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Growth, yield, and yield stability of canola in the Northern Great Plains of the United States

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Abstract

Canola (*Brassica napus* L.) may diversify wheat-based cropping systems in the Northern Great Plains. However, agronomic adaptability and stability of high-yielding genotypes have not been widely evaluated over the diverse environmental conditions of South Dakota (SD). A 2-year field experiment was conducted in two contrasting environments (Brookings—eastern SD and Pierre—Central SD) to evaluate genotypes (10 in 2019 and 12 in 2020) for days to 50% flower, lodging, pods plant⁻¹, seed yield, 1000-seed weight, and yield stability. Seed yield for all genotypes in Brookings averaged 1961 and 1740 kg ha⁻¹, in 2019 and 2020, respectively, whereas at Pierre, yields averaged 1470 and 858 kg ha⁻¹. Seed oil concentration was greater at Brookings (456 and 406 g kg⁻¹ in 2019 and 2020, respectively) than at Pierre (356 g kg⁻¹ in 2019). The additive main effects and multiplicative interaction model (AMMI) evaluated eight genotypes across locations and years for genotype × environment (GE) interactions and stability. Environment was the most dominant cause of variation among genotypes, explaining 67.7%, 41.4%, and 45.7%, of the variations in pods plant⁻¹, 1000-seed weight, and seed yield, respectively, whereas GE explained most of the remaining variation. A combination of AMMI-1 biplots and AMMI stability values found variability in genotypic response to environments for seed yield suggesting cultivar recommendations should be environment specific.

1 | INTRODUCTION

Canola (*Brassica napus* L.) is the second most produced oilseed crop in the world after soybean (FAO, 2021). The crop is in increasing demand due to its seed's healthy oil rich in omega-3 fatty acids. Canola oil is particularly rich in oleic or omega-9 fatty acids, which ensures the stability of the oil.

Abbreviations: AMMI, additive main effects and multiplicative interaction model; ASV, AMMI stability value; GE, genotype × environment interaction; NGP, Northern Great Plains; PC, principal component; SDSU, South Dakota State University.

After oil extraction, the remainder of the seed (canola meal) is processed into livestock feed. Canola meal has a lower protein content when compared to soybean [*Glycine max* (L.) Merr.] meal (36%–39% for canola vs. 45%–48% for soybean), but canola meal can substitute for soybean meal in many livestock types, especially dairy cattle and pigs. It is also fed to poultry and fish. The meal has high levels of lysine and arginine amino acids and is rich in vitamins and essential minerals (Gauthier et al., 2019).

The European Union is the world's largest producer of canola, followed by China and Canada (FAO, 2021). The

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United States produces approximately one third of the canola oil used domestically, providing an opportunity to significantly expand canola production to meet domestic demand. In 2022, 895,000 ha were planted to canola in the United States, yielding on average 2047 kg ha⁻¹ totaling 4.4 billion kg of canola (USDA-NASS, 2022). The Northern Great Plains (NGP) is the biggest canola-producing region in the United States with North Dakota leading canola production with 650,000 ha (80%). The remaining 20% of the production was located in Oklahoma, Idaho, Minnesota, Montana, and Washington (USDA-NASS, 2019). In South Dakota (SD), in 2017, canola was grown on five canola farms (<1000 ha) and is considered a new crop (USDA-NASS, 2017).

Canola has been shown to fit well in rotation with wheat (*Triticum aestivum* L.) and other small grains (Bushong et al., 2012). It has a similar growing season to spring wheat, with spring canola planted in early spring and harvested in late summer. There are over 510,300 ha dedicated to wheat production in SD (USDA-NASS, 2017). Therefore, there is a large opportunity for canola/wheat rotation in SD. Unfortunately, canola has been a high-risk crop due to problems with low heat tolerance at flowering, lodging, and pod-shattering tendencies. All of these characteristics lower harvestable yield and with shattering leading to volunteer plants in the following years. Because many of the genotypes now have herbicide-resistant genes, the management of these volunteers may be problematic. However, due to recent advanced breeding efforts, high-yielding genotypes are being released that have good standability, reduced pod shatter, and that can be straight-cut rather than swathed, which also aids in seed retention. In 2016, for example, average canola seed yield in the United States was 1976 kg ha⁻¹ (USDA-NASS, 2017), whereas in 2022, the average increased to 2047 kg ha⁻¹ (USDA-NASS, 2022).

Canola yield is highly variable based on genotype and environmental growing conditions and their interactions (GE) (Assefa et al., 2014; Gunasekera et al., 2006). Canola seed yield is a product of key yield components, pods plant⁻¹, seeds pod⁻¹, and seed weight with these components influenced by growing conditions that affect biomass accumulation, days to flowering, days to maturity, pod, and seed development (Zhang & Flottmann, 2016). Because of the high variability in this crop, it is critical that genotype evaluations be conducted in areas intended for its production to enhance the selection of best performing adapted genotypes. However, the long-standing plant breeding practice has been to focus on genotypes that have stable yields across a wide range of environments, which minimizes the complicated effects of GE interactions on yield and makes the process resource efficient. Nevertheless, specific adaptations of genotypes may improve overall yields in specific environments (Fabio et al., 2017), hence improving the profitability of the crop for producers.

Core Ideas

- Canola is a potential oilseed crop for diversifying dryland cropping systems in the Northern Great Plains (NGP) of the United States.
- Late-maturity canola genotypes have high yield potential but tend to flower during hot and dry conditions of NGP.
- Early-maturity genotypes were the most stable under lower yielding growing conditions.
- Medium- and late-maturity genotypes were more stable when temperatures were moderate and moisture not limiting.
- Environment-specific cultivar recommendations would be helpful to canola growers.

Because canola is not widely grown in SD, producers need information on its adaptation to their specific environmental conditions to facilitate its integration as an alternative crop into existing cropping systems. SD has agroecologically diverse farming regions, which could substantially impact the adaptation and performance of different canola genotypes. The west central region of SD is characterized by high summer temperatures, low precipitation, conservation till or no-till management, and is dominated by wheat production. The eastern region is dominated by corn (*Zea mays* L.) and soybean production, has humid conditions, higher precipitation, which makes crops more disease prone, and most producers use conventional tillage systems. Thus, the objective of this study was to evaluate multiple canola genotypes for growth, yield, and yield stability in these two SD agroecozones to determine if genotype recommendations should be similar or vary across these environments.

