vs. pulse		0.436	0.139	0.175	0.646	0.026	0.695	0.928	0.636
summerfallow vs. others		0.344	0.231	0.628	0.535	0.050	0.130	0.957	0.705
		---------- Mean % (SE) ----------							
cereal	50	1.7 (0.1)	53.7 (2.8)	14.8 (1.3)	3.6 (0.6)	2.2 (0.7)	7.1 (1.1)	0.8 (0.3)	11.8 (1.2)
oilseed	59	1.6 (0.1)	47.0 (2.6)	22.1 (2.3)	5.4 (0.9)	2.8 (0.9)	9.0 (1.5)	2.2 (0.8)	10.2 (1.2)
pulse	11	1.8 (0.2)	54.5 (4.0)	30.5 (5.2)	6.2 (2.3)	12.8 (5.3)	7.7 (5.0)	2.5 (1.4)	8.0 (3.2)
summerfallow	14	1.8 (0.1)	59.1 (4.1)	23.5 (3.2)	5.7 (1.8)	1.7 (1.3)	12.9 (2.7)	1.9 (1.4)	11.8 (2.9)
		---------- *P* value ----------							
Previous two crops[2]		0.617	0.001	0.002	0.903	0.006	0.000	0.944	0.002
C-C vs. C-F		0.254	0.100	0.598	0.615	0.078	0.682	0.722	0.846
C-C vs. NC-NC		0.622	0.156	0.005	0.572	0.705	0.006	0.838	0.198
C-F vs. NC-F		0.490	0.058	0.315	0.826	0.049	0.470	0.565	0.043
C-NC vs. C-F		0.127	0.338	0.190	0.613	0.003	0.018	0.877	0.693
C-NC vs. NC-F		0.537	0.126	0.019	0.691	0.640	0.015	0.509	0.001
C-NC vs. NC-NC		0.521	0.000	0.000	0.512	0.875	0.000	0.543	0.494
NC-NC vs. C-F		0.480	0.001	0.027	0.396	0.267	0.013	0.601	0.467
		---------- Mean % (SE) ----------							
C-C	15	1.6 (0.1)	46.7 (5.6)	19.9 (2.9)	4.9 (1.2)	2.1 (1.0)	10.6 (2.8)	1.3 (0.9)	13.4 (2.2)
C-NC	74	1.6 (0.1)	52.4 (2.2)	17.6 (1.7)	4.6 (0.7)	3.3 (1.0)	5.6 (0.8)	1.9 (0.6)	11.4 (1.1)
NC-NC	11	1.6 (0.1)	45.1 (5.6)	27.3 (5.1)	3.8 (1.3)	5.4 (4.1)	14.4 (4.2)	1.1 (0.8)	10.2 (2.5)
C-F	16	1.8 (0.1)	60.2 (4.0)	19.0 (2.8)	4.7 (1.6)	0.6 (0.4)	10.3 (1.9)	2.0 (1.2)	13.3 (2.7)
NC-F	19	1.8 (0.1)	46.4 (4.2)	27.9 (4.2)	5.9 (1.4)	4.7 (2.1)	14.8 (3.9)	1.0 (0.7)	4.5 (1.3)
		---------- *P* value ----------							
Previous two crops - by first crop[3]		0.749	0.001	0.000	0.702	0.642	0.000	0.161	0.016
C*-NC vs. O*-C		0.450	0.155	0.048	0.231	0.982	0.955	0.047	0.548
		---------- Mean % (SE) ----------							
C*-NC	32	1.7 (0.1)	55.9 (3.5)	13.1 (1.4)	3.1 (0.8)	2.3 (1.1)	5.9 (1.0)	0.5 (0.3)	11.0 (1.5)
O*-C	36	1.6 (0.1)	49.4 (3.4)	19.8 (2.9)	5.4 (1.2)	2.5 (1.1)	6.0 (1.4)	3.0 (1.2)	12.2 (1.7)

[1] *Cs*, *Cochliobolus sativus*; *Fus*spp., total *Fusarium* spp.; *Fav, F. avenaceum*; *Fc, F. culmorum*; *Fe, F. equiseti*; *Fg, F. graminearum*; *Mb, Microdochium bolleyi*.
[2] C, cereal; NC, noncereal; F, summerfallow; O, oilseed. Barley crops grouped according to the previous two crops, regardless of the order in the sequence (C-C, C-NC, NC-NC, C-F, and NC-F).
[3] Barley crops grouped according to first crop in the previous two-year crop sequence (e.g., C*-NC for C as the first crop, O*-C for oilseed (O) as the first crop in the C-NC sequence).

Table 2. Effect of Tillage System on Common Root Rot Index (CRRI) and Percentage Isolation of the Most Common Fungi Isolated from Subcrown Internodes, for all Barley Crops, and for those Preceded by a Cereal or an Oilseed crop, Sampled in Crop Districts 1B and 5A in Eastern Saskatchewan, 1999-2001.

