DETERMINING OPTIMUM SEEDING RATES FOR DIVERSE HARD RED SPRING WHEAT (*TRITICUM AESTIVUM* L.) CULTIVARS

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DOCTOR OF PHILOSOPHY

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ABSTRACT

Seeding rate for maximum grain yield can differ for diverse hard red spring wheat (HRSW) (*Triticum aestivum* L.) cultivars and can be derived from a seeding rate response curve. Six groups of HRSW cultivars with combinations of *Rht-B*, *Rht-D*, and *Ppd-D* with two cultivars per group were planted in 2013-2015 at five seeding rates in 23 trials throughout Minnesota (MN) and eastern North Dakota (ND), USA. Seeding rates ranged from 1.59 – 5.55 million seeds ha^{-1}. Planting dates represented optimum and delayed seeding dates. Agronomic measurements for plant height, lodging, stems per plant, protein, and yield were obtained. Stand loss measurements, defined as the amount of viable seeds that did not become established plants, ranged from 11-19% across seeding rates most commonly planted in the region. There was a seeding rate by cultivar interaction for plant height, protein, lodging, stems plant^{-1}, and yield. As seeding rate increased stems per plant consistently decreased and there were large differences in tillering capacity between cultivars. Increased seeding rate caused increased lodging for those cultivars with a capacity to lodge. Seeding rate for maximum yield of the cultivars differed. Combined over all cultivars, the seeding rate for maximum yield increased as the average yield of an environment decreased. An analysis of covariance (ANCOVA) predictive model was built for yield and tillering. The model for yield across all environments was not predictive with a validation R^2 of 0.01. However, when only the bottom six yielding environments out of the total 21 environments were used to build a yield model the predictions were more accurate with a validation R^2 of 0.44. The model built and validated for tillering was predictive for the validation environments with an R^2 of 0.71 for validation environments. Seeding rate trials continue to be useful for producers making seeding rate decisions for a range of agronomic reasons. Additionally, using regression predictions and separate training and validation datasets to predict yield and tillering with HRSW, genetic and geographic predictors show promise for recommending seeding rates for future environments.

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DEDICATION

The thesis is dedicated to my lovely wife Jenna, intrepid daughter Nora, my adventurous dog Taizy, and my supportive broader family, including but not limited to my parents, brothers, wife's parents, and extended family. Without their patience, love, and support this would not have been as fun. Additionally, this dissertation is for the birds. For it is when you are deepest into the struggles of one area of science, that your attention can become distracted by another area.

PREFACE

Determining the optimal seeding rate of Hard Red Spring Wheat (HRSW) (*Triticum aestivum* L.) is a critical management decision. Cultivars of HRSW are being released with increasing speed and diversity of genetic backgrounds from both private and public breeding programs. These new cultivars may respond differently to the range of management practices that are employed to produce a successful and profitable crop. Since there are a multitude of management practices used by producers that impact the productivity, quality, and profitability that could interact with newly released HRSW cultivars, the task of assembling a “package” of all potential practices for each new cultivar is not possible. Nevertheless, when practical to obtain, producers will benefit from information on practices that are likely to interact with new cultivars. Obtaining this information will still be expensive. The presence or absence of certain genes, specifically *Rht-B1*, *Rht-D1* and *Ppd-D1*, coupled with the known planting date, latitude, and characteristics like a cultivars ability to tiller could make it possible to determine optimum seeding rates without the need for a classical seeding rate by planting date field experiment. Instead, genotyping of new cultivars is often done in breeding programs before a cultivar is released, and could provide the necessary information to choose a seeding rate if the hypothesis of this research is met.

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Abstract

Seeding rate for maximum grain yield can differ for diverse hard red spring wheat (HRSW) (*Triticum aestivum* L.) cultivars and can be derived from a seeding rate response curve. Twelve HRSW cultivars were planted from 2013-2015 at five seeding rates in 23 trials throughout Minnesota (MN) and eastern North Dakota (ND), USA. Seeding rates ranged from 1.59 – 5.55 million seeds ha^{-1}. Planting dates represented optimum and delayed seeding dates. Seedling emergence ranged from 79 – 94% of the planted live seeds and increased as seeding rate increased. There was a seeding rate by cultivar interaction for plant height, protein, lodging, stems plant^{-1}, and yield. Cultivars varied in their ability to tiller, though tiller numbers consistently decreased as seeding rate increased. Cultivars prone to lodging had increased lodging as seeding rates increased. Seeding rate for maximum yield of an individual cultivar spanned the entire range of seeding rates planted. Combined over all cultivars, as the average yield of an environment decreased the seeding rate for maximum yield increased. Information on the response of cultivars to seeding rate can be useful when making seeding rate decisions based on cultivar and the anticipated environment in which it will be grown.

Introduction

Plant density in cereals is a critical determinant of yield, as a plant stand either side of optimum can lead to a reduction in final grain yield (Baker, 1982; Guitard et al., 1961; Hanson and Lukach, 1992; Pendleton and Dungan, 1960; and Wiersma, 2002). Plant stand in cereals is impacted by a number of factors, including crop rotation (Lafond et al., 1992), seed quality

(Rajala et al., 2011), seedbed preparation (Håkansson et al., 2002), planting date (Wiersma, 2002), seeding rate (Hanson and Lukach, 1992), seeding depth (Hadjichristodoulou et al., 1977), fertility (Mason et al., 1969), weather (Gooding and Davies, 1997), herbicide carryover (Brinkman et al., 1980), disease (Krupinsky et al., 2002), insects (Jameson et al., 1947), and weeds (Lemerle et al., 2004).

In cereal crops including HRSW a yield response curve is a useful statistical tool for analyzing yield for a range of seeding rates for a cultivar (Donald, 1963; Holliday, 1960; Hudson, 1941; and Willey and Heath, 1969). Holliday (1960) found that with increasing seeding rates, yield fits a parabolic response curve in cereal grains. As seeding rates increase the curve starts with a sharp incline to the optimum seeding rate, followed by a slow decline on the high side of the optimum seeding rate. Wiley and Heath (1969) recognized that understanding the yield response curve to seeding rate would be useful to make decisions in different cropping systems and situations.

Agronomic recommendations are available for optimum seeding rate of HRSW. It was concluded that across seven HRSW cultivars in Northwest (NW) MN, USA, the seeding rate for maximum yield was 4.84-5.31 million live seeds ha^{-1}, with lower and higher seeding rates seeing a reduction in grain yield (Wiersma, 2002). Trials at nine locations in Saskatchewan, Canada, concluded that combined over eight HRSW cultivars the highest of the three seeding rates at 4.30 million seeds ha^{-1} resulted in the highest yield (Baker, 1982).

Diverse cultivars of cereal crops can respond differently to the rate they are seeded (Anderson and Barclay, 1991; Baker, 1982; Briggs and Aytenfisu, 1979; Faris and DePauw, 1981; Kirby, 1967; Pendleton and Dungan, 1960; and Wiersma, 2002). Research in Central Alberta, Canada, by Briggs and Aytenfisu (1979) found an interaction of genotype by seeding rate with the low protein utility cultivars responding differently than the high protein cultivars. Faris and DePauw (1981) found the need to include higher seeding rates than had been previously included in trials to fully account for any cultivar by seeding rate interaction. Baker (1982) found that four out of nine environments had cultivar by seeding rate interactions, with both positive and negative responses as seeding rate increased. Wiersma (2002) found a significant seeding rate by HRSW cultivar interaction in NW MN.

When determining how much to seed, seed mortality is an important consideration (Hanson and Lukach, 1992; and Wiersma, 2002). As seeding rates increase the percentage of planted seeds that become established plants decreases (Hanson and Lukach, 1992; and Wiersma, 2002). Hanson and Lukach (1992) found variable stand establishment between many field locations, demonstrating the impact of seedbed and environmental conditions on plant establishment to reach a target plant density. Wiersma (2002) found from six environments of HRSW seeding rate research in NW MN that producers should assume 20-25% of the seed will not become an established plant from mortality, a larger loss than the 10-15% previously assumed.

Grafius (1956) described grain yield in cereals as a combination of yield components; specifically stems per plant, kernels per spike, and kernel weight. Seeding rate and cultivar can have an effect on the three yield components, specifically stems per plant. The importance of tillering is environmentally dependent in HRSW, with Holliday (1960) predicting that the relationship between fertile tillers and yield was important, notably due to the amount of photosynthesis that occurs in the spike and contributes to grain yield. However, Mackey (1966) and Donald (1968) postulated that maximum yield in HRSW was at a seeding rate that resulted in uniculm plants. Kirby and Faris (1972) found certain environments would favor uniculm conditions, but that under many environmental conditions tillers were a valuable mechanism for a cereal crop to adapt and fully use resources. Tillers that do not fully mature do not grow tall enough to rob sunlight from productive spikes and tie up very small amounts of nutrients, that in part get returned to the plant before the tiller dies. Chen et al. (2008) noted that tiller growth stages and development in HRSW lag behind the main stem which can negatively impact management of the crop. Anderson and Barclay (1991) identified that three cultivars had different tillering capacity influenced by both genetics and environment in Western Australia. Rainfall was a factor in tillering, with increased moisture resulting in decreased tillers. Hucl and Baker (1988) evaluated a diverse collection of HRSW cultivars to identify the potential for tillering and concluded that genotypes with longer vegetative periods produce a greater number of spikes.

Protein has not been shown to be influenced by seeding rate (Briggs and Aytenfisu, 1979; Faris and DePauw, 1981; Pendleton and Dungan, 1960; and Puckridge and Donald, 1967). Plant height can be affected by seeding rate and cultivar in cereal crops (Darby et al., 2011, Hanson, 2001; Puckridge and Donald, 1967; and Ransom et al., 2015). Plant height in HRSW as affected by increased seeding rate has been found to be positive (Puckridge and Donald, 1967), negative (Darby et al., 2011), and have no effect (Hanson, 2001).

Stem lodging in cereals can be a major problem and is affected by cultivar and seeding rate (Berry et al., 2004; Faris and DePauw, 1981; Holliday, 1960; Kirby, 1967; Orloff, 2014; and Ransom et al., 2015). Holliday (1960) identified the yield reduction potential of lodging in cereals, and that seeding rate response trials can be influenced by lodging. Faris and DePauw (1981) did not see lodging at every environment in British Columbia and Alberta, Canada, but observed that lodging increased as seeding rate increased. Furthermore, a seeding rate by cultivar interaction showed that certain cultivars lodged more than others as seeding rate increased.

The objective of this research was to evaluate the effect of 12 HRSW cultivars and five seeding rates on stems per plant, plant height, lodging, and protein in diverse environments across eastern ND and MN in an effort to determine the optimum seeding rate for maximum grain yield.

Materials and Methods

Site Description

Field experiments were conducted from 2013 to 2015 across a large geographic area of HRSW production in eastern ND and western MN (Table 1). In 2013, experiments were established in four locations: Prosper, ND, and Perley, Crookston, and Hallock, MN. Six locations were used in 2014 and 2015: Prosper, ND, and Lamberton, Kimball, Perley, Crookston, and Hallock, MN.

Treatments and Experimental Design

The experimental design at Lamberton, Prosper, and Crookston locations was a randomized complete block with a split-split plot arrangement and three replicates (Table 2). The whole plot was planting date, the sub-plot was cultivar (Table 3), and the sub-sub plot was seeding rate. At the Kimball, Perley, and Hallock locations the design was a randomized complete block with a split-plot arrangement and three replicates. The whole plot was cultivar and the sub-plot was seeding rate. Prosper had no planting date factor in 2013, so the design was a split-plot without planting date with the main plot as cultivar and sub-plot as seeding rate.

Table 1. Soil series[†], taxonomy, and slope at Prosper, ND, and Lamberton, Kimball, Perley, Crookston, and Hallock, MN, 2013-2015.

Location[‡]	Year	Soil Series	Soil Taxonomy[§]	Slope
				%
Lamberton, MN	2014-15	Webster[‡]	Fine-loamy, mixed, superactive, mesic Typic Endoaquolls	0-2
		Normania	Fine-loamy, mixed, superactive, mesic Aquic Hapludolls	0-2
Kimball, MN	2014	Fairhaven	Fine-loamy over sandy or sandy-skeletal, mixed, superactive, mesic Typic Hapludolls	0-2
	2015	Dakota	Fine-loamy over sandy or sandy-skeletal, mixed, superactive, mesic Typic Argiudolls	2-6
		Ridgeport	Coarse-loamy, mixed, superactive, mesic Typic Hapludolls	2-6
Prosper, ND	2013-15	Kindred-Bearden	Fine-silty, mixed, superactive, frigid Typic Endoaquolls	0-2
Perley, MN	2013-15	Fargo	Fine, smectitic, frigid Typic Epiaquerts	0-1
Crookston, MN	2013, 2015	Wheatville	Coarse-silty over clayey, mixed over smectitic, superactive, frigid Aeric Calciaquolls	0-2
		Bearden-Colvin	Fine-silty, mixed, superactive, frigid Aeric Calciaquolls	0-2
	2014	Wheatville	Coarse-silty over clayey, mixed over smectitic, superactive, frigid Aeric Calciaquolls	0-2
		Gunclub	Fine-silty, mixed, superactive, frigid Aeric Calciaquolls	0-2
Hallock, MN	2013-15	Northcote	Very-fine, smectitic, frigid Typic Epiaquerts	0-1

[†] Soil data obtained from (USDA-NRCS, 2016).
[‡] Listed from South to North.
[§] Soil taxonomy listed on individual lines based on hyphenated soil series name.

Of the 23 environments in this research, Lamberton, MN, late planting 2014 and Prosper, ND, late planting 2014 were not included in the final analysis as field conditions during seeding resulted in poor seedling establishment with stand losses over 40%. Stand loss for this research is defined as the amount of viable seeds that did not become established plants. Therefore, a total of 21 environments were included in the combined analysis unless otherwise noted.