2 | MATERIALS AND METHODS

2.1 | Site description

A 2-year study was conducted at Aurora Research Farm near Brookings, SD (44°18'40.8863" N, 96°47'54.1957" W) and Dakota Lakes Research Farm near Pierre, SD (44°22'5.9362" N, 100°21'3.4794" W) in 2019 and 2020. The soil type at the Brookings site was a Brandt silty clay loam (fine silty, super active, frigid Calcic Hapludolls; Malo, 2003). At the Pierre site, the soil was a Dorna silty loam soil (coarse-silty over clayey, superactive, mixed over smectitic, mesic Fluventic Hapludolls). The previous crop was winter wheat in Brookings and corn in Pierre. At Brookings, fields were tilled to a depth of about 10 cm before planting (conventional till),

TABLE 1 Monthly rainfall and maximum and average temperatures during the growing seasons in 2019 and 2020 at Brookings and Pierre, South Dakota

Location, year	April		May		June		July		August		Total	
Rainfall (mm)												
Brookings, 2019	62.8		105.7		67.1		132.4		62.3		430.3	
Brookings, 2020	15.3		61.8		67.3		83.6		35.4		263.4	
30-year average	63.0		90.0		111.0		84.0		84.0		432.0	
Pierre, 2019	17.4		67.0		12.9		69.7		79.1		246.1	
Pierre, 2020	6.5		48.7		88.6		61.4		29.6		234.7	
30-year average	54.1		81.0		93.0		65.0		56.0		349.0	
Temperature (°C)												
	Max.	Avg.	Max.	Avg.	Max.	Avg.	Max.	Avg.	Max.	Avg.	Mean Max.	Mean Avg.
Brookings, 2019	11.1	6.2	16.5	11.4	25.2	19.5	26.9	21.9	24.2	19.3	20.8	15.7
Brookings, 2020	12.5	5.6	17.5	12.4	27.8	21.8	28.6	22.8	28.5	22.0	22.9	16.9
30-year average	13.3	6.9	20.0	13.9	25.0	19.7	28.3	22.2	27.2	20.8	22.8	16.7
Pierre, 2019	13.7	7.4	17.4	11.7	27.2	20.2	29.6	23.4	26.4	21.0	22.9	16.7
Pierre, 2020	14.6	6.5	19.1	13.1	28.3	22.2	31.0	24.3	31.6	23.8	24.9	17.9
30-year average	16.1	9.2	22.2	15.3	27.8	21.1	32.2	25.0	31.1	29.9	25.9	20.1

Note: 30-Year average is the average rainfall or temperature from 1985 to 2015. Numbers in bold type are long-term averages. Single season temperature and rainfall data are compared to long-term average data.

Abbreviations: Max., maximum; Avg., average.

Source: Mesonet (2020; <http://www.noaa.gov/>).

whereas at Pierre, the field was under long-term no-till system (>5 year). Preplanting soil analysis results for the two locations and years are given in Table S1.

The Koppen climate classification subtype for Brookings was “Dfb” (humid continental climate), which is characterized by warm, relatively humid summers, and cold, dry winters, and Pierre was “Dfa” (hot-summer humid continental climate) characterized by hot, humid summers, and cold, windy, snowy winters (<https://www.weather-base.com/search/search.php3?query=south+dakota>). The weather data for the study locations were accessed from Mesonet at South Dakota State University (SDSU) (Mesonet, 2020) and the 30-year average data from 1985 to 2015 was accessed from National Weather Services and used for comparison (Table 1).

2.2 | Experimental design and planting

The experimental design was a randomized complete block (RCBD) with treatments consisting of 10 canola genotypes in 2019 and 12 genotypes in 2020 replicated 4 times (Table 2). Genotypes were supplied by seed companies for inclusion in these trials, and there were eight common genotypes between years and sites. Seed companies commonly replace genotypes with newer hybrids from year-to-year making it difficult to evaluate the same genotypes every single year. The individual plot size was 1.62 × 9.14 m (14.86 m²). In 2019, the plant-

ing dates were 3 May at Pierre and 18 May at Brookings. In 2020, the planting dates were 28 April at Pierre and 8 May at the Brookings location. Planting was done using a seven-row Hege 500 (Wintersteiger, Austria) drill. Each plot had seven rows, 22 cm apart. Seeding rate was based on seed size with a target population of 148 plants m⁻².

Soil test results showed adequate levels of P and K at both sites, so these nutrients were not applied. In both years and sites, urea (46% N) and ammonium sulfate (21% N; 24% S) were applied at a rate to supply 112 kg ha⁻¹ N and 22 kg ha⁻¹ S. Fertilizers were split applied to ensure continuous supply nutrients. The first application occurred at planting, and the second application occurred close to bolting (30–35 days after planting). The fertilizers were broadcast using a Whirl Hand-Powered Spreader (The Scotts Company of North America) to ensure even distribution.

Weeds were managed with a preplanting application of Prowl H₂O [pendimethalin: *N*-(1-ethylpropyl)-3,4-dimethyl-2,6-dinitrobenzenamine; BASF] at the rate of 2.8 L ha⁻¹ (1.26 kg ai ha⁻¹) disked to 5 cm deep approximately 15 days prior to planting in both years at Brookings and applied to the soil surface with no incorporation at Pierre. After crop emergence, Poast {sethoxydim: 2-[2-(ethoxyimino)butyl]-5-[2-(ethylthio)propyl]-3-hydroxy-2-cyclohexene-1-one; BASF} was applied at the rate of 2.1 L ha⁻¹ (0.38 kg ai ha⁻¹) 4 weeks after planting to control grass weeds. Broadleaf weeds were managed by hand pulling from within each plot every 2 weeks.

TABLE 2 Genotypes evaluated in 2019 and 2020 field experiments at Brookings and Pierre, South Dakota

Entry	Name	Type	Source	Herbicide tolerance ^a	Maturity ^b	Standability rating ^b
1	NCC101S	Hybrid	Photosyntech	None	Early	Excellent
2	CS2100	Hybrid	Meridian Seeds	RR	Early	Very good
3	CS2300	Hybrid	Meridian Seeds	RR	Late	Excellent
4	CS2500	Hybrid	Meridian Seeds	CL	Med	Excellent
5	CS2600 ^c	Hybrid	Meridian Seeds	TruFlex RR	Early/Med	Very good
6	DKTF91SC	Hybrid	DEKALB Canola	TruFlex RR	Early	–
7	DKTF92SC	Hybrid	DEKALB Canola	TruFlex RR	Late	Excellent
8	DKTFLL21SC ^d	Hybrid	DEKALB Canola	TruFlex RR	Early	Excellent
9	DKTF96SC ^d	Hybrid	DEKALB Canola	TruFlex RR	Med	Excellent
10	DKLL82SC ^d	Hybrid	DEKALB Canola	LL	Early	Excellent
11	DKL7114BL ^e	Hybrid	DEKALB Canola	RR	Early	–
12	InVigor L233P	Hybrid	BASF Corporation	LL	Early	Good
13	InVigor L140P	Hybrid	BASF Corporation	LL	Med/Late	Excellent

^aHerbicide technology: RR: Roundup Ready; LL: Liberty Link; CL: Clearfield; TruFlex RR: extended window of Roundup application.

^bBased on seed company ratings for maturity and standability.

^cEvaluated only at Brookings in 2019 and then at both locations in 2020.

^dEvaluated in 2020 only.

^eEvaluated in 2019 only.

2.3 | Data collection

The number of days from planting to flowering (50% of flowers open in each plot) and the number of days from planting to maturity (50% of plants with pods turned yellow in each plot) were recorded for each plot at Brookings. At physiological maturity (when 90% of the pods plot⁻¹ reached a tan color), plant height was determined by measuring the height of five random plants within each plot from soil line to the top of the plant. A sample of 10 plants was cut about 5 cm above soil level from each plot and used to determine number of pods plant⁻¹. Because canola has an indeterminate growth habit and continues to produce new flowers as long as moisture and nutrients are available, an application of Roundup {glyphosate: [*N*-(phosphonomethyl)glycine]; Monsanto} was applied at the rate of 2.24 L ha⁻¹ (1.07 kg ae ha⁻¹) 10 days before harvest to desiccate the plants. Lodging notes were taken before harvesting on a scale of 0–9 (0 = no lodging, 9 = completely lodged) (Jan et al., 2016; Johnson & Hanson, 2003; Mahmood et al., 2018). Plots were harvested using a Kincaid 8XP crop research combine (Kincaid Equipment and Manufacturing) with the assistance of the H2 High-Capacity GrainGage (Juniper Systems, Inc.). Seed from each plot was dried, weighted, and corrected for 8.5% moisture.

