



Crop sequence effects of 10 crops in the northern Great Plains

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Abstract

Dynamic cropping systems, which involve a long-term strategy of annual crop sequencing, require detailed information on management components known to influence crop performance. Considering that proper sequencing of crops is an important component for successful dynamic cropping systems, a research project was undertaken to determine the advantages and/or disadvantages of previous crop and crop residues for numerous crop sequences. A multi-disciplinary team of scientists evaluated crop sequence effects of 10 crops (barley, canola, crambe, dry bean, dry pea, flax, safflower, soybean, spring wheat, and sunflower) on seed yield, soil coverage by residue, soil water use, surface soil properties, and plant diseases in central North Dakota. Two years were required to establish a crop by crop residue matrix (crop matrix). During the second year (site 1, 1999; site 2, 2000) 10 crops were evaluated with a crop matrix. During the third and fourth year spring wheat (site 1, 2000; site 2, 2001) and sunflower (site 1, 2001; site 2, 2002), respectively, were seeded over the crop matrix. The seed yield of four crops (crambe, flax, safflower, and soybean) of the 10 crops evaluated in the crop matrix was influenced by the preceding crop at site 1 in 1999 an above average moisture year. The seed yield of eight crops (canola, crambe, dry bean, flax, safflower, soybean, spring wheat, and barley) was influenced by the preceding crop at site 2 in 2000 a more average precipitation year. Some of the lowest seed yields were obtained when a crop was seeded on its own residue. A synthesis of seed yield data from a given year provided overall values for

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positive and negative effects of crops and crop residue on subsequent crops. In general, the three legume crops had positive effects in contrast to non-leguminous crops, which usually had negative effects. However, sunflower was an exception among the non-leguminous crops; at site 2 in 2000, sunflower was positive for subsequent crops compared with canola or crambe, which had negative effects. Crop sequences composed of small cereal grains had the highest soil coverage by residue while sequences of two dicotyledonous species had considerably lower coverage. Soil water use among crops varied, ranging from sunflower with the numerically highest soil water use to dry pea with the least. Significant changes in surface soil properties due to crops were generally not detected in this short-term project. Given the variation in *Sclerotinia* disease incidence for canola, crambe, safflower, and sunflower within the crop matrix, it was difficult to detect significant differences based on the previous crop. Differences were evident two years later when the highest incidence of *Sclerotinia* basal stalk rot for sunflower was detected in plots where crambe was grown two years earlier. During the third year, when spring wheat was seeded over a crop matrix, spring wheat yields increased following 23 and 19 crop sequence treatments out of a possible 100 at site 1 and site 2, respectively, compared to the continuous wheat treatment. All crop sequence treatments that yielded better than the continuous wheat treatment were comprised of mostly non-cereal crops, demonstrating the positive impact of crop diversity on cereal crop production. The severity of leaf spot diseases on spring wheat were affected by crop sequence and fungal spore production was greatest on the continuous wheat treatment. Even though decreases in leaf spot disease severity and modest yield increases were obtained with some crop sequence treatments, significant yield increases due to reduced leaf spot disease severity were not obtained under our conditions. © 2005 Elsevier Ltd. All rights reserved.

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1. Introduction

The northern Great Plains of North America is recognized throughout the world for its fertile soils, which contribute to the production of large quantities of cereal grain, oilseed, and pulse crops. This area, which includes most of Montana, North Dakota, South Dakota, and parts of Wyoming and Nebraska in the United States as well as arable regions of Manitoba, Saskatchewan, Alberta, and British Columbia in Canada, contains approximately 52 Mha of cropland and contributes over \$20 billion in annual agricultural output (Padbury et al., 2002; Statistics Canada, 2003; US Census Bureau, 2002). Despite this impressive level of production, there are concerns about the sustainability of cropping systems within the region. High climatic variability within the northern Great Plains leads to economic instability of crop production practices (Peterson, 1996). This instability is exacerbated by historical and current trends that include a lack of crop diversity (Brummer, 1998; Peterson et al., 1996), declines in soil organic matter (Campbell et al., 1996; Lyon et al., 1997), and improper management of crop nutrients (Westfall et al., 1996).

Diversification, opportunism, risk avoidance, and flexibility are four principles considered essential to create a more sustainable agriculture in highly dynamic eco-regions such as the northern Great Plains (Behnke et al., 1993; Dhuyvetter et al.,

1996; Sandford, 1982). Development and utilization of more diverse cropping systems is closely aligned with these principles. Diverse cropping systems have been proposed to reverse many of the negative socio-economic and environmental impacts of predominant crop production practices in the region (Zentner et al., 2001). For such a reversal to occur, however, information on the agronomic potential, environmental impact, and economics of alternative crops is needed. Obtaining such information is complicated by the fact that individual crops interact differently with numerous management components, such as tillage methods, crop sequencing, cultivar selection, nutrient management, and weed and disease control. Understanding how individual crops and management components interact is essential in the development of practical, efficient, and cost-effective cropping systems capable of stabilizing crop production while minimizing deleterious effects on the environment (Hanson et al., 2003).

Tanaka et al. (2002) developed the concept of dynamic cropping systems to facilitate the determination of causal relationships between crop performance and specific management components. As defined, dynamic cropping systems refer to a long-term strategy of annual crop sequencing that optimizes crop and soil use options and the attainment of production, economic, and resource conservation goals by using sound ecological management principles (Tanaka et al., 2002). Optimizing cropping options to meet these goals requires detailed information on multiple management components known to influence crop performance. This information should provide clearer recommendations for proper crop sequencing, which has long been viewed as crucial for cropping system success (Leighty, 1938; Pierce and Rice, 1988).

The objective of this study was to determine the advantages and/or disadvantages of previous crop and crop residues for numerous crop sequences in the northern Great Plains. Specifically, we sought to evaluate the effects of crop sequencing on crop performance, soil coverage by residue, soil water use, surface soil properties, and plant diseases in a crop matrix.

2. Methodology

2.1. Description of experiment

The research project was located at the Area IV Soil Conservation Districts/USDA-ARS-Northern Great Plains Research Laboratory Research Farm approximately 6 km southwest of Mandan, ND (46°46'22"N, 100°57'09"W). The site, occupying approximately 12.2 ha, was on gently rolling uplands (0–3% slope) with a silty loess mantle overlying till. The predominant soil at the site was a Wilton silt loam (fine-silty, mixed, superactive frigid Pachic Haplustoll). Average soil bulk density, soil pH, and total C in the surface 7.5 cm was 1.34 Mg m⁻³, 6.1, and 21.7 Mg ha⁻¹, respectively. Prior to initiating the experiment, the site was in a hard red spring wheat (*Triticum aestivum* L.)-winter wheat-sunflower (*Helianthus annuus* L.) rotation under reduced tillage management for 14 yr. From 1914 to 2000, annual precipitation averaged 409 mm, with 79% of the total received during the growing season from April through September. Average annual temperature was 4 °C, though daily

averages range from 21 °C in the summer to –11 °C in the winter. Long-term precipitation and temperature data were recorded about 5 km northeast of the study site.

An experimental crop by crop residue matrix design was used to allow the simultaneous evaluation of numerous crop sequences in the same experiment under similar weather and soil conditions. Two years were required to form a crop by crop residue matrix (referred to hereafter as crop matrix) in which 10 crops were direct seeded into the crop residue of the same 10 crops (Fig. 1). In 1998, a field was divided into two sites (approximately 6.1 ha each). During the first year (1998 and 1999 for the site 1 and site 2, respectively; Table 1), four replicates of 10 crops (barley [*Hordium vulgare* L.], dry bean [*Phaseolus vulgaris* L.], canola [*Brassica napus* L.], crambe [*Crambe abyssinica* Hochst. ex R.E. Fr.], flax [*Linum usitatissimum* L.], dry pea [*Pisum sativum* L.], safflower [*Carthamus tinctorius* L.], soybean [*Glycine max* (L.) Merr.], sunflower, and spring wheat) were direct seeded in 9-m wide strips with a John Deere 750 no-till drill into a uniform cereal residue (winter wheat in the east field; barley in the west field). During the second year (Table 1), the same 10 crops were direct seeded perpendicular over the residue of the previous year's crops. This established a 10 × 10 matrix with 100 treatment combinations, where each crop was grown on 10 crop residues (Fig. 1). Treatments were replicated four times each year following a strip-block design with individual 9 × 9 m plots considered as experimental units. In the third year (Table 1), spring wheat was uniformly seeded over a previous crop matrix. In the fourth year (Table 1), sunflower was uniformly seeded

Crop by crop residue matrix, 100 plots												
											Crop	
1	2	3	4	5	6	7	8	9	10	1	First year, ten crops seeded in strips	
11	12	13	14	15	16	17	18	19	20	2		
21	22	23	24	25	26	27	28	29	30	5		
31	32	33	34	35	36	37	38	39	40	9		
41	42	43	44	45	46	47	48	49	50	7		
51	52	53	54	55	56	57	58	59	60	10		
61	62	63	64	65	66	67	68	69	70	6		
71	72	73	74	75	76	77	78	79	80	3		
81	82	83	84	85	86	87	88	89	90	4		
91	92	93	94	95	96	97	98	99	100	8		
5	2	7	1	8	4	6	9	3	10	Crop	Second year, ten crops seeded perpendicular over crop residue	

Fig. 1. Design of one replicate of a crop matrix used to evaluate the influence of crop sequence. During the first year 10 crops (numbered 1 through 10) were seeded into a uniform crop residue. During the second year the same crops were no-till seeded perpendicular over the residue of the previous year's crop. Individual plot numbers were assigned for each of the four replications.