Effect/Contrast	No.	CRRI	*Cs*[1]	*Fus*spp.	*Fav*	*Fc*	*Fe*	*Fg*	*Mb*
		---------- *P* value ----------							
All previous crops		0.074	0.001	0.011	0.026	0.663	0.445	0.008	0.742
CT vs. MT, ZT[2]		0.016	0.000	0.006	0.012	0.907	0.187	0.005	0.391
		---------- Mean % (SE) ----------							
CT	28	1.9 (0.1)	62.6 (3.2)	14.6 (2.3)	3.4 (0.9)	3.0 (1.3)	6.3 (1.7)	0.2 (0.2)	9.9 (1.9)
MT	82	1.6 (<0.1)	49.0 (2.1)	20.5 (1.7)	4.6 (0.7)	3.6 (0.9)	8.5 (1.2)	2.1 (0.6)	10.4 (0.9)
ZT	23	1.6 (0.1)	45.8 (3.9)	25.7 (2.6)	7.2 (1.4)	2.2 (1.9)	11.7 (2.2)	2.0 (1.0)	13.4 (2.3)
		---------- *P* value ----------							
Cereal		0.138	0.045	0.000	0.114	0.004	0.258	0.178	0.583
CT vs. MT, ZT		0.513	0.032	0.001	0.090	0.227	0.070	0.058	0.091
		---------- Mean % (SE) ----------							
CT	11	1.9 (0.2)	65.9 (5.5)	8.4 (1.8)	1.9 (0.9)	0.6 (0.4)	5.1 (1.5)	0.0 (0.0)	9.8 (2.7)
MT	31	1.6 (0.1)	50.6 (3.6)	16.0 (1.8)	4.1 (0.9)	3.3 (1.1)	6.5 (1.4)	1.3 (0.5)	11.5 (1.4)
ZT	8	1.7 (0.1)	48.9 (6.4)	19.0 (2.2)	3.8 (1.5)	0.0 (0.0)	12.3 (2.6)	0.0 (0.0)	15.9 (3.9)
		---------- *P* value ----------							
Oilseed		0.904	0.003	0.551	0.014	0.025	0.401	0.700	0.000
CT vs. MT, ZT		0.553	0.001	0.411	0.007	0.518	0.892	0.491	0.000
		---------- Mean % (SE) ----------							
CT	9	1.6 (0.1)	63.8 (5.5)	17.5 (5.2)	3.6 (1.7)	5.0 (3.5)	6.1 (3.8)	0.6 (0.6)	3.3 (1.6)
MT	39	1.6 (0.1)	44.4 (3.1)	21.9 (3.0)	5.0 (1.1)	3.0 (1.1)	8.5 (1.8)	2.6 (1.0)	10.5 (1.4)
ZT	10	1.6 (0.1)	42.0 (6.2)	27.0 (4.6)	8.7 (2.0)	0.2 (0.2)	13.8 (4.0)	2.2 (1.5)	15.3 (3.3)

[1] *Cs*, *Cochliobolus sativus*; *Fus*spp., total *Fusarium* spp.; *Fav, F. avenaceum*; *Fc, F. culmorum*; *Fe, F. equiseti*; *Fg, F. graminearum*; *Mb, Microdochium bolleyi*.
[2] CT, conventional-till; MT, minimum-till; ZT, zero-till.

Table 3. Effect of Herbicide Use (Previous 18 Months) on Common Root Rot Index (CRRI), and Percent Isolation of Fungi, of Barley Crops within each Tillage System, Sampled in Crop Districts 1B and 5A in Eastern Saskatchewan, 1999-2001.