In 2019, dried seed samples for three genotypes representing early-, medium-, and late-maturity groups from two replications at each location were sent to SGS Mid-West Seed Services, Inc. for oil content analysis using a hexane solvent extraction method. These results were used to calibrate our

laboratory's nuclear magnetic resonance (NMR) instrument (minispec mq, Bruker) for oil content analysis. A 5-g seed subsample for all genotypes and in all replications in 2019 and 2020 was analyzed using the calibrated NMR instrument. Oil yield was calculated by multiplying the total seed yield by the oil concentration (percent basis). Thousand seed weight was measured by counting 1000 clean dry seeds and taking their weight using a high precision scale (Sartorius Model TE3 13S-DS).

2.4 | Statistical analysis

Data from the four site-years were initially combined and analyzed together using the analysis of variance (ANOVA) for RCBD in R Studio (version 4.1.0) using the package “agricolae” (de Mendiburu, 2017). Genotype and location were considered fixed effects, whereas replication and years were considered random effects. Significant locations/environments by genotype interactions were noted for most traits; hence, data from each site-year were analyzed separately. Fisher's least significant difference was used to compare the differences among treatments within site and years at the 95% confidence level. Pearson correlation analysis was conducted using data from four site-years to determine relationship between yield and yield-related traits (Yan & Frégeau-Reid, 2018; Yan et al., 2007).

The additive main effect and multiplicative interaction (AMMI) analysis, a principal component (PC)-based method

(Gauch, 2013; Purchase et al., 2000) in R studio version 4.0.1 (Ajay et al., 2019; de Mendiburu, 2017), was used to determine the effect of genotype, environment, and their interaction on three traits (pods plant⁻¹, seed yield, and 1000-seed weight) that were measured at all four environments using the eight genotypes that were present in all four environments. The AMMI model is a combination of ANOVA and PCA analysis (PCA), and it subjects the GE interaction to PCA and partitions the interaction sum of squares (SS) into a series of interaction PC analysis axes with the PC1 being the first interaction PC (Fabio et al., 2017). When PC1 was significant, AMMI biplots were used as a tool for interpreting the AMMI analysis (Ajay et al., 2019; De Mendiburu, 2017; Fabio et al., 2017; Purchase et al., 2000). In the biplots, the additive effects of GE for each trait were plotted on the *x*-axis and the interaction PC1 scores were plotted on the *y*-axis as square roots of the trait in question (Fabio et al., 2017; Zahuski et al., 2020). The vertical reference line at the center represents the grand mean of the trait and the points on the left of the line are the characteristic of performance lower than the grand mean. The horizontal line intersects the PC1 axis at zero. Points that are farther away from the horizontal line indicate genotypes and environments with large interactions, whereas genotypes located close to the horizontal line are stable for the trait in question across environments. Genotypes and environments having the same PC score sign have positive interactions, whereas opposite signs indicate negative interactions.

AMMI stability values (ASVs) (Bocianowski et al., 2019; Purchase et al., 2000) were used to compare the stability of the genotypes for traits of interest across locations and years. Unlike the AMMI-1 biplot that breaks down genotypic adaptation by location and year, the ASV compares the stability of genotypes across years and locations with the lower ASV values indicating a genotype more stable [has similar traits (yield, 1000-seed weight, etc.) regardless of the environment] (Purchase et al., 2000). This does not imply that the genotype will be the greatest yielding every year but will be a steady performer no matter the environment. The ASV values were then compared with the ranking of each genotype for the trait of interest using means.

3 | RESULTS AND DISCUSSION

3.1 | Environmental conditions

In general, the Brookings location was cooler, wetter, and more similar to the long-term average in 2019 compared to 2020, and cooler in both years than the Pierre location. The experimental period (2019–2020) was characterized by varied weather conditions at different stages of spring canola growth and development. In 2019, the growing season rainfall

at Brookings was close to the long-term average, whereas at Pierre, it was 103 mm lower (Table 1). In June, the rainfall was 44 (Brookings) and 80 mm (Pierre) below the 30-year average. In July, precipitation was 51.4 (Brookings) and 4.7 mm (Pierre) above the long-term average. The year 2020 was drier at both locations compared to the 30-year average. Rainfall totals were 169 (Brookings) and 114.3 mm (Pierre) below the 30-year average (Table 1). Again, June was drier than the 30-year average at both locations.

Temperature from April through August varied among the four site–years of the study (Table 1). In 2019, the mean maximum temperature at the Brookings location was 2°C lower than the long-term average, whereas Pierre was 3°C cooler. The maximum temperatures during June were comparable to the 30-year average at both locations, whereas July was 1.4°C cooler at Brookings and 2.6°C warmer at Pierre, respectively. In 2020, the mean maximum temperature was comparable to the long term at Brookings, whereas Pierre was 1°C warmer than the long-term average.

The lower than optimum precipitation in April and May of 2020 at both locations resulted in reduced early growth, and vigor affecting overall agronomic trait expressions, whereas heat stress during June and July constrained flowering, pod setting, and seed filling that reduced seed yield and seed oil concentration. Drought was more severe at Pierre due to extremely dry conditions (rainfall 114.3 mm below 30-year average) and elevated temperatures (more consecutive days of extreme hot days [temperature above 25°C] compared with the Brookings location [Table S2]). This may have resulted in the reduced plant growth, pollen fertility, and number of pods plant⁻¹, which consequently led to lower seed yield and seed oil concentration for all genotypes compared to the Brookings location.

3.2 | Vegetative growth

Past studies have reported that canola plants can vary in height, averaging between 75 and 175 cm (<https://www.canolacouncil.org/canola-encyclopedia/growth-stages/>). Tall plants tend to partition more nutrients to biomass production rather than yield and generally have increased stem lodging susceptibility due to a higher gravitational point and thinner nonlignified stem tissues. In the current study, canola height was collected in three of four site–years as plants were too lodged to determine plant height at Brookings in 2019. Genotypes in the measured areas differed in plant height (Tables 3 and 4). The shortest genotype NCC101S was 85.7, 96.1, and 93.8 cm tall at Brookings in 2020 and Pierre in 2019 and 2020, respectively. The tallest genotype at Pierre in 2019 (124 cm) and at Brookings in 2020 (117 cm) was CS2300. Plant height across genotypes was similar (averaging 95 cm) at Pierre in 2020 (Table 4).