Table 1
Crops and sites used to evaluate the influence of crop sequence

Year	Crop	Site 1 ^a	Site 2 ^a
1	Ten crops ^b	1998	1999
2	Crop matrix, 10 crops ^c	1999	2000
3	Spring wheat seeded over crop matrix	2000	2001
4	Sunflower seeded over crop matrix	2001	2002

^a In 1998 a field was divided into two sites to provide two site years.

^b Two years were required to establish a crop matrix (crop by crop residue matrix). During the first year 10 crops were seeded in strips to provide residue into which 10 crops were seeded during the second year.

^c Two years were required to establish a crop matrix. During the second year 10 crops were seeded perpendicular over the crop residue from the first year to form a crop matrix.

following spring wheat on a previous crop matrix. At site 1 the sunflower crop was compromised by a damaging wind storm. Thus, sunflower yield data are not included in this paper. However, *Sclerotinia sclerotiorum* (Lib.) De Bary disease data obtained from site 2 are presented.

Cultural practices used during the experiment were similar to those of local no-till producers. Planting and harvesting operations were conducted based on locally optimal time periods for each crop (Table 2). Seed yield was determined by harvesting 11.4 m² area with a plot combine. Nitrogen was applied as a mid-row (between every other row) band application of NH₄NO₃ at 67 kg N ha⁻¹ during seeding of all crops. Phosphorus was applied with the seed as 0-44-0 at 11 kg P ha⁻¹. Appropriate fungicide seed treatments were used except for dry bean, dry pea, and soybean to which recommended inoculants were applied. Weeds were controlled with herbicides following standard no-till recommendations for each crop and crop sequence.

Table 2
Cultivars, seeding rate, and seeding and harvesting dates used for the 10 crops in the crop matrix

Crop	Cultivar	Viable seeds ha ⁻¹	Seeding date	Harvest date
Canola	Dynamite	2.5 million	Late April to mid-May	Early to late August
Crambe	Meyer	2.0 million	Late April to mid-May	Early to late August
Dry bean	T-39 (1999) Black shadow (1998, 2000)	222,000	After all possible chance of frost to early June	Late August to late September
Dry pea	Profi	864,000	Early April to mid-May	Early to mid-August
Flax	Omega	9.9 million	Late April to mid-May	Early August to mid-September
Safflower	Montola 2000	494,000	Late April to mid-May	Late August to mid September
Soybean	Jim	494,000	Late May to first week in June	Mid to late September
Sunflower	Cenex 803	69,000	Mid-May to early June	Early to late October
Spring wheat	Amidon	3.2 million	Late March to mid-May	Early to late August
Barley	Stander	3.2 million	Late March to mid-May	Early to late August

Volunteer crops as well as weed problems were minimal because of weather conditions and management practices.

2.2. *Residue carryover*

In the third year, when spring wheat was seeded over the crop matrix in 2001 (site 2), soil coverage by crop residue was measured with a transect technique (Tanaka and Hofman, 1994). Counts of residue presence were taken at 25 points equally spaced along a 7.6-m cable, which was stretched across each plot four times to count the number of residue contacts for a total of 100 points. On each plot, two V patterns were formed, which pointed in the same direction of seeding. When residue intersected with a point on the cable, it was counted as a contact. Total number of residue contacts and number of obvious wheat residue contacts were recorded. Counts were done soon after spring wheat seeding, before emergence.

2.3. *Soil water*

Soil water measurements were taken in the spring to determine the amount of soil water present after the 10 crops were grown. Measurements were done immediately following spring wheat seeding in plots on which the 10 alternative crops had been grown the previous year. Selected plots were located at site 1 in 1999 and at site 2 in 2000 and 2001 (Table 1). Access tubes (steel pipes, 2.7 m in length and 40 mm inside diameter) were installed in the center of each treatment plot of interest. Soil water measurements were taken in these access tubes to a depth of 2.1 m at 0.3 m intervals. Water contents were measured with a Model DR503 nuclear moisture gauge (CPN International Inc.). Moisture gauge calibration was achieved through comparison of moisture gauge readings with volumetric water content measurements, which combined gravimetric soil water and soil bulk density determinations.

2.4. *Surface soil properties, crop matrix*

Prior to the uniform seeding of spring wheat on the experimental area soil samples were collected within plots where a crop was seeded on its own crop residue (e.g., barley/barley) in the spring of 2000 (site 1) and 2001 (site 2). During each year, soil samples were collected in three replicates of the experiment where inherent soil conditions were most uniform based on inspection of a soil survey map. In each plot, 10 soil cores were collected from the 0 to 7.5 cm depth using a 3.1 cm (i.d.) step-down probe. To ensure composite soil samples were representative of soil conditions in each plot, four cores each were collected from the row, four from the non-wheel tracked interrow, and two from the wheel tracked interrow. Each sample was saved in a double-lined plastic bag, placed in cold storage at 5 °C, and analyzed for chemical and biological attributes within 2-wk of collection.

Soil samples were processed by sieving through a 2.0-mm sieve at field moisture content and subsampled for chemical and biological analyses. Identifiable plant material retained on the sieve was dried at 55 °C and weighed. Soil pH was estimated

from a 1:1 soil–water mixture (Watson and Brown, 1998). Particulate organic matter (POM) was estimated by weight loss-on-ignition for the 0.053–0.5 and 0.5–2.0 mm size fractions (Cambardella et al., 2000). Potentially mineralizable nitrogen was estimated from the $\text{NH}_4\text{-N}$ accumulated after a 7-d anaerobic incubation at 40 °C (Bundy and Meisinger, 1994). Soil microbial biomass carbon was estimated using the microwave irradiation technique (Islam and Weil, 1998). Fifty grams of field moist soil was incubated 10-d at 55% water-filled pore space in the presence of 10 ml of 2.0 M NaOH. Carbon dioxide content was determined by single end-point titration with 0.1 M HCl (Paul et al., 1999). Flush of CO_2 -carbon following irradiation was calculated without subtraction of a 10-d control as suggested by Franzuebbers et al. (1999). Soil microbial biomass nitrogen was estimated from a 10-d mineral nitrogen flush between irradiated and non-irradiated soil following the method of Shen et al. (1984). Soil $\text{NO}_3\text{-N}$ and $\text{NH}_4\text{-N}$ were estimated from 1:10 soil–KCl (2 M) extracts using cadmium reduction followed by a modified Griess–Ilosvay method and indophenol blue reaction (Mulvaney, 1996). Gravimetric data were converted to a volumetric basis by sampling depth using field measured soil bulk density (Blake and Hartge, 1986). All data were expressed on an oven-dry basis.

2.5. Leaf spot disease on spring wheat following crop matrix

Leaf spot disease severity on spring wheat and barley following 10 crops in the crop matrix (sites 1 and 2) was previously reported (Krupinsky et al., 2004). In the third year, when spring wheat was uniformly seeded over each crop matrix (Table 1), spring wheat was evaluated for leaf spot disease severity at both sites as in a previous study (Krupinsky et al., 2004). The total percentage of necrosis and chlorosis was visually assessed for individual spring wheat leaves (20 leaves per plot for each evaluation) and used as an indicator of the severity of leaf spot diseases. The leaves evaluated for disease severity were the flagleaf (the uppermost leaf), flagleaf-1 (first leaf below the flagleaf), flagleaf-2, and flagleaf-3.