General Procedures

The germination percentage of each seed lot was determined by placing 100 seeds between two wet sheets of Anchor Paper Co. germination paper, rolling them up loosely and keeping them in the dark at room temperature for about five days (Fabrizius, 2007). The seeding rate treatments were packed for each cultivar using kernel weight, germination percentage, and plot size. Trials were grown according to University of Minnesota and North Dakota State

University extension recommendations with regards to cultivation, fertilization, and pesticide application (Table 4) (Wiersma and Ransom, 2012).

Table 2. Design, factors, and treatments for experiments at Prosper, ND and Lamberton, Kimball, Perley, Crookston, and Hallock, MN, 2013-2015.

Location (Latitude)	Design	Factor	Treatment
Lamberton (44.24) Prosper (46.99) Crookston (47.82)	RCBD with split-split plot arrangement	Planting date	Optimum
			Late
		Cultivar	Albany
			Briggs
			Faller
			Kelby
			Knudson
			Kuntz
			Marshall
			Oklee
			Rollag
			Sabin
			Samson
			Vantage
		Seeding Rate	1590000 seeds ha^{-1}
			2580000 seeds ha^{-1}
			3570000 seeds ha^{-1}
			4560000 seeds ha^{-1}
			5550000 seeds ha^{-1}
Kimball (45.39) Perley (47.15) Hallock (48.80)	RCBD with split plot arrangement	Cultivar	Albany
			Briggs
			Faller
			Kelby
			Knudson
			Kuntz
			Marshall
			Oklee
			Rollag
			Sabin
			Samson
			Vantage
		Seeding Rate	1590000 seeds ha^{-1}
			2580000 seeds ha^{-1}
			3570000 seeds ha^{-1}
			4560000 seeds ha^{-1}
			5550000 seeds ha^{-1}

The plot size for the experimental unit at Prosper, ND was 1.24 m by 3.65 m and had 0.19 m row spacing with 7 rows of HRSW. The plot size at Kimball, Perley, Crookston, and Hallock was 1.52 m by 4.57 m and had 0.15 m row spacing with 10 rows of HRSW. The plot size at Lamberton was 1.52 m by 2.43 m and had 0.19 m row spacing with 8 rows of HRSW. Optimum seeding rates were calculated from the first derivative of the regression equation for individual cultivars for the quadratic response curve. For the linear response curves optimum seeding rate was determined by the seeding rate treatment for maximum yield.

Table 3. Characteristics of HRSW cultivars used from 2013-2015, ND and MN. †

Cultivar	Origin	Year	Height	Straw Strength	Day to Heading	Stem Rust	Leaf Rust	Fusarium Head Blight
			--cm--	1-9‡	DAP§			
Albany	Limagrain	2008	81	5	67	NA¶	MR	M
Briggs	SDSU	2002	89	7	61	R/MR	MR/MS	S
Faller	NDSU	2007	89	5	65	R	S	M
Kelby	AgriPro	2006	76	4	62	R/MR	MR/MS	M
Knudson	AgriPro	2001	81	5	60	MR	MR	MS
Kuntz	AgriPro	2007	79	4	65	R	MS	M
Marshall	UMN	1982	81	4	63	R	S	MS/S
Oklee	UMN	2003	79	4	64	R	MS	M
Rollag	UMN	2011	81	3	63	R	MR/MS	MR
Sabin	UMN	2009	84	6	65	R	MR/MS	M
Samson	Westbred	2007	79	2	63	NA	MR/MS	S
Vantage	Westbred	2007	81	2	67	MR	R	MS

† Sources: Anderson et al., (2015); Ransom et al., (2008); Ransom et al., (2012); Ransom et al., (2015).

‡ 1-9 scale where 1 = strongest, 9 = weakest.

§ DAP = days after planting.

¶ R = resistant; MR = moderately resistant; M = intermediate; MS = moderately susceptible; NA = Not adequately tested; S = susceptible.

Data Collection

Density and spike counts were obtained by counting plants and spikes in two rows between two stakes that were placed 0.91 m apart in between two adjacent interior rows. Stand counts were taken to calculate established plants and to verify the seeding rate was correct at approximately Feekes 1, before the plants began to tiller (Large, 1954). This plant stand was entered into an equation for stand loss: stand loss = ((live seed planted – initial plant population)/live seed planted)*100. Productive stem/spike counts followed at approximately Feekes 11. These two measurements were used in a calculation of stems per plant.

Table 4. Site location and year characteristics for trials conducted in ND and MN, 2013-2015.

Location / Year	Previous Crop	Seeding Date	Harvest Date	Yield (Mg ha^{-1})
Lamberton				
2014	Soybean[‡]	21-Apr	20-Aug	5.14
2014[†]	Soybean	16-May	20-Aug	4.21
2015	Soybean	4-Apr	12-Aug	5.62
2015	Soybean	27-Apr	12-Aug	4.55
Kimball				
2014	Soybean	26-Apr	14-Aug	5.54
2015	Soybean	8-Apr	31-Jul	5.97
Prosper				
2013	Soybean	16-May	22-Aug	4.69
2014	Soybean	27-May	3-Sep	4.43
2014[†]	Soybean	18-Jun	7-Oct	2.80
2015	Soybean	9-Apr	21-Aug	4.67
2015	Soybean	22-May	25-Aug	3.62
Perley				
2013	Soybean	8-May	16-Aug	5.80
2014	Soybean	22-May	2-Sep	6.00
2015	Soybean	13-Apr	11-Aug	7.03
Crookston				
2013	Soybean	10-May	8-Aug	6.14
2013	Soybean	29-May	26-Aug	6.38
2014	Soybean	17-May	27-Aug	4.95
2014	Soybean	4-Jun	27-Aug	4.55
2015	Soybean	23-Apr	21-Aug	6.35
2015	Soybean	22-May	25-Aug	5.38
Hallock				
2013	Soybean	16-May	3-Sep	7.27
2014	Soybean	23-May	6-Sep	5.45
2015	Soybean	16-Apr	13-Aug	5.62

[†] Environment not included in analysis due to 40-50% stand loss.
[‡] *Glycine Max* (L.) Merr.

Height and lodging were measured for every plot, with lodging on a 1-9 scale where 1 was erect and 9 was flat. Plot yield was collected from the entire plot with a small plot combine. Grain yield was adjusted to 13.5% moisture. Grain characteristics of moisture, test weight, and protein (13.5% moisture) were collected at harvest or during post-harvest processing.

Statistical Analysis

The statistical analysis was performed with SAS 9.4 (SAS Institute, SAS Circle, Cary, NC). Seeding rate and cultivar were considered fixed effects in the model, while replicate and environment were considered to be random effects. All interactions of fixed effects were considered fixed, while any interaction with a random term was considered random. Proc MIXED method=type3 was used for LSMEANS with means separations done through the PDIFF function and a least significant difference calculation. Proc REG was used for linear and quadratic regression analysis on the LSMEANS only. An alpha level of 0.05 was used for all hypothesis tests.

Results

Plant Height

Combined over 21 environments the interaction of seeding rate and cultivar was significant for plant height (Table 5). Comparisons among cultivars are not important within the objectives of this research, as cultivar characteristics are available from variety trial results and a farmer would need specific reasons to look between cultivars, such as combating lodging. Among the 12 cultivars for plant height, there were positive, negative, and neutral responses as seeding rate increased. The cultivars Faller, Knudson, Kuntz, Marshall, Oklee, Rollag, and Samson had no plant height response to increased seeding rate. Albany, Briggs, and Sabin height decreased when seeding rate increased. Kelby and Vantage were the only two cultivars that were taller with increased seeding rate. Kelby and Vantage had a positive increase in the quadratic response to height as seeding rate increased to the middle rate and then plateaued.

Table 5. Seeding rate and cultivar interaction effect on height combined over 21 environments, 2013-2015, ND and MN.

	Seeding Rate (million seeds ha^{-1})						
Cultivar	1.59	2.58	3.57	4.56	5.55	Quadratic Equation[†]	R^2
			-------------------cm-------------------				
Albany	82.0	81.1	81.1	79.8	79.9	$y=0.044x^2-0.802x+82.698$	0.91
Briggs	87.7	88.1	86.8	86.7	86.2	$y=-0.035x^2-0.233x+88.172$	0.79
Faller	86.4	87.0	86.7	87.1	87.1	$y=-0.031x^2+0.347x+86.154$	0.67
Kelby	74.5	75.5	76.0	75.6	75.8	$y=-0.181x^2-1.357x+73.394$	0.89
Knudson	81.8	82.9	82.1	81.7	81.3	$y=-0.168x^2+0.792x+81.42$	0.64
Kuntz	77.7	77.8	78.2	78.6	78.2	$y=-0.084x^2+0.694x+76.932$	0.77
Marshall	80.0	79.9	79.8	80.4	80.3	$y=0.052x^2-0.200x+80.116$	0.59
Oklee	84.6	85.9	85.5	85.7	85.3	$y=-0.196x^2+1.300x+83.648$	0.71
Rollag	78.1	78.5	78.9	78.5	78.5	$y=-0.100x^2+0.670x+77.592$	0.70
Sabin	85.1	83.7	83.3	83.3	82.9	$y=0.168x^2-1.488x+86.288$	0.92
Samson	76.7	77.4	77.6	77.1	77.9	$y=-0.030x^2+0.388x+76.476$	0.45
Vantage	80.9	82.1	82.9	82.8	83.2	$y=-0.191x^2+1.677x+79.454$	0.97
LSD 0.05[‡]			1.4				

[†] Equation from PROC REG.

[‡] LSD calculated to compare within whole plot means, and within sub plot means, but not among whole and sub plot means.

Stand Establishment and Mortality

Stand establishment in HRSW can be impacted by environmental conditions around planting. In the Northern Great Plains, USA, HRSW is among the earliest crops sown in the spring, just after the snow melts and a suitable seedbed can be prepared. Combined over 21 environments and 12 cultivars, the counted plant populations did not reach the planted seeding rate at any seeding rate (Table 6). Mean stand loss ranged from 6.3% to 20.7% and increased as seeding rate increased. Stand loss was best fit with a linear regression curve for the combined 20 environments.

Table 6. Seeding rate effect on plant population combined over 21 environments, 2013-2015, ND and MN.

Seeding Rate	Combined
million seeds ha^{-1}	---------plants ha^{-1} (% stand loss)---------
1.59	1.49 (6.3%)
2.58	2.29 (11.2%)
3.57	3.05 (14.6%)
4.56	3.70 (18.9%)
5.55	4.40 (20.7%)
Equation	$y=3.39+3.65x$[†]
R^2	0.97
LSD 0.05[‡]	0.04

[†] Equation for % stand loss from proc REG.

[‡] LSD calculated to compare within whole plot means for plants ha^{-1}.

Stem Lodging

Seeding rate and cultivar had a significant effect on lodging when combined over 21 environments (Table 7).

Table 7. Seeding rate and cultivar interaction effect on lodging combined over 21 environments, 2013-2015, ND and MN.

	Seeding Rate (million seeds ha^{-1})						
Cultivar	1.59	2.58	3.57	4.56	5.55	Quadratic Equation[†]	R^2
	-----------Lodging (1 – 9)[‡]-----------						
Albany	1.3	1.5	2.0	2.1	2.1	$y=-0.064x^2+0.612x+0.663$	0.97
Briggs	1.9	2.4	3.5	3.8	4.2	$y=-0.081x^2+1.102x+0.748$	0.97
Faller	1.4	1.9	2.3	2.4	2.5	$y=-0.068x^2+0.675x+0.843$	0.99
Kelby	1.5	1.5	1.5	1.6	1.5	$y=-0.003x^2+0.025x+1.495$	0.99
Knudson	1.4	1.6	1.6	1.9	2.1	$y=0.024x^2+0.011x+1.419$	0.98
Kuntz	1.3	1.3	1.4	1.5	1.6	$y=0.015x^2-0.019x+1.288$	0.99
Marshall	1.1	1.2	1.3	1.4	1.5	$y=-0.006x^2+0.124x+0.992$	0.97
Oklee	1.7	2.2	2.9	3.1	3.4	$y=-0.068x^2+0.86x+0.844$	0.99
Rollag	1.1	1.2	1.2	1.3	1.4	$y=-0.009x^2+0.006x+1.101$	0.97
Sabin	1.8	2.4	3.0	3.6	4.1	$y=-0.023x^2+0.729x+1.040$	0.99
Samson	1.2	1.2	1.3	1.3	1.4	$y=0.008x^2-0.005x+1.203$	0.98
Vantage	1.0	1.0	1.0	1.0	1.0	$y=0.002x^2-0.014x+1.047$	0.36
LSD 0.05[§]			0.4				

[†] Equation from PROC REG.

[‡] Lodging rating scale: 1=erect plant and 9=flat plant.

[§] LSD calculated to compare within whole plot means, and within sub plot means, but not among whole and sub plot means.

Lodging for half the cultivars in the experiment including Kelby, Kuntz, Marshall, Rollag, Samson, and Vantage was not impacted by seeding rate, and was additionally not severe with values below two. The other half of the cultivars had increased lodging as seeding rate increased. The cultivars Albany, Faller, and Knudson showed intermediate lodging peaking from 2.1-2.5. The lodging plateaued at the highest seeding rates for Albany, Faller, and Knudson though the exact seeding rate for plateau differed by one seeding rate level. Lodging for the cultivar Oklee peaked one level higher than the three cultivars in the intermediate group. Briggs and Sabin were the two cultivars with the highest lodging at almost every seeding rate, peaking at a lodging score over four.

Grain Protein

The interaction of seeding rate and cultivar was significant for grain protein combined over 21 environments (Table 8). Ten of the individual cultivars had no interaction with seeding rate for grain protein. Grain protein for the cultivars Albany and Vantage decreased as yield increased.