TABLE 3 Growth and yield traits for canola genotypes grown at Brookings and Pierre, South Dakota, in 2019

Genotypes	Brookings 2019				Pierre 2019	
	Lodging (0–9) ^a	Days to flower	Days to maturity	Pod number (plant ⁻¹)	Plant height (cm)	Pod number (plant ⁻¹)
CS2100	4.7 abcd	45 bcd	95 bc	95	107.8 de	67
CS2300	5.0 abcd	46 abc	94 cd	68	123.9 a	70
CS2500	1.7 d	47 a	96 ab	69	113.5 b	60
CS2600	7.7 a	46 abc	94 cd	87	–	–
DKL7114BL	6.7 ab	44 de	95 bc	78	108.2 cde	67
DKTF91SC	5.5 abc	43 e	92 e	91	106.8 e	82
DKTF92SC	4.5 abcd	45 bcd	93 de	74	110.9 bcd	58
L140P	3.5 bcd	47a	95 bc	64	112.1 bc	57
L233P	4.5 abcd	46 bcd	97 a	106	114.8 b	80
NCC101S	3.2 cd	40 f	86 f	92	96.1 f	71
Mean	4.7	45	94	82	110.5	68
<i>p</i> -Value	0.029	<0.000	<0.000	0.114	<0.000	0.258
SEM	1.09	0.68	0.50	10.3	1.40	7.5

Note: Mean values followed by same lowercase letters within the column are not significantly different at $p \leq 0.05$.

Abbreviation: SEM, standard error of the mean.

^aLodging rating scale: 0 = none, 9 = completely flat on the ground.

TABLE 4 Growth and yield traits for canola genotypes grown at Brookings and Pierre, South Dakota, in 2020

Genotype	Brookings 2020				Pierre 2020		
	Plant height (cm)	Lodging (0–9) ^a	Days to flower	Days to maturity	Pod number (plant ⁻¹)	Plant height (cm)	Pod number (plant ⁻¹)
CS2100	89.4 b	5.8 ab	39 cd	80 cd	26 c	94.2	22
CS2300	117.0 a	0.3 b	45 a	93 a	57 a	100.0	22
CS2500	97.3 b	3.8 b	42 abc	83 bcd	44 abc	100.0	32
CS2600	92.7 b	3.5 b	40 bc	85 bcd	54 ab	100.4	33
DKLL82SC	88.0 b	5.3 b	41 bc	85 bc	33 abc	98.0	30
DKTF91SC	88.1 b	6.3 ab	40 bc	79 d	18 c	90.0	23
DKTF92SC	89.1 b	4.3 b	40 bc	84 bcd	40 abc	103.0	24
DKTF 96SC	96.4 b	4.5 b	44 ab	84 bcd	30 bc	72.3	19
DKTFLL21SC	93.7 b	8.5 a	40 bc	81 cd	25 c	93.4	23
L140P	94.3 b	2.5 b	43 ab	88 ab	40 abc	102.4	23
L233P	87.8 b	3.5 b	41 bc	83 bcd	38 abc	94.1	21
NCC101S	85.7 b	3.3 b	36 d	79 d	20 c	93.8	20
Mean	93.3	4.3	41	84	35	95.1	24
<i>p</i> -Value	0.001	0.021	0.002	0.001	0.014	0.520	0.524
SEM	4.1	1.3	1.2	2.0	7.7	4.2	5.0

Note: Mean values followed by same lowercase letters for each treatment within the column are not significantly different at $p \leq 0.05$.

Abbreviation: SEM, standard error of the mean.

^aLodging rating scale: 0 = none, 9 = completely flat on the ground.

Stem lodging data were collected at the Brookings site only as no lodging occurred at Pierre in either year. This is likely due to the fact that plant populations were lower under the no-till systems resulting in plants with thick

stems and less susceptible to lodging. In both years, lodging severity was influenced by genotype (Tables 3 and 4). In 2019, the genotype with the highest lodging score was CS2600 (7.7), whereas the genotype with the lowest lodging score was

TABLE 5 Pearson correlation coefficients between yield, days to flowering, days to maturity, pod number per plant, 1000-seed weight, and lodging

Trait	df	DFL (days)	DM (days)	PD (plant ⁻¹)	TSW (g)	YLD (kg ha ⁻¹)	LD (0–9)	PH (cm)
DFL (days)	94	1	0.69**	0.55**	0.28*	0.22*	0.02 ^{ns}	0.11 ^{ns}
DM (days)	94		1	0.77***	0.49***	0.14 ^{ns}	-0.04 ^{ns}	-0.05 ^{ns}
PD (plant ⁻¹)	190			1	0.34**	0.38***	0.00 ^{ns}	0.16 ^{ns}
TSW (g)	190				1	-0.04 ^{ns}	0.02 ^{ns}	0.39**
YLD (kg ha ⁻¹)	190					1	0.10 ^{ns}	0.02 ^{ns}
LD (0–9 scale)	94						1	-0.19 ^{ns}
PH (cm)	94							1

Abbreviations: DFL, number of days to flowering; DM, number of days to maturity; PD, number of pods plant⁻¹; TSW, 1000-seed weight; YLD, seed yield; LD, lodging (0–9); PH = plant height.

*Significant at $p \leq 0.05$.

**Significant at $p \leq 0.01$.

***Significant at $p \leq 0.001$.

^{ns}Nonsignificant.

CS2500 (1.7). In 2020, the genotype with the highest score was DKTFLL21SC (8.5), whereas the genotype with the lowest lodging score was CS2300 (0.3) and was rated by the seed supplier as excellent in standability (Table 2).

Working with *B. carinata* genotypes under similar SD growing conditions, Alberti et al. (2019) reported a correlation between plant height and lodging. Likewise, Pan et al. (2016) found that lodging severity positively increased as plant height increased among canola hybrids. However, the correlation between plant height and lodging in this study was negative but not significant ($r = -0.19$; Table 5). The lack of correlation of lodging with plant height at Brookings demonstrates an advantage of growing recently developed genotypes that are being selected for standability. But some of the company ratings did not match with observed field ratings, which indicates that we should be cautious when selecting genotypes for a specific trait.

Days to 50% flowering and maturity data were collected at the Brookings location only. The 3-h drive from Brookings to the Pierre location made it very difficult to collect reliable flowering and maturity data at Pierre. On average, all canola genotypes flowered 2–4 days and matured 1–15 days earlier in 2020 compared to 2019, likely due to early season drought and mid-season heat stress initiating early transitioning from vegetative to reproductive growth and shortening time to maturity. We also found that number of days to flowering and maturity varied by genotype (Tables 3 and 4). The earliest genotype to flower was canola NCC101S (designated as early) reaching 50% flowering at 40 and 36 days after planting, in 2019 and 2020, respectively. This genotype also reached maturity earlier than all other genotypes (86 and 79 days) in 2019 and 2020 (Tables 3 and 4), which agreed with maturity rating provided by the seed company. The genotypes that flowered the latest were CS2500 (designated as medium) and L140P (designated

as late) at 47 days after planting in 2019 and CS2300 (late) at 45 days after planting in 2020, whereas the latest maturing genotypes were L233P in 2019 and CS2300 in 2020. The maturity period for some of the genotypes (notably NCC101S, CS2300, and L140P) corresponded to seed company designation, whereas others (L233P) did not (Table 2). At this time, maturity ratings across the industry are not standardized (as in soybean), and these data point out that research results at specific locations for specific genotypes would be helpful for producers when choosing genotypes/hybrids for their fields.