Spring wheat was evaluated for disease severity following selected crop sequence treatments. Evaluated crop sequence treatments included: (1) spring wheat after nine alternative crops (one year without spring wheat: spring wheat/alternative crop/spring wheat); (2) spring wheat after two alternative crops (two years without spring wheat: alternative crop/alternative crop/spring wheat); and (3) spring wheat after spring wheat. The spring wheat after spring wheat treatments (spring wheat/spring wheat/spring wheat and flax/spring wheat/spring wheat) were considered to be most favorable for disease development. For the first two evaluations of 2000, three replicates of 22 crop sequence treatments were evaluated for leaf spot disease severity at site 1. Afterwards, additional crop sequence treatments in which a crop was seeded on its own crop residue (e.g. barley/barley/spring wheat) were included, giving a total of 29 crop sequence treatments for evaluation. Even though seeding a crop on its own crop residue is not a recommended management practice, the treatments were used to obtain a more uniform crop residue of a particular crop. In 2001, four replicates of 32 crop sequence treatments were evaluated for leaf spot disease severity at

site 2. Disease severity was evaluated seven times in 2000 (June 28–July 17) and eight times in 2001 (June 27–July 17).

2.6. *Fungal spores, spring wheat following crop matrix*

Fungal conidia of *Pyrenophora tritici-repentis* [Died.] Drechs., cause of tan spot disease on wheat, were monitored during the 2001 season within several crop sequence treatments using spore samplers at site 2. Ten spore samplers (Rotorod samplers, Model 82, Multidata, St. Louis Park, MN) were placed within spring wheat in two replicates of the flax/dry bean/spring wheat, flax/safflower/spring wheat, and dry pea/crambe/spring wheat treatments to provide residue treatments without spring wheat for two years. Considering the field size and distances between plots these treatments were selected because they could be efficiently monitored. Spore samplers were also placed in four replicates of continuous wheat for comparison. The samplers operated 10% of the time and the “I” rods were changed daily, mounted, stained and stored as previously described (Krupinsky, 1992). The fungal spores were examined microscopically on an 18 mm section of the sampling rod (under the 18 mm cover slip) with a compound Zeiss microscope illuminated with an Illuminator 100. Spore production was monitored from May 16 (DOY 136) to July 6 (DOY 187).

2.7. *Sclerotinia disease, crop matrix; sunflower following crop matrix*

The fungus, *S. sclerotiorum*, causes Sclerotinia stem rot (white mold) on canola and crambe, Sclerotinia stem rot and head rot (head blight) on safflower and sunflower (Bailey et al., 2003; Nyvall, 1999). Canola, crambe, safflower, and sunflower plants were evaluated for Sclerotinia diseases within the crop matrix at both sites. Canola and crambe plants with bleached (white) stems, stems sometimes shredding, were rated positive for Sclerotinia at both sites (100 plants per plot) (Lamey, 1995). Safflower heads were rated positive for the incidence of Sclerotinia head blight when a sclerotium (hard fungal body) was present under a necrotic head. Fifty and 100 heads per plot were evaluated at site 1 and 2, respectively. Sunflower plants were rated positive for Sclerotinia basal stem rot (50 and 25 plants per plot at site 1 and 2, respectively) when a basal stem canker was present at the base of the plant. A tan, grayish or green-brown canker forms at the base of a Sclerotinia infected plant and, as the decay progresses, the stalk becomes bleached with a shredded appearance (Gulya et al., 1994).

In the fourth year, sunflower was uniformly seeded following spring wheat over the crop matrix (Table 1). Because Sclerotinia basal stem rot on sunflower is initiated by root contact with the fungus (Gulya et al., 1994), sunflower was used as a Sclerotinia-indicator crop. Thus, sunflower provided an assessment of Sclerotinia carryover associated with various crop sequence treatments. Sunflower plants grown on four replicates of 100 treatments were evaluated for presence of Sclerotinia basal stem rot (60 plants per plot) on September 4 and 18 at site 2.

2.8. Statistical analysis

Crop production and soil water data were analyzed using the GLM procedure (SAS, 8.0, SAS Inst., Cary, NC). Statistical comparisons within each evaluation were made with Tukey's HSD test. Crop residue data were analyzed using the GLM procedure and statistical comparisons were made with Scheffe's test. When spring wheat was seeded over each previous crop matrix during the third year (Table 1), Dunnett's one-tailed test was used to make comparisons between crop sequence treatments and the continuous wheat treatment, which was considered to have the lowest yield potential. Mean values of soil properties as affected by crop were compared using PROC MIXED (Littell et al., 1996). All statistical differences were evaluated at a probability level of $p \leq 0.05$.

Severity of leaf spot diseases associated with various crop sequences was compared using the GLM procedure (SAS, 8.0, SAS Inst., Cary, NC). Dunnett's one-tailed test was used to make comparisons between the crop sequence treatments and the continuous wheat treatment, which was considered to be the most favorable for leaf spot disease development. For Sclerotinia diseases, the GLM procedure was conducted using the number of infected heads or plants for each field evaluation. Statistical comparisons within each evaluation were made with Student–Newman–Keuls' test. All statistical differences were evaluated at a probability level of $p \leq 0.05$.

2.9. Synthesis of data

In order to understand the overall crop sequential effects, the crop matrix yield data were interpreted with relative values to assess overall positive or negative effects. The crop matrix yield data (Tables 3 and 4) were evaluated by a t -test and, based on the t -test, scores were assigned, which were converted to relative values to better understand the overall crop sequential effects. To begin with, the differences between crop yields due to previous crop within a column (crop), and the annual crop average were determined by a one-tailed t -test (Tables 3 and 4). In order to quantify the effect of the residue crop on the subsequent crop, scores were assigned when a significant difference was detected between a crop yield and the annual crop average (yield across all residue treatments). If the difference was significant at $p \leq 0.10$, then it was assigned a score of 1 for a positive effect and -1 for a negative. If it was significant at $p \leq 0.05$, then it was assigned a score of 2 for a positive effect and -2 for a negative effect. Scores for positive and negative effects were separately totaled along rows and overall residue crop scores were tabulated (Table 5).

The 40 residue crop scores were converted to relative values so that the average relative value for a crop was 10. With this process, the numerical values can be interpreted on a percentage basis. An example of this process: with dry bean as the residue crop in 2000 (Table 4), canola was assigned a score of 2 because canola yield following dry bean was significantly higher than the annual crop mean for canola at the $p \leq 0.05$ level. Sunflower was assigned a score of 1 because sunflower yield following dry bean was significantly higher than its annual crop mean at the $p \leq 0.10$ level. Thus, the total score for yields in 2000 with dry bean as the residue crop

Table 3
Seed yield (kg ha⁻¹) of 10 crops influenced by previous crops, crop matrix, 1999 (site 1)^a

Previous crop	1999 Crop									
	Canola	Crambe	Dry bean	Dry pea	Flax	Safflower	Soybean	Sunflower	Spring wheat	Barley
Canola	1413a	1688ab	1241a	2335a	1639a	1012a	2032ab	1597a	3591a	4680a
Crambe	1290a	1769ab	968a	§2148a	1605a	869a	2039ab	1738a	3217a	4981a
Dry bean	1400a	1559b	1175a	2550a	1521a	888a	2237ab	1609a	3308a	4189a
Dry pea	1530a	*2362a	1216a	2581a	1430a	§1042a	2112ab	1768a	3114a	4674a
Flax	1543a	1791ab	1131a	2660a	**690b	867a	1995ab	1769a	3651a	4617a
Safflower	1220a	§1518b	§816a	2532a	1387a	**458b	*1735b	1196a	§3031a	4579a
Soybean	1239a	1649ab	1098a	2300a	*1752a	886a	**2501a	1498a	3466a	4363a
Sunflower	1363a	1763ab	989a	2610a	1625a	760ab	1951b	1306a	3388a	4852a
Spring wheat	1312a	1879ab	§758a	*3045a	1571a	1026a	§1844b	1499a	3428a	4728a
Barley	1480a	2025ab	§1332a	2549a	1641a	*1106a	2090ab	1758a	3385a	4482a
Annual crop mean	1379	1800	1072	2531	1486	891	2054	1574	3358	4614
Tukey's HSD	605	735	659	949	504	374	531	1183	818	1321

Significance is indicated: § = $p \leq 0.10$, * = $p \leq 0.05$, ** = $p \leq 0.01$.