Herbicide group	Tillage system	Herbicide use	No.	CRRI	*Cs*[1]	*Fus*spp.	*Fav*	*Fc*	*Fe*	*Fg*
				P value						
Group 1	CT[2]			0.193	0.448	0.651	0.384	0.941	0.283	1.000
	MT			0.371	0.899	0.020	0.205	0.074	0.232	0.880
	ZT			0.520	0.821	0.713	0.763	0.554	0.622	0.110
Group 2	CT			0.441	0.335	0.616	0.489	0.325	0.630	1.000
	MT			0.142	0.435	0.290	0.682	0.754	0.424	0.397
	ZT			0.412	0.284	0.034	0.375	0.278	0.140	0.528
Group 4	CT			0.053	0.025	0.636	0.075	0.520	0.047	1.000
	MT			0.436	0.860	0.722	0.879	0.277	0.839	0.260
	ZT			0.016	0.149	0.138	0.001	0.280	0.887	0.399
Group 9	CT			0.165	0.125	0.229	0.448	0.923	0.472	1.000
	MT			0.934	0.033	0.027	0.296	0.056	0.667	0.092
	ZT			0.494	0.219	0.765	0.021	0.325	0.377	0.815
				Mean % (SE)						
Group 1	CT	No[3]	7	1.6 (0.3)	50.5 (5.0)	20.7 (3.6)	3.7 (1.6)	5.2 (3.0)	9.3 (4.1)	0.0 (0.0)
	CT	Yes	9	2.1 (0.2)	60.4 (5.7)	19.2 (5.4)	5.3 (1.9)	4.5 (3.3)	7.3 (3.9)	0.0 (0.0)
	MT	No	18	1.7 (0.1)	49.1 (4.3)	29.1 (4.0)	5.8 (1.1)	6.9 (2.3)	12.5 (2.9)	2.5 (1.7)
	MT	Yes	63	1.6 (0.1)	49.5 (2.4)	18.2 (1.8)	4.2 (0.8)	2.7 (0.9)	7.6 (1.3)	2.0 (0.6)
	ZT	No	8	1.8 (0.1)	45.4 (6.6)	27.1 (5.7)	7.7 (2.2)	0.7 (0.5)	12.2 (5.1)	4.6 (2.3)
	ZT	Yes	13	1.5 (0.1)	45.5 (5.0)	25.3 (2.9)	7.4 (1.9)	3.3 (3.3)	11.1 (2.2)	0.6 (0.6)
Group 2	CT	No	11	1.9 (0.2)	57.9 (4.5)	17.7 (3.3)	4.1 (1.2)	3.3 (2.1)	7.7 (2.8)	0.0 (0.0)
	CT	Yes	6	1.9 (0.1)	51.9 (6.4)	24.4 (7.9)	5.7 (3.1)	8.1 (5.2)	9.3 (6.7)	0.0 (0.0)
	MT	No	42	1.7 (0.1)	52.3 (2.9)	19.1 (2.0)	4.4 (0.7)	3.1 (1.0)	9.5 (1.8)	1.6 (0.6)
	MT	Yes	39	1.5 (0.1)	46.3 (3.1)	22.3 (2.9)	4.7 (1.2)	4.2 (1.5)	7.8 (1.6)	2.6 (1.0)
	ZT	No	9	1.5 (0.1)	42.2 (5.9)	30.3 (4.7)	5.8 (1.3)	5.2 (4.6)	15.5 (4.3)	2.1 (1.5)
	ZT	Yes	12	1.7 (0.1)	47.8 (4.8)	22.7 (2.7)	8.8 (2.2)	0.2 (0.2)	8.5 (2.2)	2.2 (1.4)
Group 4	CT	No	4	2.1 (0.2)	60.3 (10.0)	26.9 (9.1)	9.0 (2.8)	10.3 (8.4)	3.8 (1.8)	0.0 (0.0)
	CT	Yes	13	1.8 (0.2)	55.1 (4.1)	18.2 (3.4)	3.6 (1.3)	3.5 (1.9)	9.2 (3.1)	0.0 (0.0)
	MT	No	23	1.6 (0.1)	50.1 (4.4)	21.0 (3.8)	3.7 (1.4)	5.6 (1.9)	7.5 (1.9)	3.4 (1.7)
	MT	Yes	58	1.6 (0.1)	49.2 (2.4)	20.5 (1.9)	4.9 (0.8)	2.8 (1.0)	9.1 (1.5)	1.6 (0.5)
	ZT	No	5	1.4 (0.1)	38.9 (9.1)	31.2 (1.4)	12.0 (3.7)	0.0 (0.0)	13.8 (3.3)	1.5 (1.4)
	ZT	Yes	16	1.7 (0.1)	47.5 (4.1)	24.3 (3.5)	6.1 (1.3)	3.1 (2.7)	10.8 (2.9)	2.3 (1.3)
Group 9	CT	No	9	2.0 (0.2)	59.6 (6.1)	16.2 (4.7)	4.0 (1.9)	4.5 (3.4)	5.8 (3.1)	0.0 (0.0)
	CT	Yes	7	1.8 (0.2)	51.5 (4.0)	24.4 (4.5)	5.4 (1.7)	5.2 (2.9)	11.2 (4.9)	0.0 (0.0)
	MT	No	26	1.7 (0.1)	56.3 (3.0)	15.5 (2.3)	3.4 (0.9)	1.5 (0.5)	8.3 (2.1)	0.9 (0.4)
	MT	Yes	55	1.6 (0.1)	46.2 (2.6)	23.0 (2.3)	5.1 (0.9)	4.6 (1.3)	8.8 (1.5)	2.7 (0.8)
	ZT	No	2	2.0 (0.1)	61.0 (8.2)	26.8 (8.0)	4.1 (0.1)	0.0 (0.0)	18.5 (4.8)	2.1 (1.6)
	ZT	Yes	19	1.6 (0.1)	43.8 (3.5)	25.9 (2.8)	7.9 (1.5)	2.6 (2.3)	10.8 (2.5)	2.1 (1.1)

[1] *C, Cochliobolus sativus*; *Fus*spp., total *Fusarium* spp.; *Fav, F. avenaceum*; *Fc, F. culmorum*; *Fe, F. equiseti*; *Fg, F. graminearum*.
[2] CT, conventional-till; MT, minimum-till; ZT, zero-till.
[3] No, no herbicide of this group applied; Yes, herbicide of this group applied at least once in previous 18 months.