Spring-planted canola is very sensitive to heat and moisture stress. These stresses are more devastating if they coincide with flowering that occurs in late June to mid-July in SD (Alberti et al., 2019). Flower abortion and poor pod set are the results of these stresses, which ultimately negatively impacts seed yield and oil concentration (Tefsamariam et al., 2010). Late-maturing genotypes are often beneficial to prolong the growing season and optimize yields by prolonging grain filling in long growing season environments. In the NGP, however, prolonged vegetative growth would delay flowering and seed set and often expose the crop to high temperature and drought stress. This likely explains the low positive but insignificant correlation of seed yield with number of days to maturity (Table 5). Therefore, early-maturing genotypes are preferred. Over the 2-year period, the number of days to maturity for canola genotypes ranged from 79 to 97. This is a narrower range than 82–122 days reported by Gan et al. (2016) for canola hybrids grown at 16 distinct locations in Canada. The large variation in the number of days to maturity in their study was attributed to the large moisture gradient among multiple locations/environments. In the current study, genotypes were evaluated at only two locations over a period of 2 years, which had a narrower moisture and temperature gradient.

TABLE 6 Seed yield, 1000-seed weight, oil concentration, and oil yield for canola genotypes grown at Brookings and Pierre, South Dakota, in 2019

Genotypes	Brookings 2019				Pierre 2019			
	Seed yield (kg ha ⁻¹)	1000-seed weight (g)	Oil concentration (g kg ⁻¹)	Oil yield (kg ha ⁻¹)	Seed yield (kg ha ⁻¹)	1000-seed weight (g)	Oil concentration (g kg ⁻¹)	Oil yield (kg ha ⁻¹)
CS2100	1907 abc	3.4 abc	429 b	803 bc	1687 a	3.8	437 a	476
CS2300	1778 bc	3.4 abc	420 b	761 c	1409 ab	2.3	415 a	403
CS2500	1679 c	3.5 abc	475 ab	800 bc	1477 ab	3.7	432 a	552
CS2600	2012 abc	3.5 abc	516 a	1038 ab	—	—	—	—
DKL7114BL	1811 bc	3.8 abc	467 ab	843 bc	1485 ab	3.0	383 ab	504
DKTF91SC	2349 a	3.5 abc	501 ab	1178 a	1531 ab	2.9	426 a	531
DKTF92SC	1956 abc	3.0 de	477 ab	922 bc	1653 ab	2.1	380 ab	542
L140P	1927 abc	2.8 e	469 ab	903 bc	1237 c	2.8	387 ab	409
L233P	2178 ab	3.2 cd	467 ab	1017 ab	1400 ab	3.3	396 a	505
NCC101S	2106 abc	4.0 a	342 c	726 c	1352 ab	3.5	216 c	368
Mean	1961	3.1	456	899	1470	3.0	365	477
<i>p</i> -Value	<0.023	<0.013	<0.002	<0.022	0.034	0.176	<0.000	0.484
SEM	171	0.21	24.7	87.7	130	0.5	26.7	68.6

Note: Mean values followed by same lowercase letters for each treatment within the column are not significantly different at $p \leq 0.05$.

Abbreviation: SEM, standard error of mean.

3.3 | Seed yield and yield traits

The 2020 growing season was much drier and warmer than the 2019 growing season (Tables 1 and S2). At Pierre, in 2020, the impact of drought stress was exacerbated with early season damage by chinch bugs (*Blissus leucopterus*) insects followed by heat stress during reproductive growth, which resulted in low yield. Seed yield varied among genotypes at both locations and in both years (Tables 6 and 7). In 2019, at Brookings, seed yield ranged from 1679 kg ha⁻¹ (CS 2500—med) to 2349 kg ha⁻¹ (DKTF91SC—early) with a mean of 1961 kg ha⁻¹. At Pierre, in 2019, seed yield ranged from 1237 kg ha⁻¹ (L140P—mid/late) to 1687 kg ha⁻¹ (CS2100—early) (Table 6). In 2020, canola seed yield at Brookings ranged from 1104 kg ha⁻¹ (DKTFLL21SC—early) to 2964 kg ha⁻¹ (L140P—mid/late) with a mean of 1740 kg ha⁻¹. At Pierre, seed yield was much lower ranging from 504 kg ha⁻¹ (L233P—early) to 1375 kg ha⁻¹ (CS2600—early/mid) with a mean of 858 kg ha⁻¹. Unlike 2019, when early-maturing genotypes had greater yield, the early season drought stress in 2020 favored late-maturing genotypes at both locations.

The 1000-seed weight is an important genotype-specific trait (McGregor, 1987) that is also influenced by environmental conditions (Harker et al., 2015). This trait is used as a selection parameter among canola genotypes as it determines seeding rate and influences seedling emergence rates, vigor, and growth (Elliott et al., 2008). Canola seed weight varied among genotypes at Brookings in 2019 ($p < 0.000$) and 2020 ($p = 0.045$) (Tables 6 and 7). In 2019, 1000-seed weight aver-

aged 3.1 g and ranged from 2.8 g (L140P) to 4.0 g (NCC101S). In 2020, 1000-seed weight averaged 2.7 g and ranged from 1.9 g (L233P) to 3.3 g (CS2500). Canola 1000-seed weight was similar among genotypes at Pierre and averaged 3 g in 2019 and 1.9 g in 2020.

Pods plant⁻¹ ranged from 19 to 106 among all genotypes and different environmental conditions. On average, plants had more pods in 2019 (82 and 68 pods plant⁻¹ at Brookings and Pierre, respectively) (Table 3) than in 2020 (35 and 24 pods plant⁻¹ at Brookings and Pierre, respectively) (Table 4). Canola genotypes had similar pod number in 2020 at Pierre, averaging 24 pods plant⁻¹, whereas at Brookings, the number of pods plant⁻¹ differed by genotype ($p = 0.014$) (Table 4). The genotype with the greatest number of pods plant⁻¹ was CS2300 (57 pods plant⁻¹), whereas the genotype with the least number of pods plant⁻¹ was DKTF91SC (18 pods plant⁻¹).

Seed yield in *Brassica* crops is a function of pods plant⁻¹, seeds pod⁻¹, and seed weight, which are key yield components (Angadi et al., 2003; Lu et al., 2011). In the current study, the correlation between number of pods plant⁻¹ and seed yield, combining the four site-years data, was positive and significant ($r = 0.38$; $p < 0.000$) (Table 5) agreeing with the above statement. However, the correlation between 1000-seed weight and seed yield was not significant (Table 5). Similarly, other researchers have reported no correlation between 1000-seed weight and seed yield (Załoski et al., 2020) or a weak correlation between individual seed weight and yield (Diepenbrock, 2000).

TABLE 7 Seed yield, 1000-seed weight, oil concentration, and oil yield for canola genotypes grown at Brookings and Pierre, South Dakota, in 2020

Genotype	Brookings 2020				Pierre 2020	
	Seed yield (g kg ⁻¹)	1000-seed weight (g)	Oil concentration (g kg ⁻¹)	Oil yield (kg ha ⁻¹)	Seed yield (kg ha ⁻¹)	1000-seed weight (g)
CS2100	1661 bc	2.7 abc	343 bc	557 bc	576 b	1.7
CS2300	1797 bc	3.1 ab	416 abc	764 b	1355 a	2.1
CS2500	1793 bc	3.3 a	449 ab	804 b	1345 a	1.9
CS2600	1600 bc	3.0 ab	312 c	510 bc	1375 a	2.0
DKLL82SC	1407 bc	3.0 ab	423 abc	603 bc	512 b	1.5
DKTF91SC	1509 bc	2.7 abc	468 a	705 bc	749 b	2.2
DKTF92SC	1697 bc	3.0 ab	436 ab	737 b	607 b	1.7
DKTF 96SC	1930 b	2.6 abc	438 ab	849 b	863 ab	2.0
DKTFLL21SC	1104 c	2.3 bc	305 c	323 c	666 b	1.8
L140P	2964 a	2.6 abc	469 a	1405 a	1084 ab	1.7
L233P	1701 bc	1.9 c	452 ab	766 b	504 b	2.3
NCC101S	1711 bc	2.9 ab	368 abc	626 bc	667 b	2.0
Mean	1740	2.7	406	720	858	1.9
<i>p</i> -Value	0.002	0.045	0.019	<0.000	0.003	0.782
SEM	232.4	0.3	37.2	118.0	185.4	0.2

Note: Mean values followed by same lower-case letters for each treatment within the column are not significantly different at $p \leq 0.05$.