^a Yields in a column followed by the same letter are not significantly different at the $p \leq 0.05$ level according to Tukey's HSD test. In order to synthesize the data, values are bolded when they are significantly different than the annual crop mean in the same column according to a t -test. Bold only values are significantly lower than the mean, whereas bold and underlined values are significantly higher than the mean in a given column.

Table 4
Seed yield (kg ha⁻¹) of 10 crops influenced by previous crops, crop matrix, 2000 (site 2)^a

Previous crop	2000 Crop									
	Canola	Crambe	Dry bean	Dry pea	Flax	Safflower	Soybean	Sunflower	Spring wheat	Barley
Canola	**1125b	**242b	§ 1522ab	2935a	§ 868b	*588b	2226ab	1120a	3319ab	3282ab
Crambe	1418ab	1072a	**1038b	3442a	959ab	882ab	*1540b	870a	3592ab	3850a
Dry bean	*1660a	929ab	1883a	3386a	1160ab	847ab	1770ab	§ 1545a	3505ab	3663ab
Dry pea	1480ab	979a	2111a	§ 2835a	1033ab	1172ab	2058ab	1537a	3367ab	3628ab
Flax	1430ab	1303a	1978a	3239a	**415c	*1367a	2296ab	1336a	3349ab	§ 3879a
Safflower	1576a	922ab	1914a	3466a	*1317a	754ab	1774ab	1004a	§ 3673a	3568ab
Soybean	1306ab	1129a	2018a	§ 3744a	§ 1284ab	913ab	2529ab	1181a	§ 3000ab	3416ab
Sunflower	1422ab	*1540a	§ 2137a	2888a	§ 1246ab	1145ab	*2779a	883a	3212ab	3192ab
Spring wheat	1476ab	1150a	2010a	3308a	1146ab	1174ab	2122ab	1306a	*2847b	3748ab
Barley	1585a	1297a	1826a	3277a	1218ab	1183ab	2394ab	1201a	3267ab	*2905b
Annual crop mean	1448	1056	1844	3252	1064	1002	2149	1198	3313	3513
Tukey's HSD	397	726	745	1052	447	681	1110	902	753	943

Significance is indicated: § = $p \leq 0.10$, * = $p \leq 0.05$, ** = $p \leq 0.01$.

^a Yields in a column followed by the same letter are not significantly different at the $p \leq 0.05$ level according to Tukey's HSD test. In order to synthesize the data, values are bolded when they are significantly different than the annual crop mean in the same column according to a *t*-test. Bold only values are significantly lower than the mean, whereas bold and underlined values are significantly higher than the mean in a given column.

Table 5

Overall positive and negative crop sequence effects based on *t*-tests between the yields of crop sequences and the annual crop mean for that particular crop (Tables 3 and 4)

Residue crop	Crop sequence effect scores				Relative values				Net sequence effect
	Negative		Positive		Negative		Positive		
	1999	2000	1999	2000	1999	2000	1999	2000	
Canola	0	-8	0	0	0	-52	0	0	-52
Crambe	-1	-4	0	0	-7	-26	0	0	-33
Dry bean	0	0	0	3	0	0	0	20	20
Dry pea	0	-1	3	0	0	-7	20	0	13
Flax	-2	-2	0	3	-13	-13	0	20	-6
Safflower	-7	0	0	3	-46	0	0	20	-26
Soybean	0	-1	4	2	0	-7	26	13	32
Sunflower	0	0	0	6	0	0	0	39	39
Spring wheat	-2	-2	2	0	-13	-13	13	0	-13
Barley	0	-2	3	0	0	-13	20	0	7
Totals (10 crops)	-12	-20	12	17	-79	-131	79	112	-19
Crop on own residue	-4	-9	2	0	-26	-59	13	0	-72

Positive values indicate yield increases and negative values indicate yield decreases following a residue crop.

was 3 (Table 5). An average was developed for all 40 residue crop scores (unsigned); then each individual crop residue score was divided by that average (1.475) and multiplied by 10 to produce the relative value for each crop residue score (Table 5). Thus, continuing with our example, a crop score of 3 was converted to a relative value of 20. The effect of seeding a crop on its own residue was summarized (Table 5) by adding crop scores along the diagonal of the crop matrix (Tables 3 and 4).

3. Results and discussion

3.1. Crop production, crop matrix, 10 crops

Growing season precipitation, May through August, was 181% of the long-term average of 26.0 cm for the 1999 crop matrix and 104% for the 2000 crop matrix (Fig. 2). Even with above average precipitation in 1999, spring wheat and barley yields were not affected by previous crops ($p \leq 0.05$ level, Table 3). Considering that cereals are thought to benefit following legume crops via a 'legume N credit,' spring wheat and barley did not show a positive yield effect from following pulse crops such as dry bean, dry pea, and soybean. It is possible that the high application rate of N fertilizer (67 kg N ha⁻¹) in this experiment may have acted to suppress N fixation by legume crops and decreased the N credit to succeeding crops. Miller et al. (2002a) found similar responses to pulse-cereal crop sequences and came to the conclusion that factors other than nitrogen fixation were responsible for crop sequence yield differences. Crambe, flax, safflower, and soybean were the only crops affected by previous crops

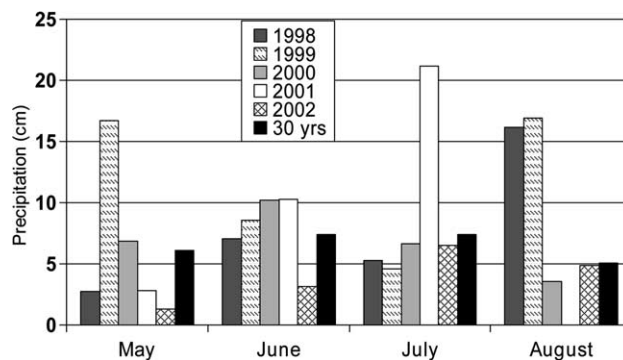


Fig. 2. Growing season precipitation for 1998–2002 compared to 30 year average. Only trace of precipitation (0.03) was detected during August in 2001.

in 1999 ($p \leq 0.05$ level, Table 3). Safflower and flax had their lowest seed yield when they were seeded on their own crop residue. Plant diseases were a contributing factor. Safflower seeded on its own crop residue was heavily infected with *Alternaria* blight (*Alternaria carthami* Chowdhury). Flax seeded on its own crop residue turned brown with premature ripening from flax wilt (*Fusarium oxysporum* Schlechtend.:Fr. f. sp. *lini* [Bolley] W.C. Snyder & H.N. Hans) and pasmo (*Septoria linicola* [Speg.] Garassini). In contrast, soybean had a high yield when it was seeded on its own residue. Considering that soybean was a new crop to this site and *Sclerotinia* disease was not a factor, one can speculate that favorable soil microbiological factors contributed to the increased yield response of this second year crop.

Seed yield for eight of the 10 crops at site 2 was influenced by the previous crop in 2000, which had average growing season precipitation, compared to only four crops in 1999. The annual-crop mean, for seed yield, for five of the 10 crops in 2000 (Table 4) was greater than their annual-crop mean in 1999 (Table 3), even though precipitation was 77% greater in 1999. This was not expected, but growing seasons that are cool and wet, such as the 1999 growing season, usually result in some of the lowest water-use efficiencies (Miller et al., 2001). The increased precipitation, in contrast to the intermittent wet-dry periods associated with normal precipitation in the northern Great Plains area that often limits plant disease development (Krupinsky et al., 2002), may have increased the prevalence of plant diseases. The present data indicate that wet growing seasons do not always enhance crop sequence influences or increase seed yields.

Numerically, barley, spring wheat, flax, and canola had their lowest seed yield when they were seeded on their own residues in 2000 at site 2. As mentioned above, an increase in plant diseases was obvious when flax was seeded on its own crop residue. The factors associated with the lower yields of barley, spring wheat, and canola were not as obvious, indicating that further investigation is warranted on the detrimental influences of 'crop stacking' (the concept of growing the same crop two years in a row). When the previous crop was either canola or crambe, seed yields were numerically the lowest for dry bean, canola, crambe, safflower, and soybean in

2000. Therefore, choosing a proper crop sequence with canola and/or crambe can be crucial if optimum seed yields are to be obtained by a succeeding crop. Dry pea and sunflower were the only crops not influenced by previous crops in 2000.