Stems per Plant

Seeding rate and cultivar had a significant interaction on stems per plant (Table 9). The response of all individual cultivars for stems per plant to seeding rate decreased with a quadratic response, and very high R^2 ranging from 0.97 to 0.99. The fit of the quadratic regression was significant for all cultivars. Albany and Knudson had the highest intercept at 6.10 and 5.83, while Kuntz and Vantage had the lowest intercept at 4.27 for both cultivars. Stems per plant is directly related to tillering, with stems per plant minus one being the true number for tillers per plant. The physiological response of uniculm plants, where only one stem per seed is produced, was not found at even the highest density seeding rates across 21 environments.

Table 8. Seeding rate and cultivar interaction effect on grain protein combined over 21 environments, 2013-2015, ND and MN.

Cultivar	Seeding Rate (million seeds ha^{-1})					Quadratic Equation†	R^2
	1.59	2.58	3.57	4.56	5.55		
	---------------- g kg^{-1}----------------						
Albany	131	131	127	129	133	$y=0.105x^2-0.593x+13.639$	0.73
Briggs	145	145	145	145	144	$y=0.001x^2-0.013x+14.499$	0.89
Faller	136	136	135	136	136	$y=0.002x^2-0.019x+13.598$	0.16
Kelby	146	145	146	145	145	$y=0.002x^2-0.021x+14.613$	0.09
Knudson	134	133	134	133	133	$y=0.008x^2-0.073x+13.480$	0.76
Kuntz	138	138	138	137	137	$y=0.003x^2-0.033x+13.812$	0.78
Marshall	135	133	133	133	133	$y=0.041x^2-0.282x+13.726$	0.99
Oklee	143	142	142	143	143	$y=0.012x^2-0.062x+14.330$	0.27
Rollag	147	146	146	145	145	$y=0.008x^2-0.101x+14.795$	0.86
Sabin	144	142	144	144	144	$y=0.008x^2-0.009x+14.309$	0.31
Samson	138	138	138	136	137	$y=0.016x^2-0.138x+13.976$	0.68
Vantage	151	149	149	148	147	$y=0.001x^2-0.105x+15.186$	0.94
LSD 0.05‡			3				

† Equation from PROC REG.

‡ LSD calculated to compare within whole plot means, and within sub plot means, but not among whole and sub plot means.

With some exceptions, as seeding rate increased stems per plant decreased within individual cultivars (Table 9). For a few cultivars, specifically Marshall and Oklee, it was only at the highest two seeding rates that stems per plant were similar. Albany was the cultivar with the highest overall tillering capacity. At the lowest seeding rate Albany had more stems per plant than any other cultivar. At the second lowest seeding rate Albany had more stems per plant than all cultivars except Briggs and Knudson.

Table 9. Seeding rate and cultivar interaction effect on stems per plant combined over 21 environments, 2013-2015, ND and MN.

	Seeding Rate (million seeds ha^{-1})						
Cultivar	1.59	2.58	3.57	4.56	5.55	Quadratic Equation[†]	R^2
	-------------stems plant^{-1}-------------						
Albany	4.62	3.10	2.51	2.10	1.75	$y=0.180x^2-1.755x+6.098$	0.99
Briggs	4.06	2.89	2.38	2.04	1.68	$y=0.128x^2-1.331x+5.191$	0.99
Faller	3.97	2.79	2.10	1.76	1.53	$y=0.161x^2-1.557x+5.334$	0.99
Kelby	3.48	2.55	1.99	1.69	1.47	$y=0.120x^2-1.205x+4.535$	0.99
Knudson	4.38	3.01	2.29	2.00	1.64	$y=0.174x^2-1.695x+5.832$	0.99
Kuntz	3.29	2.44	1.88	1.67	1.43	$y=0.111x^2-1.116x+4.269$	0.99
Marshall	3.85	2.86	2.23	1.84	1.65	$y=0.132x^2-1.335x+5.041$	0.99
Oklee	3.39	2.52	2.02	1.53	1.48	$y=0.117x^2-1.185x+4.453$	0.99
Rollag	3.84	2.81	2.29	1.86	1.65	$y=0.125x^2-1.283x+4.964$	0.99
Sabin	3.82	2.49	2.09	1.79	1.45	$y=0.148x^2-1.430x+4.993$	0.97
Samson	3.61	2.48	1.91	1.63	1.42	$y=0.150x^2-1.425x+4.830$	0.99
Vantage	3.39	2.43	2.07	1.83	1.55	$y=0.104x^2-1.052x+4.266$	0.98
LSD 0.05[‡]			0.21				

[†] Equation from PROC REG.

[‡] LSD calculated to compare within whole plot means, and within sub plot means, but not among whole and sub plot means.

Maximum Yield

The twelve cultivars in this research did not all have the same response to seeding rate or the same seeding rate for maximum yield (Table 10). Linear and quadratic regression functions were fit to least squares means for all seeding rate by cultivar interactions. Among all 12 cultivars only Sabin had a better fit with a linear regression than quadratic. The linear regression for Sabin had a negative slope as seeding rate increased. Only the highest and lowest seeding rate for Sabin had different yields with the lowest seeding rate yielding 0.25 Mg ha^{-1} higher. The other 11 cultivars all had quadratic seeding rate responses with slightly differing seeding rate peaks for maximum yield (Table 10). The R^2 for the 11 cultivars was generally high with most at 0.90 or above, with Faller having the lowest R^2 due to a slight cubic response from the 4th to 5th seeding rate.

Table 10. Seeding rate and cultivar interaction effect on yield combined over 21 environments, 2013-2015, ND and MN.

	Seeding Rate (SR) (million seeds ha^{-1})							
Cultivar	1.59	2.58	3.57	4.56	5.55	Peak SR[†]	Regression Equation	R^2
		--------Mg ha^{-1}--------						
Albany	5.79	6.04	5.99	5.83	5.64	2.62	$y=-0.073x^2+0.382x+5.507$	0.93
Briggs	5.24	5.43	5.40	5.33	5.23	2.89	$y=-0.046x^2+0.266x+5.037$	0.88
Faller	5.76	5.90	5.94	5.85	5.87	3.32	$y=-0.025x^2+0.166x+5.638$	0.69
Kelby	5.10	5.40	5.45	5.45	5.50	4.14	$y=-0.038x^2+0.315x+4.860$	0.91
Knudson	5.47	5.67	5.67	5.65	5.65	3.58	$y=-0.030x^2+0.215x+5.309$	0.83
Kuntz	4.94	5.15	5.19	5.19	5.29	5.03	$y=-0.019x^2+0.191x+4.794$	0.90
Marshall	5.07	5.15	5.24	5.24	5.26	4.60	$y=-0.015x^2+0.138x+4.943$	0.97
Oklee	5.29	5.48	5.45	5.45	5.33	3.10	$y=-0.042x^2+0.260x+5.086$	0.88
Rollag	5.08	5.39	5.53	5.59	5.66	4.63	$y=-0.041x^2+0.380x+4.756$	0.99
Sabin	5.63	5.54	5.49	5.49	5.38	1.59	$y=-0.055x+5.673$	0.99
Samson	5.51	5.84	5.97	5.98	5.99	4.02	$y=-0.055x^2+0.442x+5.140$	0.99
Vantage	4.96	5.15	5.25	5.28	5.30	4.26	$y=-0.031x^2+0.264x+4.733$	0.99
LSD 0.05[‡]			0.19					

[†] SR = Seeding rate. Peak derived from first regression of the quadratic regression equation, or the treatment for maximum yield of the linear equation for the cultivar Sabin.

[‡] LSD calculated to compare within whole plot means, and within sub plot means, but not among whole and sub plot means.

Environment on Maximum Yield

Yield is a dependent variable that could be used to describe environments from this research as there was a range of low, medium, and high yielding environments. The range in yield of the 21 environments across all seeding rates and cultivars was 3.65 Mg ha^{-1}, from a lowest average yield of 3.62 Mg ha^{-1} to a highest average yield of 7.27 Mg ha^{-1}. The mean average yield of all 21 environments was 5.48 Mg ha^{-1}. The fit of the regression line and the resulting R^2 was generally more accurate in the combined analysis over 21 environments than dividing the environments into two or three groups (Table 11). There were certain cultivars where the fit improved when looking into environments characterized by yield, however the improvements were small. For other cultivars the R^2 fit decreased sharply when the environments were broken into smaller groups.

Table 11. Goodness of fit for the quadratic regression of seeding rate by cultivar yield means split in half by average environment yield, split in thirds, and combined over 21 environments, 2013-2015, ND and MN.

Cultivar	Combined	Bottom 1/2	Top 1/2	Bottom 1/3	Mid 1/3	Top 1/3
	------------------------------------R^2------------------------------------					
Albany	0.93	0.98	0.95	0.81	0.76	0.98
Briggs	0.88	0.95	0.81	0.91	0.91	0.82
Faller	0.69	0.95	0.73	0.69	0.57	0.95
Kelby	0.91	0.98	0.89	0.89	0.85	0.45
Knudson	0.83	0.97	0.81	0.76	0.86	0.23
Kuntz	0.90	0.89	0.94	0.90	0.92	0.61
Marshall	0.97	0.99	0.73	0.94	0.97	0.27
Oklee	0.88	0.88	0.90	0.71	0.72	0.68
Rollag	0.99	0.91	0.99	0.96	0.99	0.97
Sabin	0.92	0.67	0.97	0.82	0.96	0.77
Samson	0.99	0.97	0.92	0.99	0.99	0.80
Vantage	0.99	0.99	0.90	0.95	0.96	0.64
Average	0.91	0.93	0.88	0.86	0.87	0.68

There is more power when a greater number of environments are included in an analysis. When a smaller subset of environments were used, environmental stresses such as lodging and disease, among other biotic and abiotic stresses, may have been behind the decreased fit of the quadratic regression curve for certain cultivars.

The seeding rate for maximum yield differed for each cultivar when all 21 environments were split into groups by the bottom third, middle third, and top third yielding environments (Table 12). When averaged across the twelve cultivars, the seeding rate for maximum yield decreased as the yield for the grouping of environments increased. The cultivars Briggs, Kuntz, Marshall, Oklee, Sabin, and Samson all followed the general decrease in optimum seeding rate as environments yielded higher. In contrast, the cultivar Vantage maximized grain yield at the highest seeding rate in the high yield environments. The four cultivars Albany, Faller, Knudson, and Rollag behaved in a quadratic trend, having the highest seeding rate for maximum yield in the middle third yielding environments and decreasing from there at both the bottom and top third environments. Kelby had a general trend towards lower seeding rates as average yield increased, but had a decrease in optimum seeding rate in the middle third yielding environments.

Table 12. Seeding rate for maximum yield of 12 cultivars split into thirds for the bottom third yielding, middle third yielding, and top third yielding environments by average yields from a total of 21 environments, ND and MN, 2013-2015.

Cultivar	Bottom 1/3	Middle 1/3	Top 1/3
	---------million seeds ha^{-1}---------		
Albany	2.44	3.21	2.37
Briggs	3.70	2.76	2.54
Faller	2.97	3.70	2.96
Kelby	4.63	3.58	3.89
Knudson	3.62	3.77	3.06
Kuntz	5.76	4.00	3.89
Marshall	7.72	5.17	2.80
Oklee	3.40	3.21	2.67
Rollag	3.67	5.46	4.55
Sabin	2.52	1.48	1.42
Samson	4.71	4.36	3.34
Vantage	4.04	4.10	5.93
Average	4.10	3.73	3.29

Discussion

Stand Establishment and Mortality

Some mortality should be expected based on our data from 21 environments even though certain environments may have had very little stand loss (Table 6). Producers in the region should predict a 11-19% stand loss at seeding rates from 2.58-4.56 million seeds ha^{-1}. This estimate was not far off from mortality estimates given by the ND and MN extension services (Wiersma and Ransom, 2012). However, this estimate is less than the 20-25% stand loss that was reported by Wiersma (2002) over six environments for a similar geography. The variability that was found among environments demonstrates the need for a stand loss variable when calculating seeding rate.

Lodging and Plant Height

Lodging has been recognized as a confounding effect for seeding rate studies (Holliday, 1960). Lodging was unavoidable in this research given the current straw strength for cultivars being grown and tested in ND and MN (Anderson et al., 2015; and Ransom et al., 2015). The results for lodging were expected given the diverse collection of genotypes included in this seeding rate study. Lodging ranged from non-existent to extreme with the combination of cultivars, seeding rates, and environments in this research. Lodging increased as seeding rate increased for many cultivars, similar to what has been reported in wheat and barley (*Hordeum vulgare* L.) (Faris and DePauw, 1981; Kirby, 1967; and Orloff, 2014). Knowledge of a cultivar's straw strength and tendency to lodge is critical when selecting seeding rates for diverse HRSW cultivars, especially in lodging prone environments (Anderson et al., 2015; Faris and DePauw, 1981; and Ransom et al., 2015). The dominant lack of any response for 7 of 12 cultivars is in agreement with Hanson (2011). The positive and negative lodging responses for cultivars can in part be explained by known characteristics of overall plant height and lodging (Table 3, 5, and 7). The tallest cultivars in this study results were in line with Darby et al. (2011), where increased seeding rates caused severely increased lodging (Tables 5 and 7). The cultivars Kelby, the shortest cultivar in the study, Vantage, a cultivar with tall growth but the strongest straw strength and tendency not to lodge, Rollag, and Samson all had no increase in lodging as seeding rate increased, similar to findings by Puckridge and Donald (1967). Yield loss can be high in certain cultivars where seeding rate causes extreme lodging. Lodging further decreases economic viability of a HRSW crop because of the decreased speed at which a lodged HRSW crop can be combined.

Plant height and the interaction of plant height with seeding rate is important for producers. The prevalence of negative associations of lodging in high yielding environments and the height of some available cultivars on the market have producers looking for ways to decrease plant height. The 12 cultivars used in this research provide evidence that shorter statured HRSW do not reach a decline in the yield response curve at the highest seeding rate tested in this research like was seen for the taller cultivars (Table 10).