Abbreviation: SEM, standard error of mean.

The partitioning and accumulation of growth assimilate into the seed endosperm determines seed weight, and this can vary depending on the availability of nutrients and moisture during critical seed development and maturation stages. Under optimal conditions, canola seed weight ranges from 2 to 6 g 1000 seeds⁻¹ (Elliott et al., 2008; Harker et al., 2015). In the current study, canola seed sizes were smaller, ranging from 1.7 to 4.0 g 1000 seeds⁻¹ due to drought and heat stress conditions during seed development (Tables 1 and S2). Moisture and heat stresses have also been reported to negatively impact seed yield in *Brassica* crops (CCC, 2018; Morrison & Stewart, 2002). Other studies have reported higher yields under irrigation compared to nonirrigated controls under extremes of drought and heat stress (Mohtashami et al., 2020; Taylor et al., 1991), suggesting that supplemental irrigation at the Pierre location in 2020 may have reduced yield penalties associated with drought and heat stress. However, in SD, only about 40,500 ha are under irrigation, so that dryland conditions, especially in the western part of the state, would be the norm.

The number of pods per plant in the current study (ranging from 19 to 106) is in the lower end of the range of 44–200 pods plant⁻¹ reported in a study by Angadi et al. (2003). The discrepancy could be due to a combination of factors. The effects of heat and moisture stress on *Brassica* crops have been reported in different studies to negatively impact pod number and seed fill reducing yield (Angadi et al., 2000; Nuttal et al., 1992; Singh et al., 2014). High temperatures

(>25°C), during bud and flowering stages, can result in the abortion of flowers and pods in *Brassica* spp. and the failure of seeds to properly develop (Angadi et al., 2000; Gan et al., 2004). Drought stress during the reproductive growth stages creates a hormone imbalance that inhibits pod formation and seed development, causing *Brassica* species to drop damaged flowers and direct energy into younger flowers (Canola Watch, 2016). Although both locations recorded temperatures higher than 25°C during critical growth stages of canola, temperatures were elevated for a longer period, and moisture conditions were less favorable at Pierre than at Brookings (Table S2).

3.4 | Oil concentration and oil yield

Genotypes differed in seed oil concentration and oil yield at Brookings and at Pierre in 2019 and at Brookings in 2020 (Tables 6 and 7). Oil concentration and oil yield were not measured at Pierre in 2020 because drought stress impacted seed development resulting in extremely small and shriveled seeds. At Brookings, in 2019, oil concentrations ranged from 342 g kg⁻¹ (NCC101S) to 516 g kg⁻¹ (CS2600), whereas in 2020, the range in oil concentration among genotypes was narrower from 305 g kg⁻¹ (DKTFLL21SC) to 469 g kg⁻¹ (L140P) (Table 7). At Pierre, seed oil concentration was lower ranging from 216 g kg⁻¹ (NCC101S) to 437 g kg⁻¹ (CS2100) in 2019 (Table 6). In 2019, at Brookings, oil yield ranged from 726 kg ha⁻¹ (NCC101S) to 1178 kg ha⁻¹ (DKTF91SC)

with a mean of 899 kg ha⁻¹. At Pierre, in the same year, oil yield was much lower ranging from 368 kg ha⁻¹ (NCC101S) to 542 kg ha⁻¹ (DKTF92SC) and a mean of 477 kg ha⁻¹. At Brookings, in 2020, oil yield ranged from 323 kg ha⁻¹ (DKTFLL21SC) to 1405 kg ha⁻¹ (L140P).

Seed oil concentration in canola has been reported to range from 370 to 510 g kg⁻¹ under optimum field conditions and averaged 340 g kg⁻¹ under drought stress (332 mm of precipitation) (Jackson, 2000). Canola oil content is also influenced by the environmental conditions that affect seed endosperm development and maturation (Zhang & Flottmann, 2016). At Pierre, in 2019, the total growing season precipitation was 246 mm, which was lower than that reported by Jackson (2000) and helps explain the low oil concentration and yield. At Brookings, precipitation was 430 mm and 263 in 2019 and 2020, respectively. This explains the lower oil concentration at Brookings in 2020 (406 g kg⁻¹) when compared to the same location in 2019 (456 g kg⁻¹). Low oil concentration in semiarid environments has been attributed to accelerated growth and short growing season as reported by Getinet et al. (1996), which negatively impacts seed development and maturation and ultimately reduces seed oil accumulation. Periods of high temperatures and low soil moisture during flowering and seed-filling periods in canola have been shown to reduce seed oil concentrations (Morrison & Stewart, 2002), which helps explain the low oil yield among all genotypes at Pierre compared to Brookings.

3.5 | Genotype by environment interaction

Acclimatizing a new cultivar to a new environment for optimum yield demands that both genotype and environment interact (GE interaction) to influence yield (Gunasekera et al., 2006), although this may complicate selection for multiple environments (Shafii & Price, 1998). The results of the AMMI analysis for three traits of interest (pod plant⁻¹, 1000-seed weight, and seed yield) for eight genotypes that were present at all four site-years of this study are presented in Table 8. Environmental effects were significant and explained 45.7%, 41.4%, and 67.7% of the variation in seed yield, 1000-seed weight, and pods plant⁻¹, respectively. Genotypic effects were only significant for the 1000-seed weight and explained 7.7% of the variation. On the other hand, GE interactions were significant for two of the three traits of interest (seed yield and pod per plant) and explained 18.1% of the variation in seed yield and 11.3% for pods plant⁻¹. Recent research assessing GE interaction for canola has mostly focused on seed quality traits (Bocianowski et al., 2019; Liersch et al., 2020). However, Zaluski et al. (2020) reported significant environmental, genotypic, and GE interactions effects on seed yield and 1000-seed weight in camelina [*Camelina sativa* (L.)], a member of the Brassicaceae family. In their study,

environmental effects were the dominant factor influencing yield explaining 72.7% of observed variation, whereas genotypic effects were the dominant factor influencing 1000-seed weight and explained 73.3% of the observed variation (Zaluski et al., 2020). GE interaction impacts were smaller than observed in the current study only explaining 5.7% and 4.1% of the observed variation for seed yield and 1000-seed weight, respectively.

When a GE interaction SS were partitioned into interaction PCs, first PC (PC1) of GE was significant for all three traits (Table 8). The second PC of GE was significant for only seed yield. For seed yield, PC1 and PC2 explained 93% of observed GE variation, whereas PC1 accounted for 75.9% of the observed GE variation for 1000-seed weight and 84.4% in pods plant⁻¹, respectively (Table 8).