3.2. Crop production, spring wheat following crop matrix

During the third year, when spring wheat was seeded over the crop matrix in 2000 (site 1), seed yield was reduced by an average of 22% following spring wheat, which was a second year crop in the crop matrix (Fig. 3). Eight of the 10 first year crop residue treatments had a lower seed yield when the second year crop residue treatment was spring wheat (data not shown). Therefore, spring wheat following spring wheat resulted in reduced yield no matter what the previous crop. This is similar to results Gan et al. (2003) reported for durum wheat grown after pulse and oilseed crops in Swift Current, SK. In 2001 (site 2), spring wheat seed yields were reduced by an average of 8% following spring wheat included as a second year crop (Fig. 4), indicating the influence of previous crop sequences on spring wheat seed yield was not as evident in 2001 compared to the 2000 season. Only two of the 10 first year crop residue treatments that had spring wheat as the second year residue had lower yields, possibly because of above average precipitation in July (Fig. 2). We anticipated monoculture cereal crop sequences would be antagonistic to spring wheat seed yield. Miller et al. (2002b) found similar results when comparing residues of spring wheat and selected pulse and oilseeds. They found pulse crops the previous year

First year crop residue	Second year crop residue									
	Canola	Crambe	Dry Bean	Dry Pea	Flax	Safflower	Soybean	Sunflower	Wheat	Barley
Canola	2905	3061	3360	3124	3133	3401	3052	3356	2594	2935
Crambe	3253	3150	3090	3064	3073	3310	3190	3312	2430	2726
Dry Bean	3173	3125	3459	3100	3258	3281	3181	3382	2434	2801
Dry Pea	2972	2930	2924	2944	2668	3249	2946	3059	2146	3092
Flax	2876	3142	3038	3197	2870	3439	2999	3170	2439	2819
Safflower	3131	3073	2947	3114	3013	3128	2977	3300	2440	3016
Soybean	3042	2966	3456	2878	3028	2896	3039	3287	2238	2832
Sunflower	3086	3252	3471	3303	2993	3240	3237	3171	2816	3028
Wheat	2996	3071	2764	2919	2562	2784	2823	2711	2485	2926
Barley	2997	2938	3316	3116	2682	3428	3186	3337	2107	2999

Fig. 3. Spring wheat yield (kg ha^{-1}) influenced by previous crop sequences, 2000 (site 1). Spring wheat yield following 23 crop sequences was higher (gray background) than the continuous wheat treatment (2485 kg ha^{-1}), which was used as the control in Dunnett's one-tailed test. Crop sequences including spring wheat are indicated with dot-filled background.

First year crop residue	Second year crop residue									
	Canola	Crambe	Dry Bean	Dry Pea	Flax	Safflower	Soybean	Sunflower	Wheat	Barley
Canola	4122	4454	4283	4319	4400	4153	4253	3957	4027	4312
Crambe	3907	3904	4008	4011	4078	3677	3972	3884	3629	3939
Dry Bean	4109	4250	4089	4179	4322	3785	4221	3698	3866	3901
Dry Pea	4009	4254	4085	3524	4428	3997	4369	4101	3835	4216
Flax	4047	4396	4063	4382	4686	4396	4495	4175	3840	4193
Safflower	4211	4082	4230	4129	4194	3952	4021	4096	4070	4240
Soybean	4098	4177	4447	4279	4297	4239	4303	4093	3728	4180
Sunflower	4360	4389	4315	4376	4499	4009	4343	3987	3745	4117
Wheat	4110	4057	3988	4346	4319	3878	4043	4062	3567	3881
Barley	3950	4450	4253	4202	4200	4370	4350	3802	3690	3749

Fig. 4. Spring wheat yield (kg ha^{-1}) influenced by previous crop sequences in 2001 (site 2). Spring wheat yield following 19 crop sequences was higher (gray background) than the continuous wheat treatment (3567 kg ha^{-1}), which was used as the control in Dunnett's one-tailed test. Crop sequences including spring wheat are indicated with dot-filled background.

increased spring wheat seed yield by 21% when compared to spring wheat the previous year. Similarly, Stevenson and van Kessel (1996) found wheat seed yield was greater when preceded by dry pea compared to wheat, with most of the yield advantage attributed to a non-N rotation benefit.

Crops grown two years previous to a cereal crop can influence seed yield (Wright, 1990). Our data suggest a similar response with several crop sequence treatments. In 2000 (site 1), spring wheat seed yield was reduced following the spring wheat/sunflower, barley/spring wheat, and dry pea/spring wheat crop sequence treatments (data not shown). In 2001 (site 2), spring wheat had lower seed yields following the dry pea/dry pea and crambe/safflower crop sequence treatments (data not shown). In general, spring wheat seed yield was influenced to a greater extent by the second year crop residue than by the first year crop residue. Considering the reported impact of previous crops on subsequent cereal crops (Wright, 1990), the first year crop residue was expected to have a greater impact on spring wheat seed yield than the data indicated. Second year crop residues from spring wheat and barley were expected to similarly impact succeeding spring wheat seed yield and second year residues from pulse crops were expected to influence a succeeding spring wheat crop but they did not. The observation that spring wheat following the dry pea/dry pea crop sequence had a yield lower than the continuous wheat treatment (Fig. 4) warrants additional investigation.

In 2000 (site 1), the seed yield of spring wheat following 23 crop sequence treatments was higher (ranging from 30% to 40%) than the continuous wheat treatment (Fig. 3). Eighteen of the 23 crop sequence treatments had safflower, sunflower, or dry

bean as the second year crop. In 2001 (site 2), the seed yield of spring wheat following 19 crop sequence treatments was higher (ranging from 22% to 31%) than the continuous wheat treatment (Fig. 4). Greater yields did not appear to be highly associated with the second year crops as in 2000 but were more closely associated with the first year crops of flax and sunflower. All crop sequence treatments that yielded better than the continuous wheat treatment were comprised of mostly non-cereal crops (Figs. 3 and 4). In contrast, the crop sequence treatments with either spring wheat or barley in second year of the crop matrix (20 treatments) did not yield better than the continuous wheat treatment (Figs. 3 and 4) in either year. In addition, there was only one treatment out of 10 that included spring wheat in the first year of the crop sequence that yielded better than the continuous wheat treatment over two years. This indicates the importance of crop diversity prior to a spring wheat crop for optimizing spring wheat production. The use of alternative crops in the rotations allows time for natural enemies to destroy potential wheat pathogens (Cook and Veseth, 1991; Krupinsky et al., 2002).

Even though approximately 20% of all the crop sequences tested each year yielded significantly better than the continuous wheat treatment, only six crop sequences (sunflower/crambe, soybean/dry bean, sunflower/dry pea, flax/safflower, barley/safflower, and sunflower/soybean) were common to both years demonstrating the difficulty of selecting a specific crop sequence for all environmental conditions. As Cook and Veseth (1991) indicate, the number of years with alternative crops before returning to wheat may be more important than the crops used in the crop sequences. This again shows the need for diversity, not only in the crops used but also in the crop sequences used in a long-term cropping system.

3.3. Residue carryover

Soil coverage by crop residue influences the soil surface environment. Moisture retention is improved with soil coverage by crop residue because of reduced evaporation, increased snow trapping, and reduced surface runoff due to better water infiltration (Cook and Veseth, 1991). Higher residue coverage delays heating and drying of the soil surface, especially earlier in the growing season. Reduction in drying of the soil surface allows for greater root activity and enhancement of biological activity.

Soil coverage values measured after spring wheat seeding in 2001 (site 2) indicate that crop sequences composed of cereals had the highest residue coverage levels while sequences composed of two dicotyledonous species had considerably lower coverage (Fig. 5). Combinations of spring wheat and barley had residue coverage levels ranging from 85% to 94%, sequences with spring wheat followed by dry bean, safflower, dry pea, and sunflower had coverage ranging from 66% to 78%, and sequential combinations of these same four broadleaf crops had coverage from 35% to 52%. Crop sequences with the lowest coverage levels in the middle- and lower-residue groups (Fig. 5) contained sunflower while sequences having the next to lowest values in the two groups contained dry pea.