Grain Protein

The main effect of cultivar for protein can be explained by inherent genetic differences in protein content among the 12 cultivars that could also be found from most variety trial results (Anderson et al., 2015; and Ransom et al., 2015). Besides Albany and Vantage having small responses to grain protein when grown at different densities, no response for ten of twelve cultivars, was in agreement with what has been previously reported (Briggs and Aytenfisu, 1979; Faris and DePauw, 1981; Pendleton and Dungan, 1960; and Puckridge and Donald, 1967). The seeding rate for maximum grain protein for Albany and Vantage provided half a percent protein above the lowest protein treatment. The decrease in protein as seeding rate increased for the cultivar Vantage was likely a function of the increased yield at higher seeding rates (Table 10).

Stems per Plant

Stems per plant can be used to calculate the first yield component for cereals, spikes ha^{-1} (data not shown) (Grafius, 1956). Measuring tillering in the field under space-planted or solid-seeded conditions is a labor intensive process, requiring both an initial stand count and spike counts near harvest. Consistent with prior research, tillering capacity was not the same for all 12 cultivars in this research (Hucl and Baker, 1988). The difference between number of stems per plant for the top tillering and bottom tillering cultivars decreased as seeding rate increased. At the top seeding rate there were 1.33 stems plant^{-1} difference from the top to bottom ranked tillering cultivars, while at the highest seeding rate there was only a 0.33 stems plant^{-1} difference. Making cultivar selection decisions based on known tillering capacity is of more use at lower seeding rates than higher seeding rates, given the difference in ranges between top and bottom tillering cultivars. Correlations between grain yield or protein and tillering were not analyzed for this research. Past research has found weak correlations between tillering and yield for HRSW (Hucl and Baker, 1988). A treatment with all uniculm plants was not found at any seeding rate or cultivar combination over 21 diverse environments. These results are consistent with others reporting tillering being an important adaptation strategy to maximize HRSW production, especially in the geographic reference area of this research (Kirby and Faris, 1972).

Maximum Yield

A cultivar by seeding rate interaction was found when data were combined over 21 environments (Table 10). These results were similar to other research findings for HRSW (Anderson and Barclay, 1991; Baker, 1982; Briggs and Aytenfisu, 1979; Faris and DePauw, 1981; Pendleton and Dungan, 1960; and Wiersma, 2002). In the current research, Sabin was the only cultivar to have a linear negative slope from the lowest seeding rate to the highest seeding rate. This resulted from severe lodging for the cultivar as seeding rate increased (Table 7). The three cultivars that had a quadratic fit for the regression curve, but no significant response to increased seeding rate were Faller, Marshall, and Oklee. Faller and Oklee are both among the tallest cultivars of the twelve and have intermediate to high lodging potential (Table 6 and 7). Additionally, Faller was among the highest yielding cultivars and Oklee an intermediate yielding cultivar (Table 10). The combination of these three characteristics show that Oklee and Faller do best when seeded at a lower than average seeding rate. Marshall is an older cultivar, released in 1982, but is still included as a check in trials, not for its market share, but for its resistance to stem rust (Anderson et al., 2015) (Table 3).

Among the eight cultivars that interacted with seeding rate for yield, a quadratic fit provided the highest R^2. While a non-linear quadratic plus plateau function from PROC NLIN was significant and described the response well, quadratic polynomial models also described the fit well. Quadratic regression was used because the literature on seeding rates and the underpinning biology has focused on quadratic functions to describe seeding rates, specifically due to increased lodging at higher seeding rates (Holliday, 1960; and Hudson, 1941). Similar to other findings, Albany was a high tillering capacity cultivar that was most negatively affected by increased seeding rates (Balla, 1971). Albany was a top tillering cultivar at the lowest seeding rate and peaked for maximum yield at 2.62 million seeds ha^{-1} (Table 9 and 10). The sharp decline in yield past the peak indicates that Albany should be seeded at a lower seeding rate. The decrease in yield can in part be explained by intermediate lodging peaking just over a score of two for Albany (Table 7).

Cultivars that had a combination of good straw strength and minimal lodging, had higher seeding rates for maximum yield (Table 3, 6-7, and 10). These characteristics also resulted in no decline in yield at the highest seeding rates. The cultivars in this category were Kelby, Kuntz, Marshall, Rollag, Samson, and Vantage. The specific seeding rates for maximum yield were not the same, but the yield response curves did not have a characteristic quadratic curve where the highest seeding rates have a negative slope. For these cultivars, seeding above the middle rate was not ill-advised for agronomic reasons, however the economic return was not likely to be positive.

Conclusions

When calculating seeding rates, germination percentage, kernel weight, and a stand loss calculation of 11-19% should be added. This estimate was slightly lower than the most recent estimate in the region of 20-25% and slightly higher than the old estimate of 10-15% (Wiersma, 2002, and Wiersma and Ransom, 2012). Stand loss estimates should be increased as seeding rate is increased. A planting date by cultivar by seeding rate response was not found in this research. A seeding rate by cultivar interaction was found for stems per plant, height, lodging, protein, and yield. In the Northern Great Plains where HRSW is productive and moisture is adequate, tillering can influence the seeding rate for maximum yield. A cultivar such as Albany that has a high tillering capacity can reach maximum yield at a lower seeding rate than cultivars with less tillering capacity. Plant height can be impacted positively, negatively, and have no effect as seeding rates increase for diverse cultivars. Cultivars prone to lodging will have increased lodging at increased seeding rates while cultivars with strong straw strength may not lodge at even the highest seeding rates. Grain protein is not impacted by seeding rate and should not be used as a management strategy for protein content.

The environments included in this research were diverse for soil type, geography, and planting date. Latitude for the locations spanned 48.77 to 44.23 and longitude spanned -97.01 to -95.26. Planting dates varied from the optimum planting dates to later planting dates than producers would typically seed HRSW in the region. The knowledge of the yield potential of an environment from past production, soil type, productivity index of the soil, temperatures during tillering and spike formation, and other environmental factors is useful in determining optimum seeding rate. A general decrease in required seeding rate for maximum yield of a HRSW crop was found in this research as the environmental average yield increased (Table 12). However, the exact cause of low and high yielding environments cannot be known for sure, as it was a combination of moisture, latitude, disease, lodging, and other stresses that affected average yield. High yielding environments in this geographic reference area had cooler temperatures during tillering and grain fill, resulting in an increase in all three yield components recognized by Grafius (1956).

The seeding rate for maximum yield in HRSW was not the same for every cultivar due to known and unknown genetic, environment, and agronomic factors. Certain cultivars were found to peak for maximum yield at the lower end of the recommended seeding rate in ND and MN. These cultivars provide an opportunity for producers to cut seeding rates slightly, which is an expense in their operation, and be more profitable with the same yield as if they seeded heavier. The next step of this research is to explore how environmental factors such as latitude and planting date can be paired with known genotypic characteristics that might serve as predictive tools to select optimum seeding rates for maximum yield of a cultivar or type of cultivar. Overall, seeding rate trials continue to provide insight into the optimum seeding rate for HRSW with consideration to yield, tillering, height, and lodging.

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CHAPTER 2. USING GENETIC AND ENVIRONMENTAL PREDICTORS TO DETERMINE OPTIMUM SEEDING RATES FOR DIVERSE HRSW CULTIVARS

Abstract

Seeding rate for maximum grain yield can differ for diverse hard red spring wheat (HRSW) (*Triticum aestivum* L.) cultivars and can be derived from a seeding rate response curve. Six groups of HRSW cultivars with combinations of *Rht-B*, *Rht-D*, and *Ppd-D* genes with two cultivars per group were planted in 2013-2015 at five seeding rates in 23 trials throughout Minnesota (MN) and eastern North Dakota (ND), USA. Seeding rates ranged from 1.59 – 5.55 million seeds ha^{-1} and planting dates were optimum and delayed dates. An ANCOVA predictive model with 13 predetermined training environments was built for yield and tillering and validated with eight predetermined environments. However, the model for yield was not predictive with latitude of the environment negatively skewing the predictions from observed values. The model built and validated for tillering was predictive for the validation environments, with a validation R^2 of 0.71. A second yield model was built for the six lowest yielding environments. The validation dataset for this yield scenario resulted in a more predictive model and an R^2 of 0.44. Using regression predictions and separate training and validation datasets to predict yield and tillering with HRSW genetic and geographic predictors shows promise to help recommend seeding rates for future environments.

Introduction

Plant density in cereals is critical as grain yield is impacted by final plant stand (Baker, 1982; Guitard et al., 1961; Hanson and Lukach, 1992; Pendleton and Dungan, 1960; and Wiersma, 2002). A seeding rate by cultivar interaction is often found in cereal crop research

(Anderson and Barclay, 1991; Baker, 1982; Briggs and Aytenfisu, 1979; Faris and DePauw, 1981; Kirby, 1967; Pendleton and Dungan, 1960; and Wiersma, 2002). Faris and DePauw (1981) concluded that each new cultivar released from a breeding program should be tested at several seeding rates to fully understand the optimum seeding rate for maximum yield.

Cultivars of HRSW have genetic differences affecting plant height (Butler et al., 2005; Lanning et al., 2012; Ransom et al., 2015; and Wiersma, 2012), tillering (Anderson and Barclay, 1991; and Hucl and Baker, 1988), photoperiod sensitivity (Wiersma, 2012; and Worland, 1996), and yield (Ransom et al., 2015) among many other genetically controlled traits. Spikes per plant in cereal grains is a quantitative trait affected by environment conditions, soil fertility, planting date, and other agronomic practices (Friend, 1965; and Li et al., 2002). Li et al. (2002) identified that many quantitative trait loci (QTL) influence tillering. A region on the short arm of chromosome 6A has the greatest impact on stems per plant, with a region on the short arm of chromosome 1D and the region of *Ppd-D1* also contributing.

Semi-dwarf genes have been widely incorporated into HRSW cultivars, though yield improvements still remain dependent on environment (Butler et al., 2005; and Lanning et al., 2012). Ciha (1983) reinforced that the semi-dwarf growth habit has changed agronomic performance characteristics such as lodging and yield in HRSW. As the prevalence of standard height cultivars has declined, research has been conducted to find proper agronomic practices for semi-dwarf HRSW cultivars (Anderson and Barclay, 1991; Baker, 1982; Baker, 1990; Ciha, 1983; Faris and DePauw, 1981; Hanson and Lukach, 1992; Miralles and Slafer, 1995; and Wiersma, 2002). The genetic basis of semi-dwarf growth habit in HRSW is from *Rht-8*, *Rht-B1* and *Rht-D1* genes (Borojevic, 2005). *Rht-B1* and *Rht-D1* occur on homologous chromosomes 4B and 4D, respectively, while *Rht-8* occurs on the short arm of chromosome 2D (Gale and Marshall, 1976; Gale et al., 1975; and Gale et al., 1982).

Photoperiod sensitivity in HRSW cultivars is imparted from the *Ppd-A1*, *Ppd-B1*, and *Ppd-D1* genes (Worland, 1996). Furthermore, these three genes have been ranked for their contribution to photoperiod sensitivity in the order *Ppd-D1* > *Ppd-B1* > *Ppd-A1*. These genes are located on the long arm of 2A for *Ppd-A1*, short arm of 2B for *Ppd-B1*, and long arm of 2D for *Ppd-D1* (Scarth and Law, 1984). *Ppd-D1a* is the wild-type allele with no photoperiod sensitivity, while *Ppd-D1b* is the photoperiod sensitive allele. Flowering time in wheat is a characteristic that makes a wheat cultivar suitable for a specific environment (Davidson and Christian, 1984). The yield benefit of photoperiod sensitivity is dependent on environment (Busch et al., 1984; Dyck et al., 2004; Marshall et al., 1989; Worland et al., 1994; and Worland, 1996).

In cereal crops, a yield response curve is a useful statistical tool for analyzing the yield for a range of seeding rates for a cultivar (Donald, 1963; Holliday, 1960; Hudson, 1941; and Willey and Heath, 1969). Holliday (1960) found that with seeding rates, yield fits a quadratic response curve in cereal grains. The curve, as seeding rates increase, starts with a sharp incline to the optimum seeding rate, followed by a slow decline on the high side of the optimum seeding rate. Wiley and Heath (1969) recognized that understanding the yield response curve to seeding rate was useful for making seeding rate decisions in different cropping systems and situations.

The first objective of this research was to determine if genetic traits such as plant stature, photoperiod sensitivity, and easily measured phenotypic traits like capacity to tiller, in addition to geographic indicators such as planting date, day length at planting, and latitude, can be used to predict the optimum seeding rate for maximum yield of a newly released cultivar without the need for conducting classical seeding rate response experiments. The first objective was investigated by building an ANCOVA regression model for yield and tillering using covariates as predictors with a training data set. The second objective was to validate the regression model for yield and tillering with an out-of-sample validation dataset to gauge the models predictive power. The third objective, if the model was found to be predictive, was to use the entire data set as a database to enter a cultivars known characteristics, expected planting date, and location latitude to determine the optimum seeding rate for maximum yield of the cultivar.

Materials and Methods

Site Description

Field experiments were conducted from 2013 to 2015 in ND and MN. In 2013, experiments were established in four locations: Prosper, ND, and Perley, Crookston, and Hallock, MN. Six locations were used in 2014 and 2015: Prosper, ND, and Lamberton, Kimball, Perley, Crookston, and Hallock, MN. Table 13 lists the soil series, soil taxonomy, and slope at each location and year.

Treatments and Experimental Design

The locations were set up in pairs, with Kimball, Perley, and Hallock being model validation sites for the model training sites Lamberton, Prosper, and Crookston, respectively. The experimental design at Lamberton, Prosper, and Crookston was a randomized complete block with a split-split plot arrangement and three replicates (Table 14). The whole plot was planting date, the sub-plot was cultivar, and the sub-sub plot was seeding rate. In 2013, Prosper had no planting date factor so the design was a split-plot without planting date.

Table 13. Soil series[†], taxonomy, and slope at Prosper, ND, and Lamberton, Kimball, Perley, Crookston, and Hallock, MN, 2013-2015.