In terms of environmental adaptability, Brookings 2019 (B19) and Pierre 2019 (P19) were similar, but the Brookings 2019 environment had greater than grand mean yields, whereas yields were lower than the grand mean at Pierre (Figure 1a). Pierre 2019 (P19) and Brookings 2020 (B20) differed greatly in terms of genotype adaptability, as indicated by opposite PC1 scores. In general, the Brookings 2020 and Pierre 2020 (P20) environments interacted positively but with the Pierre 2020 discriminating, as indicated by longer distance from the origin and with no genotypes adapted to this very harsh environment. The Brookings 2020 environment, on the other hand, supported greater than grand mean yields and had a positive interaction with three genotypes [CS2300—late (2), CS2500—med (3), and L140—med/late (6)]. The first two (CS2300 and CS2500) were the most stable in this environment indicated by closeness to the horizontal axis. L140P (6) had the greatest yield at the Brookings 2020 environment but was unstable as it is located farthest along the right side of the center axis. This genotype showed adaption to above-average high-yielding environments with adequate moisture to support growth and mild temperatures (Brookings 2019 and 2020) and showed a negative interaction with the lower yielding environments with inadequate moisture and high temperatures during flowering/seed filling (Pierre 2019 and 2020) (Figure 1a). The Pierre 2019 environment supported below grand mean yield and interacted positively with the greatest number of genotypes, and four genotypes [NCC101S—early (8), DKTF92SC—early (5), CS2100—early (1), and L233P—early (7)] were relatively stable under this environment, whereas DKTF91SC—early (4) was the least stable. On average, seed yield was greatest for genotypes L140P (6) and lowest for L233P (7) (Figure 1a).

Again, the 2019 environments were more favorable for seed weight with the Brookings 2019 producing the largest seed weight (Figure 1b). Pierre 2020 produced small, shriveled seeds due to hot-and-dry conditions and was the worst environment for the 1000-seed weight. The most stable genotypes

TABLE 8 The additive main effects and multiplicative interaction (AMMI) analysis of variance for yield and yield traits of eight canola genotypes, averaged across two locations (Brookings and Pierre, South Dakota) and 2 years (2019 and 2020)

Source	df	Seed yield (kg ha ⁻¹)			1000-seed weight (g)			Pods (plant ⁻¹)		
		Sum of squares (%)	F-value	p-value	Sum of squares (%)	F-value	p-value	Sum of squares (%)	F-value	p-value
Total	127	100.0			100			100		
Environment (E)	3	45.7	16.5	<0.000	41.4	24.8	<0.000	67.7	177.2	<0.000
Blocks (E)	12	11.1	3.5	<0.000	6.7	1.5	0.145	1.4	0.6	0.806
Genotype (G)	7	2.9	1.6	0.151	7.7	3.0	0.008	2.3	0.5	0.188
G × E	21	18.1	3.2	<0.000	12.6	1.6	0.067	11.3	2.7	<0.000
PC1	9	61.1	4.6	<0.000	75.9	2.8	0.005	84.4	5.2	<0.000
PC2	7	32.0	3.1	0.006	16.3	0.8	0.597	9.1	0.7	0.687
PC3	5	7.0	1.0	0.429	7.8	0.5	0.753	6.4	0.7	0.603
Residuals	84	22.2			27.2			17.2		

TABLE 9 The additive main effects and multiplicative interaction model (AMMI), stability value (ASV), rank of AMMI stability value (rASV), mean values of traits for genotypes and rank of trait mean (rY) from highest to lowest for eight canola genotypes evaluated at four environments in South Dakota

Gen	Seed yield (kg ha ⁻¹)				1000-seed weight (g)				Pods (plant ⁻¹)			
	ASV ^a	rASV ^b	Mean ^c	rY ^d	ASV	rASV	Mean	rY	ASV	rASV	Mean	rY
CS2100	15.3	3	1458	7	0.9	6	2.5	3	13.3	3	53	4
CS2300	20.7	5	1585	2	1.1	7	2.3	6	20.1	8	54	2
CS2500	22.2	6	1574	3	0.4	4	2.8	1	15.2	5	51	5
DKTF91SC	26.5	7	1535	4	0.4	3	2.4	5	19.5	7	53	3
DKTF92SC	14.0	2	1478	5	0.8	5	1.8	8	9.0	1	49	7
L140P	54.9	8	1803	1	0.2	1	2.2	7	14.9	4	46	8
L233P	17.7	4	1446	8	0.3	2	2.5	2	10.1	2	64	1
NCC101S	10.0	1	1459	6	1.1	8	2.4	4	16.7	6	51	6

^aAMMI stability value, the lower the value the higher the stability for the trait.

^bAMMI stability value ranking; 1 = most stable, 8 = least stable.

^cMean value for each trait.

^dRank of trait mean; 1 = highest value, 8 = lowest value.

for the 1000-seed weight were L140P (6), DKTF91SC (4), and L233P (7) as indicated by their closeness to the horizontal axis (Figure 1b).

For pods plant⁻¹, the 2019 environments, Brookings (B19) and Pierre (P19), were similar and favorable for pod production, whereas in 2020, both locations were less favorable with a number of pods plant⁻¹ lower than grand mean (Figure 1c). The number of pods plant⁻¹ was greatest for L233P—early (7) and lowest for L140P—late (6) agreeing with the ranking of pods plant⁻¹ in Table 9. The spread of points in the AMMI-1 biplot indicates that the number of pods per plant is an unstable trait that is greatly influenced by environmental conditions. The relatively stable genotypes in pod production were CS2100 (1), DKTF92SC (5), and L233P (7) as indicated by their relative closeness to the horizontal axis.

3.6 | AMMI stability value

When genotypes were ranked for stability using ASV values, the top four genotypes were rated as early (NCC101S, DKTF92SC, CS2100, and L233P) (Table 9). The same four genotypes were also shown to be the most stable under the Pierre 2019 environment in the AMMI-1 biplots but yielded lower than the grand mean. The next two genotypes in the ASV stability ranking (CS2300—late and CS2500—med) were the most stable in the higher yielding environment of Brookings 2020. These two genotypes had positive interactions with high-yielding environments (Brookings 2019 and 2020) meaning they are adapted to growing conditions with sufficient moisture to support growth and temperatures during flowering and seed filling that were less harsh than Pierre for canola. The ASV stability ranking characterized DKTF91SC