The highest soil coverage level reported here, 94% for the spring wheat/spring wheat sequence (Fig. 5) was rated at a very low level of relative soil erodibility

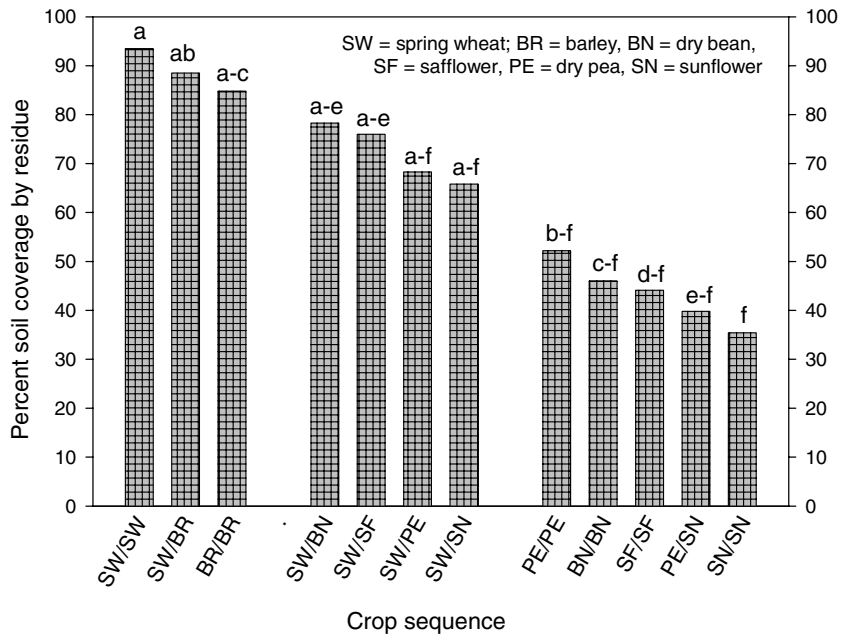


Fig. 5. Percentage of soil covered by crop residue measured in the spring of 2001 (site 2) soon after spring wheat seeding. The sequence of crops grown in 1999 and 2000 is identified. Entries possessing the same letter (note letter ranges) are not significantly different according to Scheffe's test at a probability level of $p \leq 0.05$. Previous crops: BR = barley, BN = dry bean, PE = Dry pea, SF = safflower, SN = sunflower, and SW = spring wheat.

due to wind, 3% based on the Revised Wind Erosion Equation model (evaluated for residue alone, no residue coverage = 100% relative soil erodibility; [Bilbro and Fryrear, 1994](#); [Fryrear et al., 1998](#)). A comparable rating for relative soil erodibility due to water was 4% (based on the Revised Universal Soil Loss Equation model; [Renard et al., 1997](#)). Lower soil coverage levels reported here, 35–40% for sunflower/sunflower and dry pea/sunflower, respectively ([Fig. 5](#)), were rated at moderate levels of relative soil erodibility due to wind, 23% and 19% respectively, based on the Revised Wind Erosion Equation model. Comparable ratings for relative soil erodibility due to water were 28% and 22% for sunflower/sunflower and dry pea/sunflower, respectively. Thus, low residue crop sequence treatments such as dry pea/sunflower need to be cautiously evaluated when considering crop sequences for lands that are more inherently erodible.

These results were obtained under no-till management and during years of above average to average precipitation, a combination that tends to optimize residue production. Even under these favorable conditions, marginal levels of soil coverage by residues were detected in crop sequence treatments where lower residue-providing crops were seeded into their own or each others residues ([Fig. 5](#)). Under conditions of serious precipitation limitation and drought, two years of lower residue-generating crops could result in low levels of soil coverage by residue and the hazard for potential

soil erosion will escalate. Under drought conditions, no-till management alone will not prevent unacceptable levels of soil erosion hazard from occurring due to low crop growth, low residue production, and surface soil disaggregation (Merrill et al., 1999).

3.4. Soil water

Crop growth is supported by stored soil water present in the spring and precipitation occurring during the growing season. Soil water present in the spring is dependent on two processes: (a) water remaining in the profile after the prior season's crops, and (b) water entering the soil from snowmelt as influenced by amount of snow captured by residues of the preceding crops. There is evidence that water remaining in the profile after various crops is a more important determinant of soil water availability than differences due to water entering the soil from snowmelt (Merrill et al., 2002b; Merrill et al., 2004).

In general, the amount of spring soil water present in plots following the 10 crops grown the previous year varied (Fig. 6). There was a relatively low but significant variation in amount of soil water present following the 10 crops in 1999. Numerically, the lowest amount of soil water present was measured following sunflower and safflower. The numerically highest amount of soil water present was measured following flax. The numerical difference between highest and lowest amount of soil water present was 2.7 cm. Although the amount of spring soil water varied following the 10 crops in 2000 with a range of 4.1 cm, differences were not significant. Apparently, the above average precipitation in 1999, particularly during August (Fig. 2), impacted the soil water remaining in the profile after the growing season. In 2001, differences in the amount of spring soil water following the 10 residue crops were evident (Fig. 6). Similar to 1999, lowest amount of soil water present was measured following sunflower and safflower. The numerically highest amount of soil water present was measured following dry pea. The difference between highest and lowest amount of soil water present was 8.6 cm. The higher soil water use by sunflower and safflower is consistent with their longer growing season and deeper root growth compared to the other crops (Merrill et al., 2002a). The lower soil water use by dry pea is consistent with its shorter growing season and lower rooting depth compared to the other crops (Merrill et al., 2002a,b). These results are comparable to those reported earlier (Anderson et al., 2003).

The lack of a consistent relationship between the amounts of spring soil water in 1999 and 2000 (Fig. 6) and seed yields (Tables 3 and 4) may be related to the above average precipitation during the 1999 growing season (Fig. 2). Negative effects were not obvious with crops following sunflower, a high water user. Negative effects observed in 1999 following safflower (Table 3), another high water user, were probably related to other factors, not soil water. Negative soil water effects are not evident in spring wheat yields in 2001 (Fig. 4). In contrast to our results, other researchers have shown that differential soil water depletion can play a major role in crop sequence effects under more arid conditions than experienced in the present experiment. In

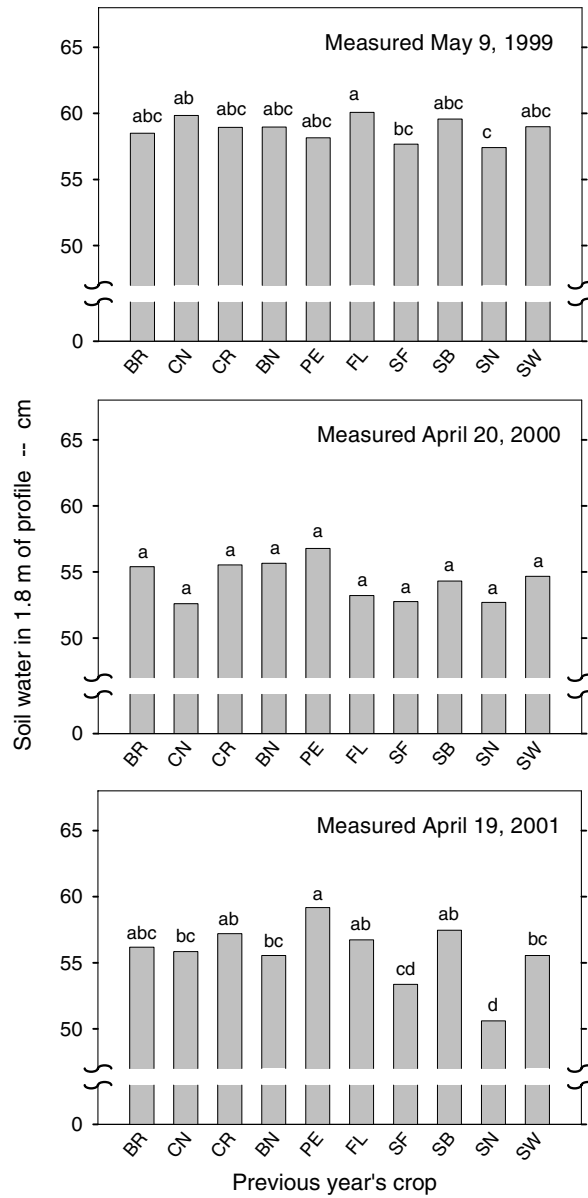


Fig. 6. Total spring soil water content in the soil profile measured to a depth of 1.8 m where the indicated crops had grown the previous year. Previous crops: BR = barley, CN = canola, CR = crambe, BN = dry bean, PE = Dry pea, FL = flax, SF = safflower, SB = soybean, SN = sunflower, and SW = spring wheat.

the central Great Plains, yield of winter wheat was negatively impacted by the higher water usage of prior sunflower and soybean crops (Nielsen et al., 1999; Norwood, 2000).