Location[‡]	Year	Soil Series	Soil Taxonomy[§]	Slope
				%
Lamberton, MN	2014-15	Webster[‡]	Fine-loamy, mixed, superactive, mesic Typic Endoaquolls	0-2
		Normania	Fine-loamy, mixed, superactive, mesic Aquic Hapludolls	0-2
Kimball, MN	2014	Fairhaven	Fine-loamy over sandy or sandy-skeletal, mixed, superactive, mesic Typic Hapludolls	0-2
	2015	Dakota	Fine-loamy over sandy or sandy-skeletal, mixed, superactive, mesic Typic Argiudolls	2-6
		Ridgeport	Coarse-loamy, mixed, superactive, mesic Typic Hapludolls	2-6
Prosper, ND	2013-15	Kindred-Bearden	Fine-silty, mixed, superactive, frigid Typic Endoaquolls	0-2
Perley, MN	2013-15	Fargo	Fine, smectitic, frigid Typic Epiaquerts	0-1
Crookston, MN	2013, 2015	Wheatville	Coarse-silty over clayey, mixed over smectitic, superactive, frigid Aeric Calciaquolls	0-2
		Bearden-Colvin	Fine-silty, mixed, superactive, frigid Aeric Calciaquolls	0-2
	2014	Wheatville	Coarse-silty over clayey, mixed over smectitic, superactive, frigid Aeric Calciaquolls	0-2
		Gunclub	Fine-silty, mixed, superactive, frigid Aeric Calciaquolls	0-2
Hallock, MN	2013-15	Northcote	Very-fine, smectitic, frigid Typic Epiaquerts	0-1

[†] Soil data obtained from (USDA-NRCS, 2016).
[‡] Listed from South to North.
[§] Soil taxonomy listed on individual lines based on hyphenated soil series name.

The locations Kimball, Perley, and Hallock were designed as a randomized complete blocks with a split-plot arrangement and three replicates. The whole plot was cultivar and the split-plot was seeding rate. Cultivars were selected in pairs based on presence of two genes controlling semi-dwarfism and one gene for photoperiod sensitivity (Table 15). The presence or absence of the genes was determined using polymerase chain reactions at the Wheat Genotyping Center in the USDA-ARS Cereal Crops Research Unit by Dr. Shiaoman Chao (Wiersma, 2012).

General Procedures

The germination percentage of each seed lot was determined by placing 100 seeds between two wet sheets of germination paper, rolling them up and keeping them in the dark at room temperature for about five days (Fabrizius, 2007). The seeding rate treatments were packed for each cultivar using kernel weight, germination percentage, and plot size. Trials were grown according to University of Minnesota and North Dakota State University extension recommendations with regards to cultivation, fertilization, and pesticide application (Table 16) (Wiersma and Ransom, 2012).

Table 14. Design, factors, and treatments for experiments at Prosper, ND, and Lamberton, Kimball, Perley, Crookston, and Hallock, MN, 2013-2015.

Location (Latitude)	Design	Factor	Treatment
Lamberton (44.24) Prosper (46.99) Crookston (47.82)	RCBD with split-split plot arrangement	Planting date	Optimum Late
		Cultivar	Albany Briggs Faller Kelby Knudson Kuntz Marshall Oklee Rollag Sabin Samson Vantage
		Seeding Rate	1590000 seeds ha^{-1} 2580000 seeds ha^{-1} 3570000 seeds ha^{-1} 4560000 seeds ha^{-1} 5550000 seeds ha^{-1}
Kimball (45.39) Perley (47.15) Hallock (48.80)	RCBD with split plot arrangement	Cultivar	Albany Briggs Faller Kelby Knudson Kuntz Marshall Oklee Rollag Sabin Samson Vantage
		Seeding Rate	1590000 seeds ha^{-1} 2580000 seeds ha^{-1} 3570000 seeds ha^{-1} 4560000 seeds ha^{-1} 5550000 seeds ha^{-1}

The plot size for the experimental unit at Prosper, ND was 1.24 m by 3.65 m and had 7 rows of HRSW with 0.19 m spacing. The plot size at Kimball, Perley, Crookston, and Hallock was 1.52 m by 4.57 m and had 10 rows of HRSW with 0.15 m row spacing. The plot size at Lamberton was 1.52 m by 2.43 m and had 8 rows of HRSW with 0.19 m row spacing. Optimum seeding rates were calculated from the first derivative of the regression equation for the quadratic seeding rate response curves. For the linear response curves optimum seeding rate was determined by the seeding rate treatment for maximum yield.

Table 15. Background genetic details of HRSW cultivars.

Group	Cultivar	*Ppd-D1*†	*Rht-B1*‡	*Rht-D1*§
1	Albany	*b*	*b*	*a*
	Faller	*b*	*b*	*a*
2	Knudson	*a*	*b*	*a*
	Samson	*a*	*b*	*a*
3	Briggs	*b*	*a*	*a*
	Vantage	*b*	*a*	*a*
4	Sabin	*a*	*a*	*a*
	Oklee	*a*	*a*	*a*
5	Kelby	*a*	*a*	*b*
	Kuntz	*a*	*a*	*b*
6	Marshall	*b*	*a*	*b*
	Rollag	*b*	*a*	*b*

† *Ppd-D1a* is photoperiod insensitive, *Ppd-D1b* is photoperiod sensitive.
‡ *Rht-B1a* is the wild-type stature allele, *Rht-B1b* is semi-dwarf stature.
§ *Rht-D1a* is the wild-type stature allele, *Rht-D1b* is semi-dwarf stature.

Data Collection

Density and spike counts were obtained by counting plants and spikes in two rows between two stakes that were placed 0.91 m apart in between two adjacent interior rows. Stand counts at approximately Feekes 1 were taken to verify that the seeding rate was correct (Large, 1954). Spike counts were taken at approximately Feekes 11. These two measurements were used in a calculation of stems per plant. Plot yield was collected from the entire plot with a small plot combine. Grain yield was adjusted to 13.5% moisture. Grain characteristics of moisture, test weight, and protein were collected at harvest or during post-harvest processing.

Table 16. Site location and year characteristics for a HRSW trial conducted in ND and MN, 2013-2015.

Location / Year	Previous Crop	Seeding Date	Harvest Date	Yield (Mg ha^{-1})
Lamberton				
2014	Soybean[‡]	21-Apr	20-Aug	5.14
2014[†]	Soybean	16-May	20-Aug	4.21
2015	Soybean	4-Apr	12-Aug	5.62
2015	Soybean	27-Apr	12-Aug	4.55
Kimball				
2014	Soybean	26-Apr	14-Aug	5.54
2015	Soybean	8-Apr	31-Jul	5.97
Prosper				
2013	Soybean	16-May	22-Aug	4.69
2014	Soybean	27-May	3-Sep	4.43
2014[†]	Soybean	18-Jun	7-Oct	2.80
2015	Soybean	9-Apr	21-Aug	4.67
2015	Soybean	22-May	25-Aug	3.62
Perley				
2013	Soybean	8-May	16-Aug	5.80
2014	Soybean	22-May	2-Sep	6.00
2015	Soybean	13-Apr	11-Aug	7.03
Crookston				
2013	Soybean	10-May	8-Aug	6.14
2013	Soybean	29-May	26-Aug	6.38
2014	Soybean	17-May	27-Aug	4.95
2014	Soybean	4-Jun	27-Aug	4.55
2015	Soybean	23-Apr	21-Aug	6.35
2015	Soybean	22-May	25-Aug	5.38
Hallock				
2013	Soybean	16-May	3-Sep	7.27
2014	Soybean	23-May	6-Sep	5.45
2015	Soybean	16-Apr	13-Aug	5.62

[†] Environment not included in analysis due to 40-50% stand loss.

[‡] *Glycine Max* (L.) Merr.

Statistical Analyses and Modeling

The statistical analysis was performed with SAS 9.4 (SAS Institute, SAS Circle, Cary, NC). Seeding rate and cultivar were considered fixed effects, while replicate and environment were considered to be random effects in the initial analysis. All interactions of fixed effects were considered fixed, while any interaction with a random term was considered random. When moving forward with the comparison of the entire dataset for creating a predictive model, environments were characterized by planting date, day length at planting, and latitude to ensure a broad and robust model.

The models for yield (Mg ha^{-1}) and tillers as the dependent variables were built using unadjusted data from each plot. An analysis of covariance (ANCOVA) model was built with data from 13 environments *a priori* considered to be the training data. The last model using only the six lowest yielding environments was built and validated without *a priori* designation of training and validation environments. The model was built with data from two randomly chosen replicates, with a third replicate for validation. The models were built using a manual technique within PROC MIXED with *Ppd-D*, *Rht-B*, *Rht-D*, stems plant^{-1}, geographic latitude of the field location, day length at planting (DL), and calendar days from January 1 (CD) as covariates. Method=type1 was the estimation method used to build the model and parameter estimate solutions were found with the solutions htype=1 statement. A model was built in the order of linear main effects, quadratic main effects, linear interactions, and quadratic interactions of all covariates. Effects that were non-significant at the 95% confidence level were removed from the end of the model to the beginning. Iterations of the model were run as effects were removed to ensure significance remained for effects below an eliminated term that may have partially explained the higher term.

Model adequacy and assumptions were assessed as the training model was nearing the final iteration using regression diagnostics (Ngo, 2012). The error mean square (EMS) was monitored so that it did not increase as the model was altered. Method=type3 was invoked to measure stability of the parameter estimates for the intercept and covariate terms as the last term in the model was added or removed. Residual plots were assessed to ensure stability in the model and to identify unusual and influential data points. Normality of the residuals around absolute zero was monitored for normality, skewness, and kurtosis. Tests were done for multi-collinearity of the factors in the model using Pearson correlation coefficients from the PROC CORR procedure as described by Ngo (2012). An R^2 estimate was calculated using PROC MIXED for the training data. Near completion, the model was further assessed for assumptions by running the validation data set through the model and assessing the same regression diagnostics and assumptions as for the training model.

Model validation was performed from the training data ANCOVA model with an outpred= statement in PROC MIXED by assigning a missing data symbol '.' as the dependent variable of the validation dataset. The residuals found by subtracting the observed minus predicted were further assessed by running the validation data through the parameter estimates as given by the solutions statement in SAS and plotting using PROC GPLOT and PROC SGPLOT. Predictions and residuals were calculated for each plot in the validation dataset to measure how predictive the model was of an out-of-sample dataset which was not used to build the model. The predictive nature of the model was assessed primarily using R^2 of the observed versus predicted plot values.

PROC REG was used for linear and quadratic regression analysis on the LSMEANS of the predicted outcomes of a seeding rate response curve for yield. The entire data set, training plus validation, was used for this analysis. An alpha level of 0.05 was used for all hypothesis tests. Single degree of freedom linear and orthogonal contrasts were written to make comparisons for main effects and interaction terms for categorical covariates. Significance indicators from the contrast statement were used to declare differences between seeding rate response curves for certain covariates.

Results

Original Yield Model

An ANCOVA regression model was built using the entire training dataset of 13 environments and validated for the entire validation dataset of eight environments across the large geographic reference area spanning nearly the entire north to south length of MN, USA. The most stable model had 11 variables and an intercept (Figure 1 and 2)

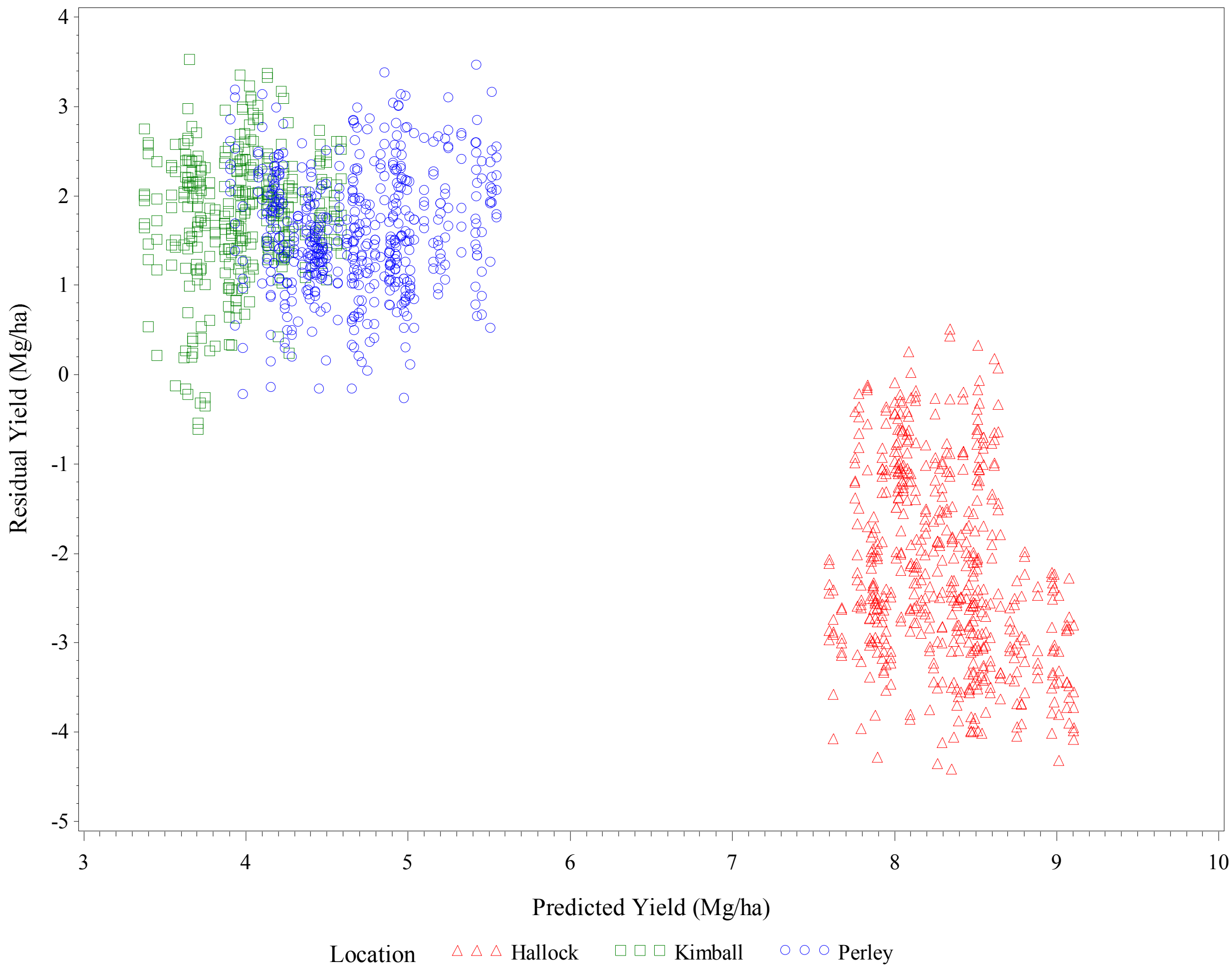

Figure 1. Validation dataset predictions plotted against actual observed yields minus the predicted yield residuals for all locations and years of validation datasets, Kimball, Perley, and Hallock, MN, 2013-2015.