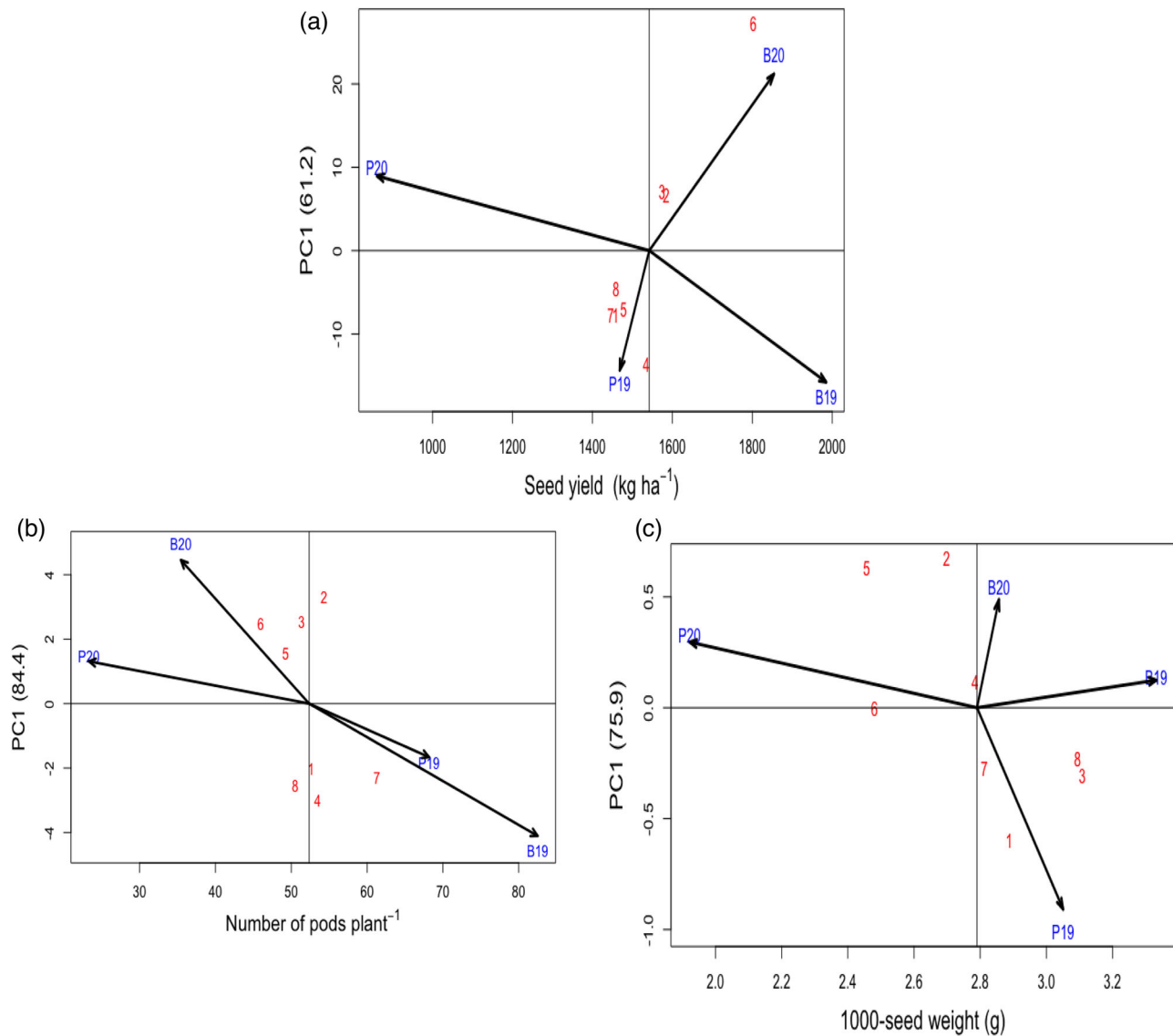


FIGURE 1 Additive main effects and multiplicative interaction model (AMMI)-1 biplot of (a) seed yield, (b) 1000-seed weight, and (c) number of pods plant⁻¹ of eight canola genotypes (red) across four environments (blue) in 2019 and 2020. Environment key: B19 = Brookings 2019, P19 = Pierre 2019, B20 = Brookings 2020, and P20 = Pierre 2020. Genotypes key: 1 = CS2100, 2 = CS2300, 3 = CS2500, 4 = DKT F91SC, 5 = DKTF92SC, 6 = L140P, 7 = L233P, 8 = NCC101S

and L140P as the least stable genotypes (Table 9) similar to the characterization of the genotypes for stability using AMMI-1 biplots (Figure 1a). Similarly, the characterization of genotypes for seed yield based on AMMI-1 biplots closely matched the ranking of genotypes for seed yield from highest to lowest yield: L140P—late, CS2300—late, CS2500—med, DKTF91SC—early, DKTF92SC—early, NCC101S—early, CS2100—early, and L233P—early (Table 9). These data indicate that the top three yielding genotypes were all classified as late maturity but had unstable yields across environments. These genotypes could be highly favored in growing conditions with high moisture and mild temperatures during flowering and seed filling but least desirable under heat and moisture stress.

GE interactions present both challenges and opportunities for agronomists and breeders (Fabio et al., 2017). The common plant breeding practice is to develop genotypes with broad adaptation across multiple environments. This selection based on stability reduces the complicating effects of GE interactions, lowers breeding costs, and eliminates the tendency to select high-yielding genotypes based only on favorable environments (Fabio et al., 2017). However, the GE component in this study is strong; therefore, it is important to capitalize on the contrasting performance among genotypes in the different environments and make recommendations based on specific adaptations. Canola is targeted for production in the central and western areas of SD as a rotational crop with winter wheat. These western regions have less

favorable growing conditions than eastern SD where moisture and temperatures are conducive to the corn–soybean rotation and outcompeting canola. Thus, subdividing SD into smaller areas and targeting genotypes' performance to the specific area can improve overall yields and profitability for local producers. The success of canola in SD will be determined by yield stability and adaptability to this specific region of the state.

4 | CONCLUSION

Even though canola can be adapted to diverse environments, genotype performance varied by environment. Greatest seed yields were observed at the Brookings environments that had higher precipitation and mild temperatures during flowering and seed filling compared to the Pierre environments, but even then, differences were noted between years. Environment was the most dominant cause of variation among genotypes, explaining 67.7%, 41.4%, and 45.7%, of variations in pods plant⁻¹, 1000-seed weight, and seed yield, respectively, whereas GE interactions explained most of the remaining variation. AMMI-1 analyses revealed that the four most stable genotypes under the low-yielding environment, with inadequate moisture to support growth and high temperatures during flowering/seed filling, were rated as early maturity (NCC101S, DKTF92SC, CS2100, and L233P), whereas the two most stable genotypes under growing conditions with adequate moisture and mild temperatures at flowering/seeding filling were rated as medium/late maturity (CS2300 and CS2500). Two of the three most stable genotypes in terms of seed weight were rated as early maturity (L233P and DKTF91SC). Pod production was less stable and highly influenced by environmental conditions.

These results demonstrate the importance of identifying genotypic adaptability as a way of developing environment-specific cultivar recommendations. Although genotypes that are stable across environments are generally preferred, in SD, canola production is targeted to low-yielding environments with inadequate moisture and high temperatures during flowering/seeding filling. These environmental conditions are less favorable than those where the crop is currently grown (ND and Canada, where cooler summer temperatures are common) meaning identifying genotypes with specific adaptation to the warmer, drier environmental conditions is critical for canola production to succeed in SD and in other regions with similar environmental conditions.

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CONFLICT OF INTEREST

The authors have no conflict of interest.

AUTHOR CONTRIBUTIONS

Unius Arinaitwe: Formal analysis; Investigation; Methodology; Project administration; Writing – original draft. **Sharon Clay:** Supervision; Writing – original draft; Writing – review & editing. **Thandiwe Nleya:** Conceptualization; Data curation; Formal analysis; Funding acquisition; Investigation; Methodology; Project administration; Supervision; Writing – original draft; Writing – review & editing.

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SUPPORTING INFORMATION

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