3.5. Surface soil properties, crop matrix

Soil surface properties including bulk density, soil pH, identifiable plant material, particulate organic matter, potentially mineralizable N and microbial biomass C and N were generally not affected by crops in this study (data not shown). The only exception was that particulate organic matter in the 0.5–2.0 mm size fraction was greater after soybean (3054 kg ha⁻¹) than after dry pea, safflower, flax and dry bean (1595–1951 kg ha⁻¹). Among the 10 crops, dry pea tended to possess the lowest values for most soil properties, presumably because of low residue input to the soil.

The short timeframe of the experiment likely contributed to the lack of significant crop effects on soil properties. However, other factors may have played a role in the prevalence of non-significant treatment effects. For instance, the field had inherently high soil fertility, had been continuously cropped under reduced-tillage management for 14 yr prior to the initiation of the experiment, and was under no-till management during the experiment. As a result, the potential for crops to have an appreciable effect on soil properties may have been small because of a ‘masking’ effect from high soil fertility and reduced-tillage.

3.6. Leaf spot disease on spring wheat following crop matrix

Leaf spot diseases were present on spring wheat during the third year, when spring wheat was seeded over the crop matrix. The most common leaf spot diseases on spring wheat were tan spot, caused by *Drechslera tritici-repentis* [Died.] Shoemaker (teleomorph = *P. tritici-repentis*) and stagonospora nodorum blotch, caused by *Stagonospora nodorum* [Berk.] Cast. et Germ. (teleomorph = *Phaeosphaeria nodorum*) [E. Müller] Hedjaroude (Krupinsky et al., 2004). When defining the relationship between yield and disease severity caused by tan spot and stagonospora nodorum blotch, Bhathal et al. (2003) recently reported losses in grain yield ranging from 18% to 31%. Other diseases present included stagonospora avenae blotch (*Stagonospora avenae* Bissett f. sp. *triticea* T. Johnson), and septoria tritici blotch (*Septoria tritici* Roberge in Desmaz) and spot blotch (*Bipolaris sorokiniana* [Sacc.] Shoemaker) (Krupinsky et al., 2004).

When spring wheat was evaluated for leaf spot disease severity in 2000 (site 1), differences in disease severity among crop sequence treatments were evident in six of seven evaluations. This indicates that disease severity was influenced by crop sequence treatments. As a group the ‘two year without spring wheat’ crop sequences could not be distinguished from the ‘one year without spring wheat’ crop sequences (Fig. 7(a)). There were individual crop sequences that had less disease severity than the continuous wheat treatment. For example, leaf spot disease severity levels early in the season on spring wheat following barley were lower than continuous wheat in 2000 (Fig. 7(b)). Similar to a previous report (Krupinsky et al., 2004), differences among treatments were more evident in the earlier evaluations indicating a greater influence of crop residue and carryover of inoculum earlier in the season compared to later. When the continuous wheat treatment was used as the control, the crambe/

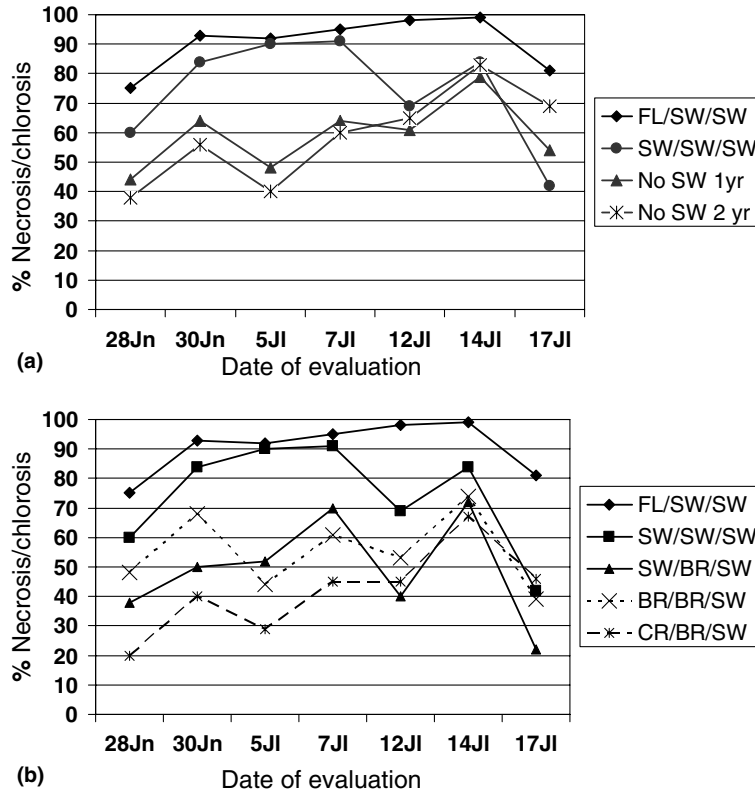


Fig. 7. Leaf spot disease severity (percentage necrosis and chlorosis) on Amidon spring wheat following crop sequence treatments: (a) Spring wheat (SW) following spring wheat compared to 'one-year-without-spring wheat' (No SW 1 yr) and 'two-year-without-spring wheat' (No SW 2 yr) crop sequences. (b) Spring wheat following spring wheat compared to spring wheat following barley (BR); FL = flax, CR = crambe.

barley/spring wheat treatment had less disease severity than continuous wheat in all analyses when differences were detected. This is consistent with an earlier observation where the risk for leaf spot disease on spring wheat was lower following barley compared to spring wheat (Krupinsky et al., 2004). Three crop sequence treatments (flax/dry pea/spring wheat, soybean/flax/spring wheat, and spring wheat/dry pea/spring wheat) had less disease than the continuous wheat treatment for three of the four times differences were detected. Although these three treatments and the crambe/barley/spring wheat treatment were distinguished from the continuous wheat treatment based on disease severity and yielded 10–29% higher than the continuous wheat treatment, they were not statistically different from the continuous wheat treatment based on seed yield (Fig. 3).

When spring wheat was evaluated for leaf spot disease severity in 2001 (site 2), there were differences among crop sequence treatments in four of eight evaluations. Similar to 2000, the 'two year without spring wheat' crop sequences, as a group,

could not be distinguished from the ‘one year without spring wheat’ crop sequences. There were crop sequence treatments that had less disease severity than the continuous wheat treatment. Those crop sequence treatments with less disease for at least three of the four times differences were detected were flax/flax/spring wheat and safflower/safflower/spring wheat. The crop sequences that were different from the continuous wheat treatment two or more times were flax/canola/spring wheat, pea/crambe/spring wheat, soybean/flax/spring wheat, spring wheat/dry bean/spring wheat, and soybean/soybean/spring wheat. Although these treatments were distinguished from the continuous wheat treatment based on disease severity and yielded 11–31% higher than the continuous wheat treatment, with one exception, they were statistically similar to the continuous wheat treatment based on seed yield (Fig. 4). This is similar to what occurred in 2000. Thus, even though there was a decrease in leaf spot disease severity with some crop sequence treatments and modest yield increases, significant yield increases because of decreases in leaf spot disease severity were not detected under our environmental conditions. It is possible that the movement of fungal spores among plots (interplot interference) diluted the impact of individual crop sequence treatments, particularly later in the season.

3.7. Fungal spores, spring wheat following crop matrix

Fungal spores were detected within the spring wheat crop following all crop sequence treatments evaluated during the 2001 season. The average number of *D. tritici-repentis* conidia per sampler for each sampling day over the total collection period was 0.22, 0.20 and 0.13 conidia per cubic meter of air sampled per day from the flax/safflower/spring wheat, flax/dry bean/spring wheat, dry pea/crambe/spring wheat treatments, respectively, compared to 0.47 conidia per cubic meter of air sampled per day for the continuous wheat treatment. Thus, *D. tritici-repentis* conidia were obtained from all treatments and at least twice as many conidia were obtained from the continuous wheat treatment compared to the other treatments. Even though spore production was statistically similar among treatments during most weeks, significantly more conidia were collected within the continuous wheat treatment during the fifth week compared to the other three treatments. When the number of conidia collected during the fifth, sixth, and seventh weeks were combined, the average number of conidia from the flax/safflower/spring wheat, flax/dry bean/spring wheat, dry pea/crambe/spring wheat treatments was 0.19, 0.10 and 0.06 conidia per cubic meter of air sampled per day respectively, compared to 0.80 conidia per cubic meter of air sampled per day for the continuous wheat treatment. During these three weeks at least four times as many conidia were obtained from the continuous wheat treatment compared to the other treatments. In the sixth week, the amount of disease severity on spring wheat plants following the continuous wheat treatment was significantly higher compared to the other treatments (data not shown). Thus, the higher level of spore production associated with the continuous wheat treatment apparently increased the potential for higher disease severity.