The 11 variables in the model were *Ppd-D*, *Rht-B*, *Rht-D*, seeding rate, calendar days from January 1 at planting (CD), latitude of the environment, rate*rate, CD*CD, latitude*latitude, *Ppd-D*Rht-B*, and *Ppd-D*Rht-D*.

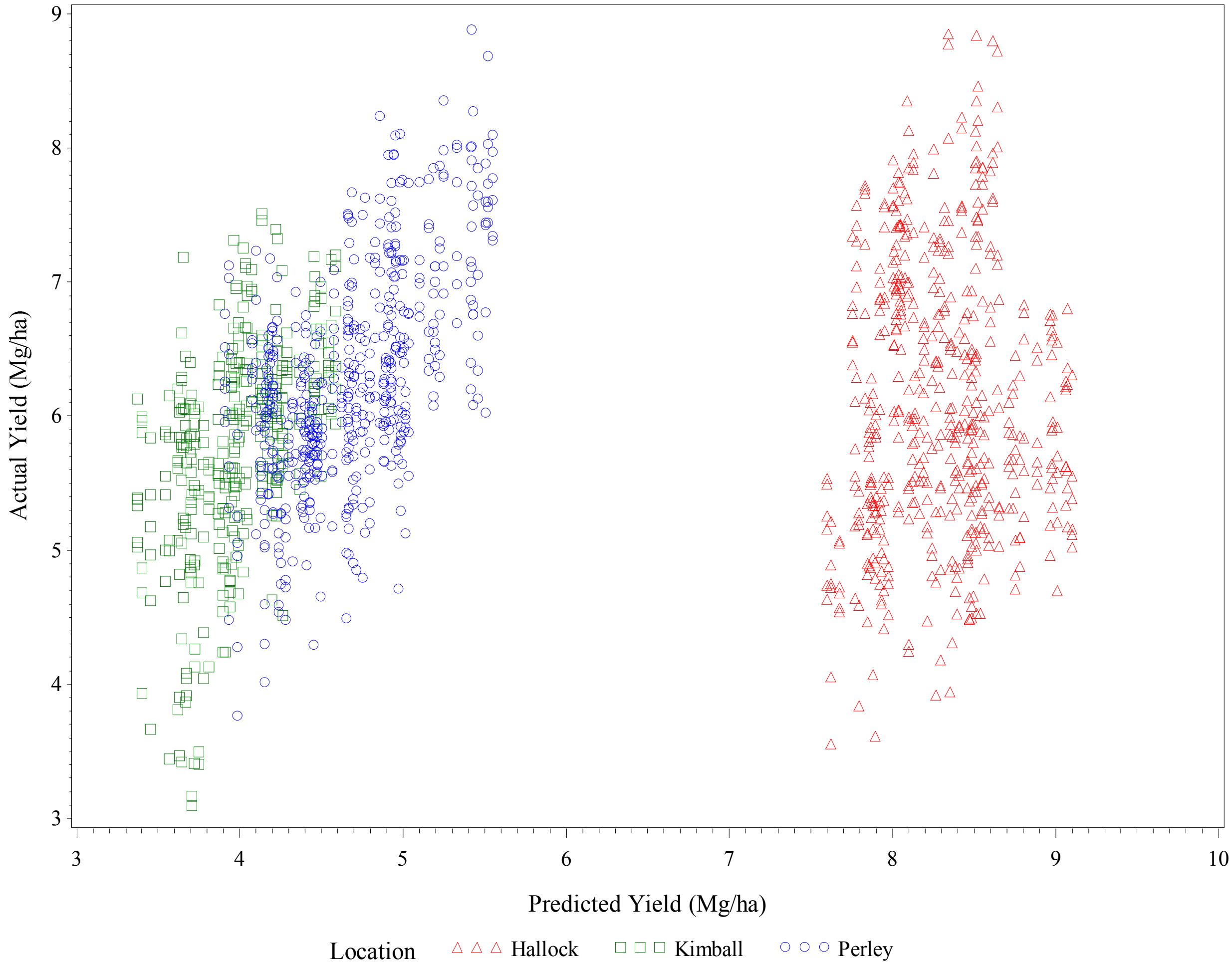

Figure 2. Validation dataset predictions plotted against actual observed yields for all locations and years of validation datasets, Kimball, Perley, and Hallock, MN, 2013-2015.

This model did not validate plot yield well at all. The original regression model for the training environments had an R^2 of 0.46 for observed versus predicted values. However, when this model was used to predict the yield of every plot from the eight validation environments, the R^2 between observed and predicted values was only 0.01, and the residual values (difference of the actual plot yield taken at harvest from the predicted yield from the model) differed substantially from zero. The residuals were not centered on zero Mg ha^{-1}, and were upwards of four Mg ha^{-1} away from the actual plot yield. Furthermore, the locations separated out from each other in fairly well-defined groups, especially Hallock, MN (Figures 1 and 2).

Model Predictions

The model for yield built for 13 environments and validated for eight environments was not predictive for out-of-sample data, however some trends for the covariates were found when all 21 environments were plotted. The four cultivars with *Rht-Bb* allele for semi-dwarf stature yielded more at all seeding rates than either the four semi-dwarf *Rht-Db* or the four wild-type stature cultivars (Figure 3).

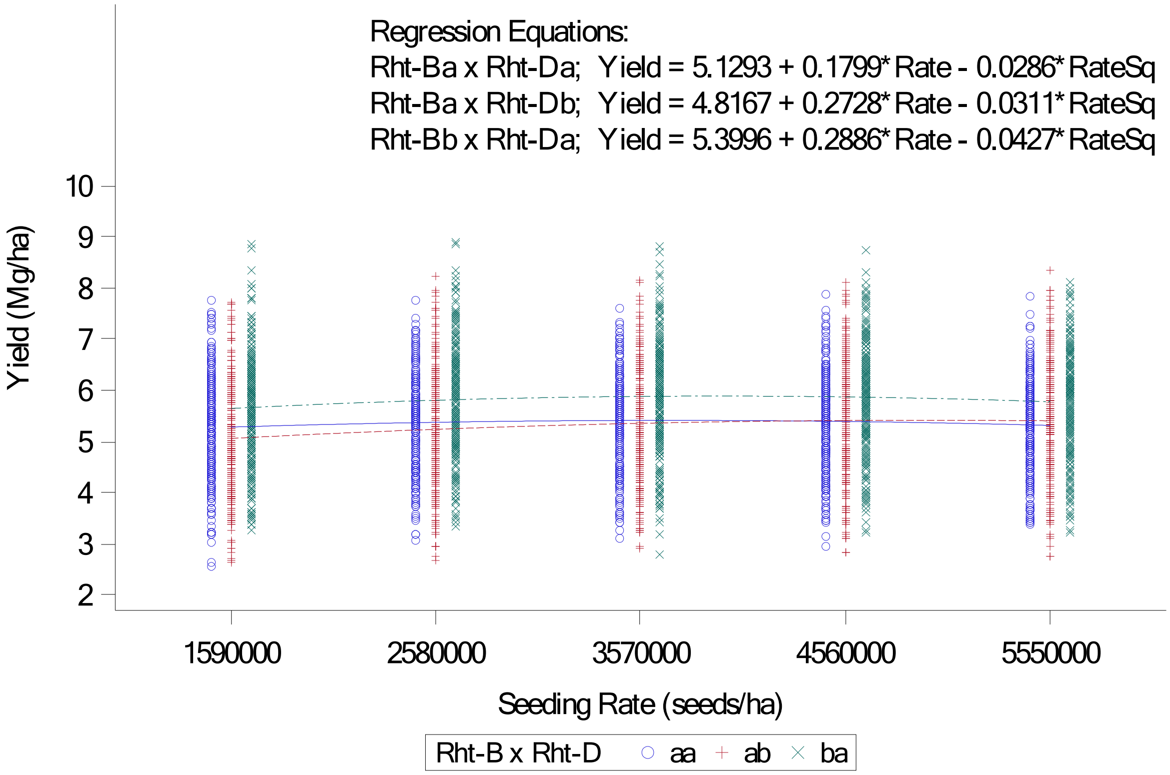

Figure 3. Influence of *Rht-Bb*, *Rht-Db*, and *Rht-a* (wild-type stature) alleles on seeding rate response for yield combined over 21 environments, ND and MN, 2013-2015.
† Seeding rate for the peak of the curve: aa = 3.41, ab = 4.40, and ba = 3.21 million seeds ha^{-1}.

Rht-Db cultivars had a crossover response interaction with wild-type stature cultivars. The *Rht-Db* cultivars peaked at 4.40 Mg ha^{-1} while the wild-type stature cultivars peaked at 3.41 Mg ha^{-1}.

The *Ppd-Da* gene for photoperiod insensitivity (PI) and *Ppd-Db* gene for photoperiod sensitivity (PS) imparted no yield advantage or differing seeding rate response curve at any seeding rate over the six cultivars with each allele combined over 21 environments (Figure 4).

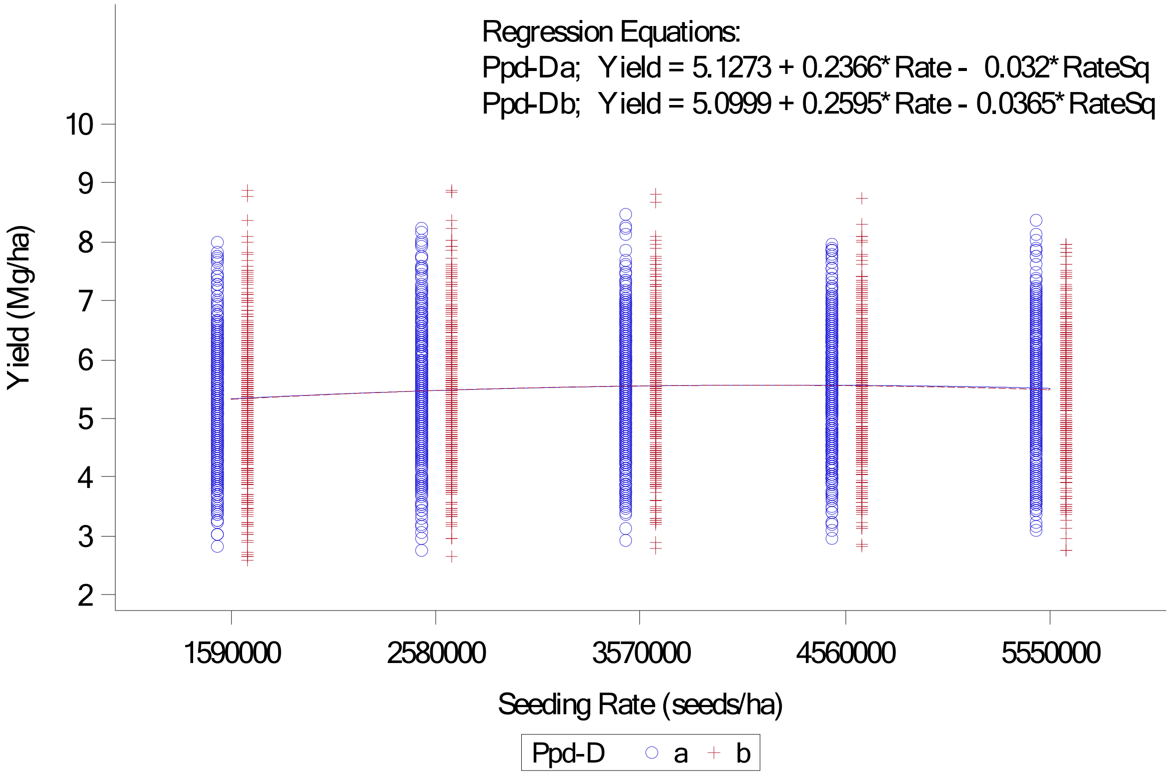

Figure 4. Influence of *Ppd-D* alleles *a* and *b* on seeding rate response for yield combined over 21 environments, ND and MN, 2013-2015.
† Seeding rate for the peak of the curve: a = 3.69, and b = 3.59 million seeds ha^{-1}.

There was an interaction of *Ppd-D* and *Rht-B* combined over all 21 environments (Figure 5). Of the combinations of cultivars with different alleles for the two genes, the main effect of *Rht-B* (Figure 3) is clearly evident. The response curves were a converging interaction within the two subgroups of *Rht-Ba* and *Rht-Bb*. The wild-type stature cultivars with *Rht-Ba* yielded more at the lowest two seeding rates when the cultivar also had PI allele *Ppd-Da*. The semi-dwarf cultivars with *Rht-Bb* yielded more at the lowest seeding rates when the cultivar also had PS allele *Ppd-Db*. Within this group the slope of the yield response curve was almost two times greater with PI than with PS.