There was an association between the quantity of conidia obtained and the residue on the soil surface, particularly obvious wheat residue. The amount of total residue on the soil surface for each of the treatments was 74% (74 residue contacts of a 100 possible), 72%, 60%, and 94% for the flax/dry bean/spring wheat, flax/safflower/spring wheat, dry pea/crambe/spring wheat, and spring wheat/spring wheat/spring wheat treatments, respectively. Greater differences were more apparent in the amount of obvious wheat residue present in the plots with 0%, 1%, 1%, and 53% (53 of a 100 possible residue contacts was obvious wheat residue) for the flax/dry bean/spring wheat, flax/safflower/spring wheat, dry pea/crambe/spring wheat, and spring wheat/spring wheat/spring wheat treatments, respectively. Thus, the higher level of wheat residue (on which conidia [inoculum] are produced) was associated with the continuous wheat treatment increasing the potential for leaf spot diseases on spring wheat in those plots. This indicates the importance of crop sequence, as a management tool, in decreasing the amount of inoculum available to initiate leaf spot diseases. Although pathogens may not be completely eliminated by crop sequence, rotating among crop types reduces the amount of inoculum pressure on the crop being grown (Krupinsky et al., 2002).

3.8. *Sclerotinia* disease, crop matrix; sunflower following crop matrix

The incidence of *Sclerotinia* head blight on safflower was low, ranging from 0% to 3% in 1999 and from 0% to 2% in 2000, with the highest level on safflower grown on crambe residue for both years. For canola, the incidence of *Sclerotinia* stem rot ranged from 0% to 6% in 1999 and from 1% to 5% in 2000, with the highest level occurring on safflower residue both years. For crambe, the incidence of *Sclerotinia* stem rot ranged from 2% to 15% in 1999 and from 10% to 60% in 2000, with the highest level occurring on safflower residue both years. Thus, the higher levels of *Sclerotinia* on canola and crambe were observed when those crops followed a safflower crop for both years even though the incidence of *Sclerotinia* head blight on the previous safflower crop was rather low. Sunflower was rated for *Sclerotinia* basal stem rot but the data are not included because no diseased plants were identified in 1999 and few infected plants (0.01%) were present in 2000. Given the variation in *Sclerotinia* disease incidence among plots, it was difficult to demonstrate significant differences among previous residue treatments at a probability level of $p \leq 0.05$. Even though there were some patterns in the incidence of *Sclerotinia* disease, one can speculate that the movement of ascospores among plots or from other areas made it difficult to detect significant differences among the individual crop residue treatments. Accordingly, crop rotation may be only partially effective because of the movement of wind-borne ascospores (Krupinsky et al., 2002).

The impact of crop rotation on *Sclerotinia* disease was more evident with the uniform sunflower crop at site 2 [crop matrix (2000)/spring wheat (2001)/sunflower (2002)]. The number of sunflower plants infected with *Sclerotinia* basal stalk rot was related to crops grown two years previous. The highest incidence of *Sclerotinia* basal stalk rot (24%) was associated with former crambe plots that had a high incidence of *Sclerotinia* disease in 2000. The sunflower seed yield (1506 kg ha^{-1}) was

31% lower in the previous crambe plots compared to the average yield obtained from the previous barley (2122 kg ha^{-1}), canola (2170 kg ha^{-1}), dry pea (2128 kg ha^{-1}), and sunflower (2286 kg ha^{-1}) plots, indicating crops grown two years previous to a sunflower crop can influence yield. The former dry pea plots (13% *Sclerotinia* basal stalk rot) and canola plots (6% *Sclerotinia* basal stalk rot) ranked second, with the remaining plots ranging from 0.5% to 3% grouped together. Although the dry pea and canola plots were not significantly different from one another, the canola plots could not be distinguished from the remaining plots. Considering *Sclerotinia* disease was not evident in the dry pea crop or in the grain harvested in 2000, further investigation is warranted to explain why intermediate levels of *Sclerotinia* disease were detected following dry pea.

4. Synthesis and conclusions

4.1. Crop production, crop matrix, 10 crops

When the three legume crops were compared to the seven non-leguminous crops, on a per-crop basis, the legumes exhibited more positive crop-sequence effects on seed yield compared to the non-leguminous crops which usually exhibited negative effects. When the crop sequential effects of the various residue crops were assessed (Table 5, rightmost column), all three legume crops had positive net relative values. Overall, a relative value of +22 per crop was associated with the legumes compared to -12 per crop for non-legumes (derived from Table 5). However, sunflower was an exception among the non-leguminous crops. Sunflower as residue crop had a positive effect on subsequent crops in 2000 with average precipitation but not in 1999, an above average precipitation year (Tables 3 and 4).

The most negative crop sequence effects on seed yield were observed when a crop was seeded on its own crop residue (Tables 3 and 4). The overall relative values for this crop sequence effect were -26 in 1999 and -59 in 2000 (Table 5). With five negative relative values out of a possible 10 in 2000 (Table 4), the negative impact of a crop being seeded on its own crop residue was more than doubled in 2000, an average precipitation year, compared to 1999, an above average precipitation year. In 1999, safflower as a residue crop had a negative impact on the seed yield of five out of 10 crops (Table 3) and a relative value of -46 for overall sequence effect (Table 5). Safflower, a xeric species, may promote allelopathic or other effects in a wet year, such as 1999. Canola and crambe had negative effects on subsequent crops in 2000, with relative values of -52 and -26, respectively, for the overall sequence effect in 2000 (Table 5). Considering that mycorrhizae can be beneficial to their host plants (Paul and Clark, 1996) and canola and crambe belong to the Cruciferae family, which includes typically non-mycorrhizal crops (Harley and Harley, 1987), growing non-mycorrhizal plants may negatively impact mycorrhizal fungi in the soil, and consequently affect subsequent mycorrhizal crops that follow.

4.2. Crop production, spring wheat following crop matrix

Spring wheat yields following diverse crop sequences were generally higher than the continuous wheat treatment. In 2000, spring wheat yields were enhanced following six and seven crop sequence treatments when sunflower and safflower, respectively, were the second year crop residue (Fig. 3). In 2001, spring wheat yields were enhanced following 10 crop sequence treatments when either sunflower or flax were the first year crop residue (Fig. 4). Safflower and sunflower were previously reported to be high water users compared to the other crops (Merrill et al., 2004). With the above average precipitation in 1999, the pattern of results suggests high water-using crops, by reducing soil wetness, may have modified soil moisture conditions for spring wheat and lessened the potential of soilborne diseases. Leaf spot disease observations (Fig. 7) indicate the inclusion of diverse crops in crop sequences may lessen disease severity compared to continuous wheat early in the season, contributing to a general increase in spring wheat yields.

4.3. Some overall considerations

In general, our results showed that the pulse legume crops dry pea, dry bean, and soybean, as a group, provided positive crop sequential enhancements to the yields of other crops compared to the non-leguminous crops. With the notable exception of sunflower, non-leguminous crops were more associated with negative crop sequential effects. Because the soil that the study was conducted on had inherently high soil fertility and had been under soil health-enhancing no-till management with adequate N-fertilization, it is difficult, or possibly impossible, to ascribe positive legume effects specifically to a “nitrogen-credit”, N-fixation effect. This important overall result points to the need to apply the research tools of soil microbiological analysis linked to soil-based plant pathological analyses in order to reach better understanding of such crop sequential effects.

The future costs of nitrogen fertilization and the local-to-global environmental burdens of off-field nitrogen flux (Follett and Hatfield, 2001) are expected to increase the value of including legumes in crop rotations. As this and other studies have shown, legume crops are inferior to non-leguminous crops in terms of maintaining soil coverage by crop residue, which is one of the most important factors for maintaining soil health. Thus, expected increased use of legumes will require a proper balancing of these crops with higher residue-providing crops such as small cereal grains. This will in turn place emphasis on research for maintenance and enhancement of no-till soil and crop management systems.

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