The interaction of *Ppd-D* and *Rht-D* did not respond similarly to *Rht-B* in the same interaction, beyond the main effect of *Rht-Db* cultivars yielding lower than the combination of wild-type stature or *Rht-Bb* cultivars (data not shown). Within the same allele of *Rht-D*, PI or PS had nearly identical seeding rate response curves with very similar slopes and peaks.

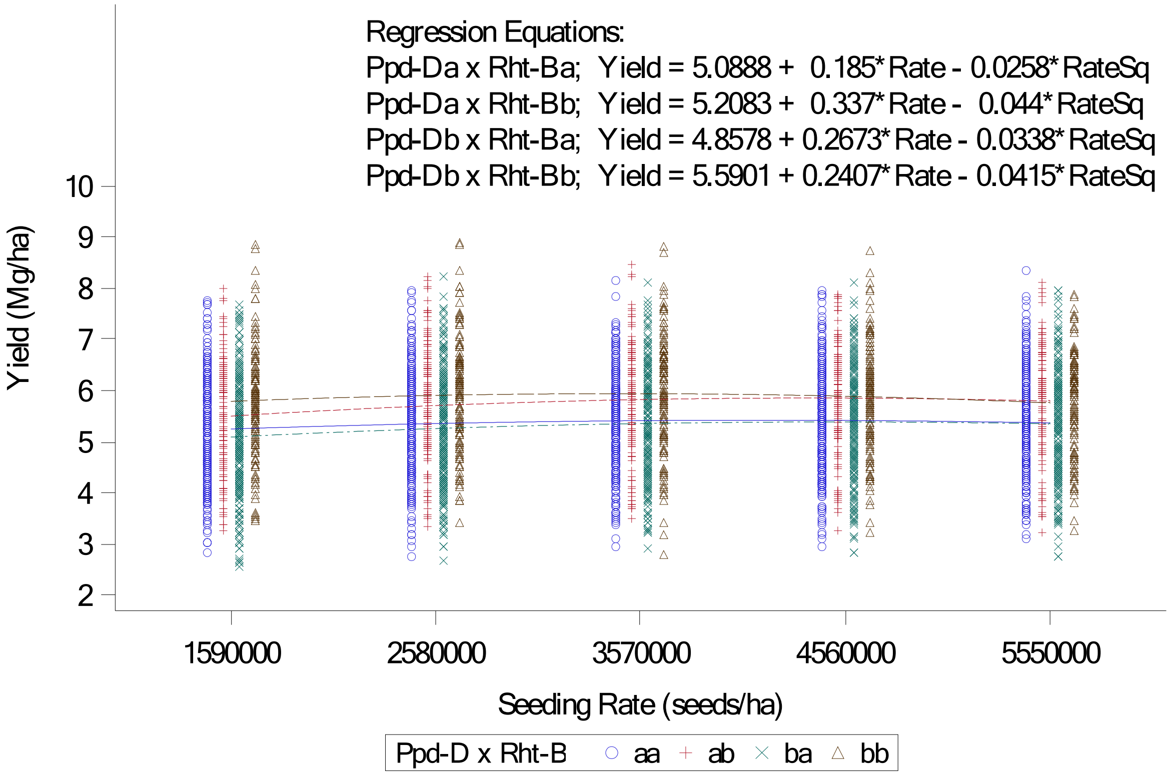

Figure 5. Yield response curves to seeding rate for the interaction between *Rht-B* and *Ppd-D* alleles combined over 21 environments, ND and MN, 2013-2015.
[†] Seeding rate for the peak of the curve: aa = 3.60, ab = 3.88, ba = 3.79, and bb = 2.94 million seeds ha^{-1}.

Latitude of an environment had an impact on seeding rate response for yield combined over all 21 environments (Figure 6). The locations were not in exactly the same location from year to year, however the difference in distance between environments within a location name was never more than about 8 km north to south (Hallock, Perley, and Kimball), and was typically more like a 1 km difference (Prosper, Lamberton, and Crookston). The relative yield potential of the environments breaks out cleanly in the order from lowest to highest of Prosper < Lamberton < Crookston < Kimball < Hallock < Perley. The higher the yield potential of the environment tended to mean a lower seeding rate was required to reach maximum yield across 12 diverse cultivars.

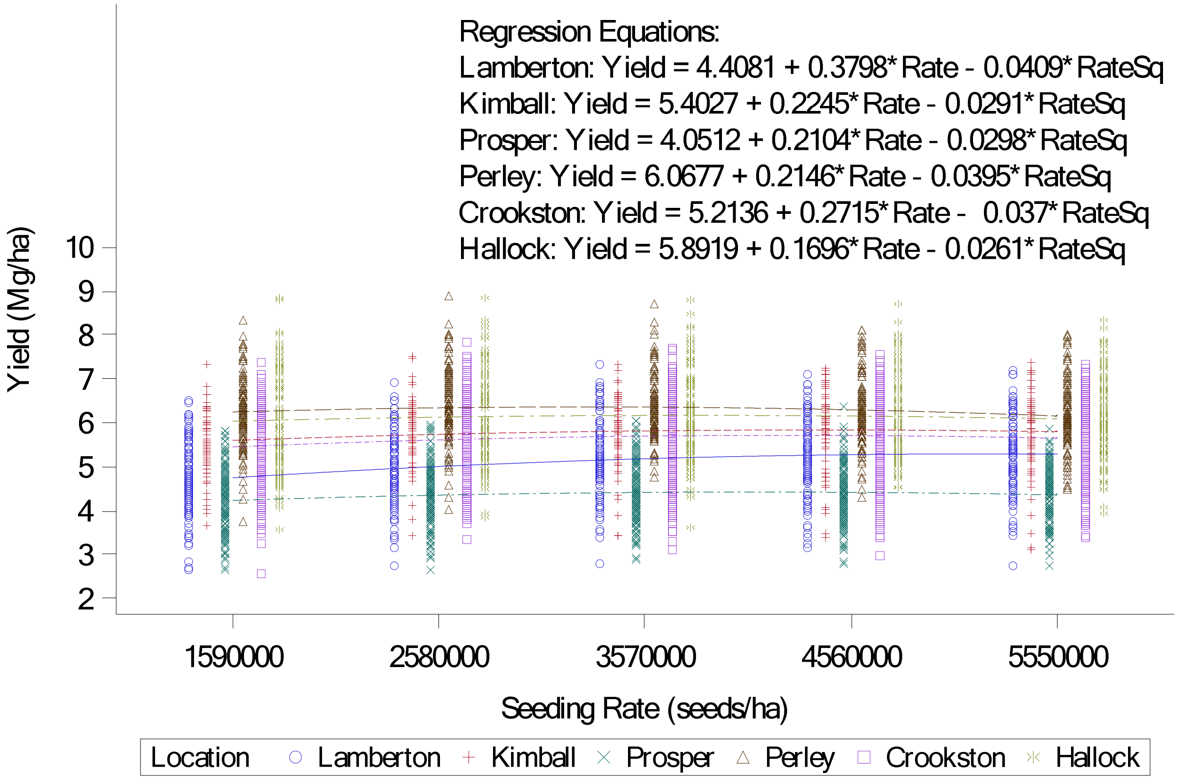

Figure 6. Yield response curves to seeding rate for latitude with each location averaged over between 2-6 environments, ND and MN, 2013-2015.

[†] Seeding rate for the peak of the curve: Lamberton = 4.62, Kimball = 3.87, Prosper = 3.51, Perley = 2.68, Crookston = 3.73, and Hallock = 3.26 million seeds ha^{-1}.

[‡] Exact latitude can be found in Table 14.

Tillering Model

With no model proving predictive for yield in the combined dataset, the predictive power of an ANCOVA model for the yield component stems per plant in HRSW was built and assessed. The ANCOVA regression model was built using the entire training dataset of 13 environments and validated for the entire validation dataset of eight environments, exactly as was done for the original yield model. The most stable model for stems plant^{-1} had 9 variables and an intercept (Figure 7 and 8).

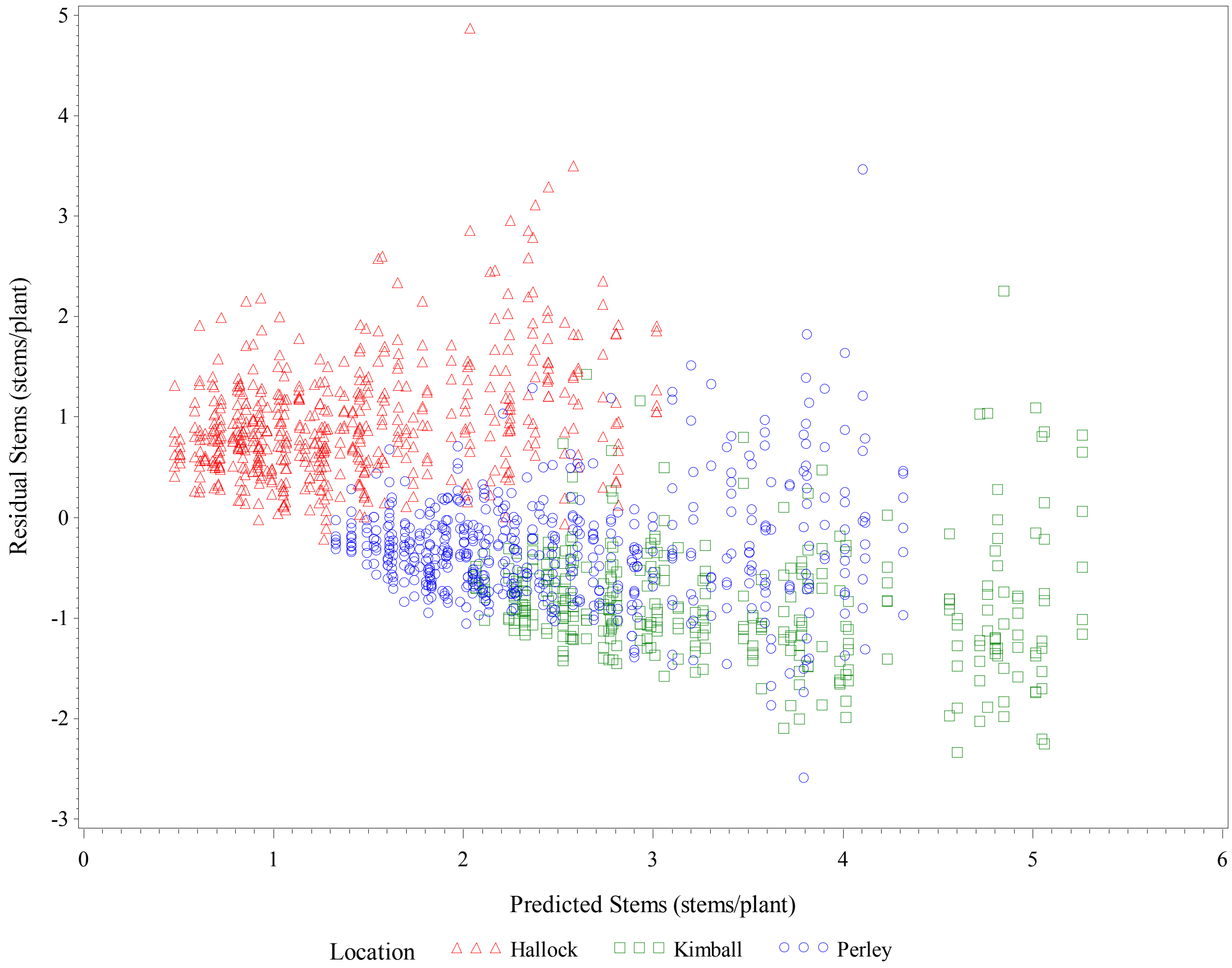

Figure 7. Validation dataset predictions plotted against actual observed stems per plant minus the predicted stems per plant residuals for all locations and years of validation datasets, Kimball, Perley, and Hallock, MN, 2013-2015.

The 9 variables in the model were *Ppd-D*, *Rht-B*, seeding rate, calendar days from January 1 at planting (CD), day-length at planting (DL), latitude of environment, rate*rate, latitude*latitude, and rate*latitude. The resulting R^2 for the training model was 0.63. When the validation data was put through the model the resulting R^2 was 0.71. The predicted and residual values were more representative of what would be expected from a predictive model. There was still a slight latitude influence. However, the trends were indicative of a predictive model.

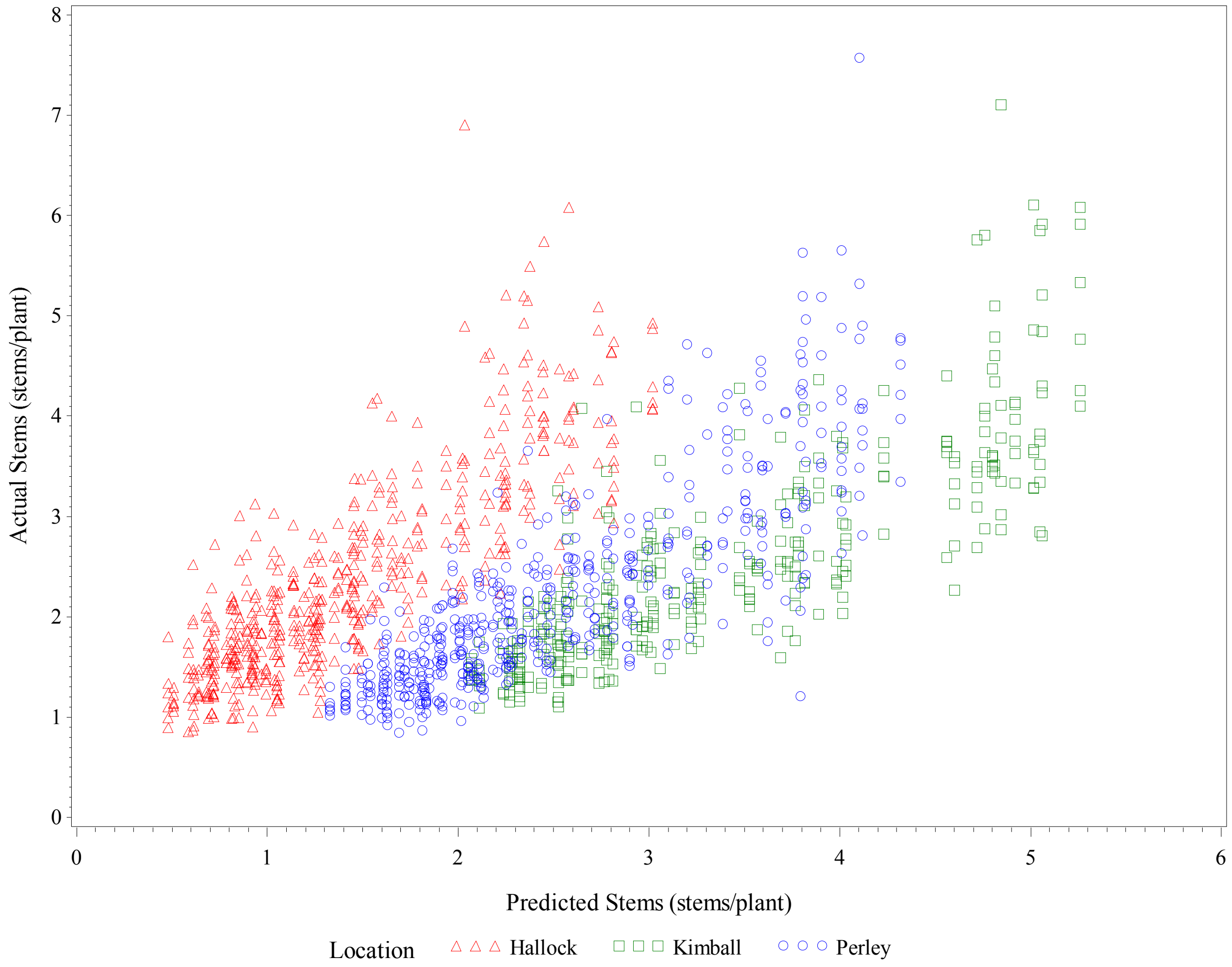

Figure 8. Validation dataset predictions plotted against actual observed stems per plant for all locations and years of validation datasets, Kimball, Perley, and Hallock, MN, 2013-2015.

Model Predictions

The genes *Rht-B*, *Rht-D*, and *Ppd-D* had an influence on stems per plant across all 21 environments (Figures 9-10). *Rht-Bb* cultivars had greater number of stems per plant at the two lowest seeding rates than *Rht-Db* or wild-type stature cultivars, though all three categories plateaued towards the highest three seeding rates (Figure 9).

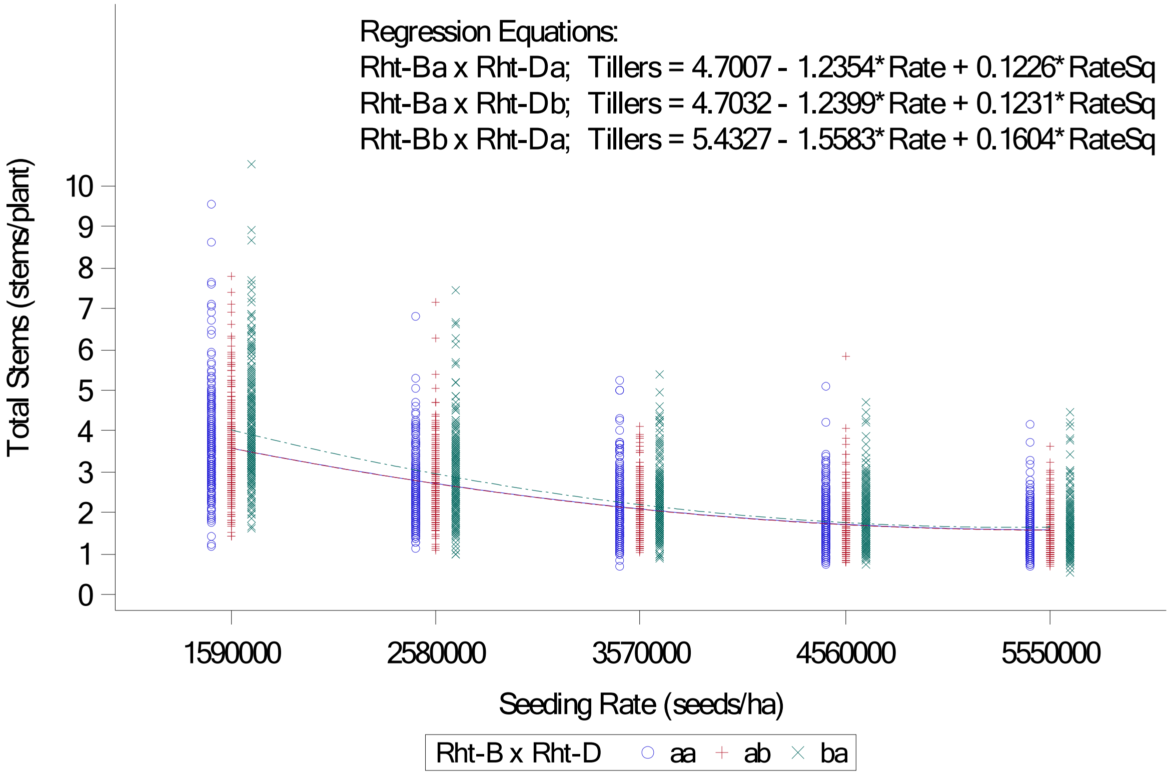

Figure 9. Influence of *Rht-Bb*, *Rht-Db*, and *Rht-a* (wild-type stature) alleles on seeding rate response for tillering combined over 21 environments, ND and MN, 2013-2015.

Photoperiod insensitive cultivars with the *Ppd-Da* allele consistently had fewer tillers than PS cultivars with the *Ppd-Db* allele (Figure 10). The tillering response curves were mirrored with very similar slopes, but different intercepts. Interactions between *Ppd-D* and either semi-dwarf gene provided only slight differences in stems per plant (data not shown). The main effect of PI cultivars having fewer stems per plant than PS cultivars was the main trend that came out of the interactions between photoperiod and semi-dwarf genes.

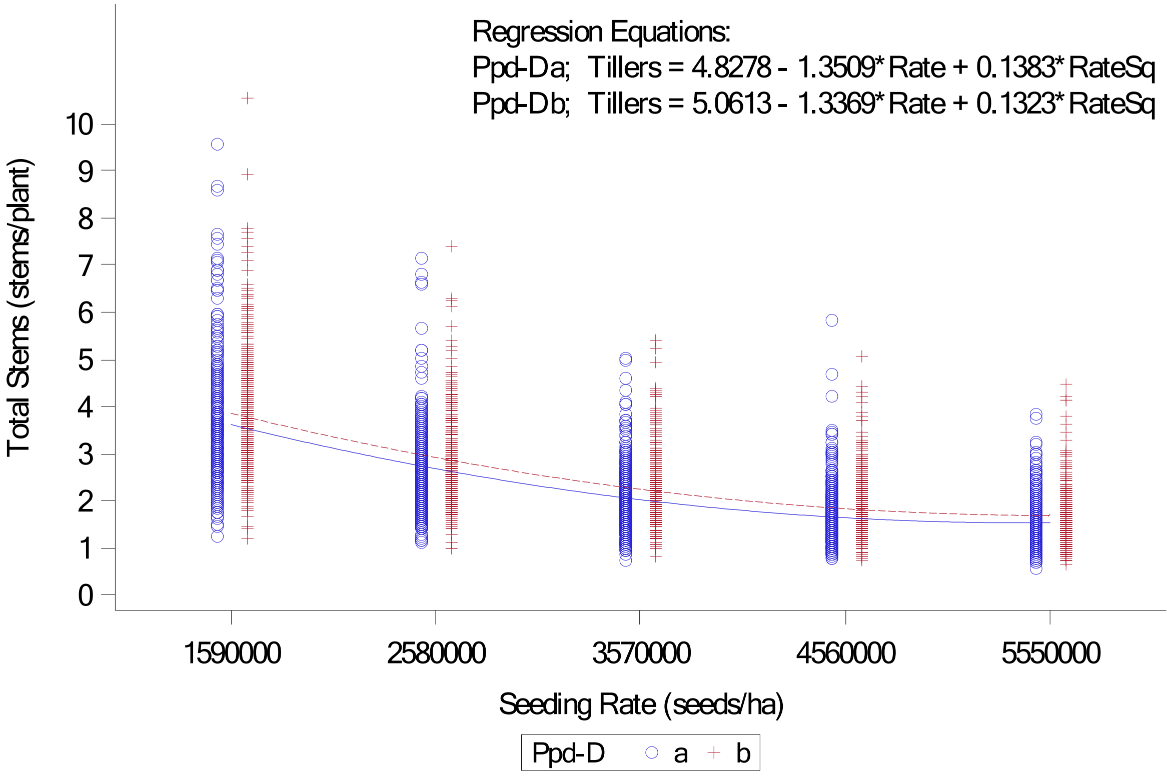

Figure 10. Influence of *Ppd-D* alleles on seeding rate response for tillering combined over 21 environments, ND and MN, 2013-2015.

Latitude had an impact on tillering combined over all cultivars (Figure 11). All of the environments at Lamberton combined to produce the highest stems per plant over all cultivars, while all the environments at Crookston combined to produce the lowest stems per plant. There was no noticeable interaction between the stems per plant response curves and latitude. The intercepts and the slopes of each latitude gives an indication of how the environments separated out for tillering capacity. Each named location could have as many as six diverse environments averaged into it from across three years and separate planting dates to represent general trends from southern to northern MN.

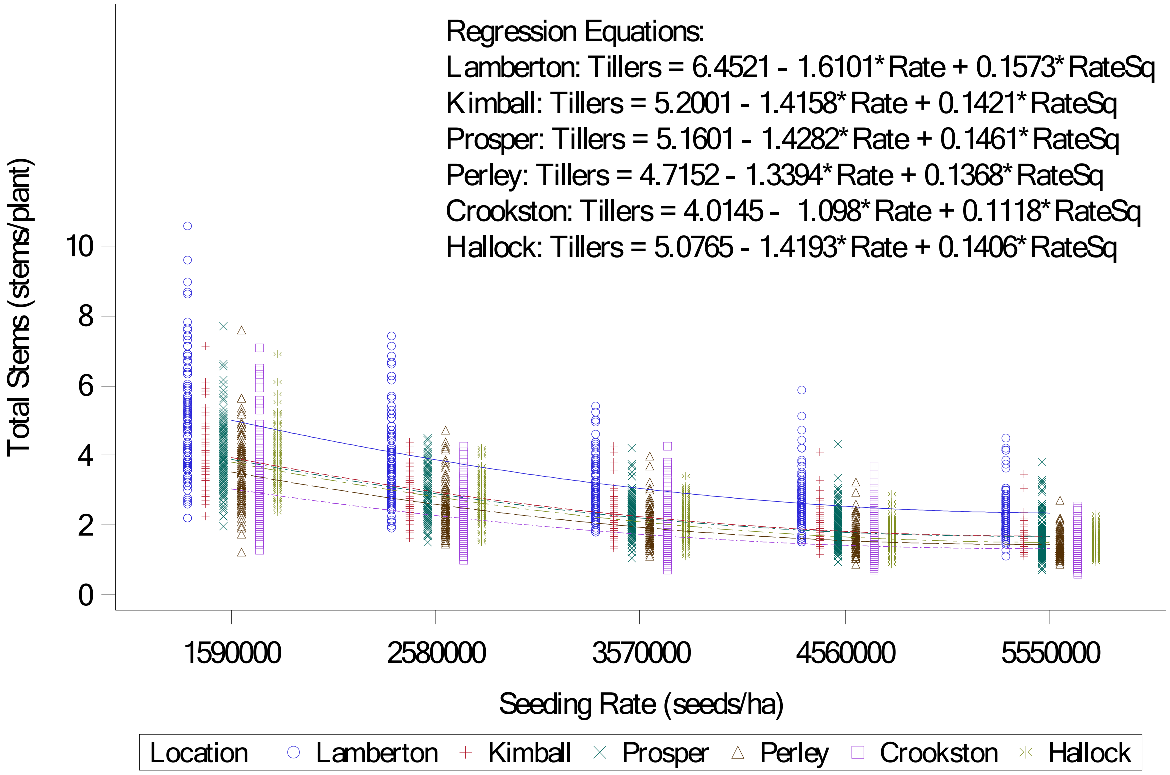

Figure 11. Tillering response curves to seeding rate for latitude with each location averaged over between 2-6 environments, ND and MN, 2013-2015.

Reworked Yield Model

The original yield model was not predictive, and the tillering model was only moderately predictive. Therefore, the yield model was looked at in a new way. One problem that plagued the three years of seeding rate research was the lack of a seeding rate response to yield at many environments due to very productive HRSW growing seasons. The yield responses were much flatter across the five seeding rates than what had previously been reported for this region (Wiersma 2002). The large difference in yield potential between the 21 environments in this research has been well documented in chapter 1. Therefore, an ANCOVA model was built to test the predictive nature of the covariates for yield of only the bottom six average yielding environments where seeding rate response curves were more pronounced. Thirteen covariates remained in the final model for the bottom third yielding environments including *Ppd-D*, *Rht-B*, *Rht-D*, seeding rate, DL, CD, latitude, rate*rate, CD*CD, latitude*latitude, *Ppd-D**Rht-B*, *Rht-B**DL, and *Rht-D**DL. The model for yield of the six bottom third yielding environments had a training R^2 of 0.42. The model was validated three times, with one of the three replicates serving as the validation dataset while two of the replicates were the training dataset. With replicate one, two, and three as the validation dataset the respective R^2 were very consistent at 0.43, 0.44, and 0.44 (Figures 12 and 13). When the bottom two-thirds yielding environments were run through the same scenario with a new model, the resulting R^2 averaged 0.20, therefore the bottom one third yielding environments was the focus of this final model.

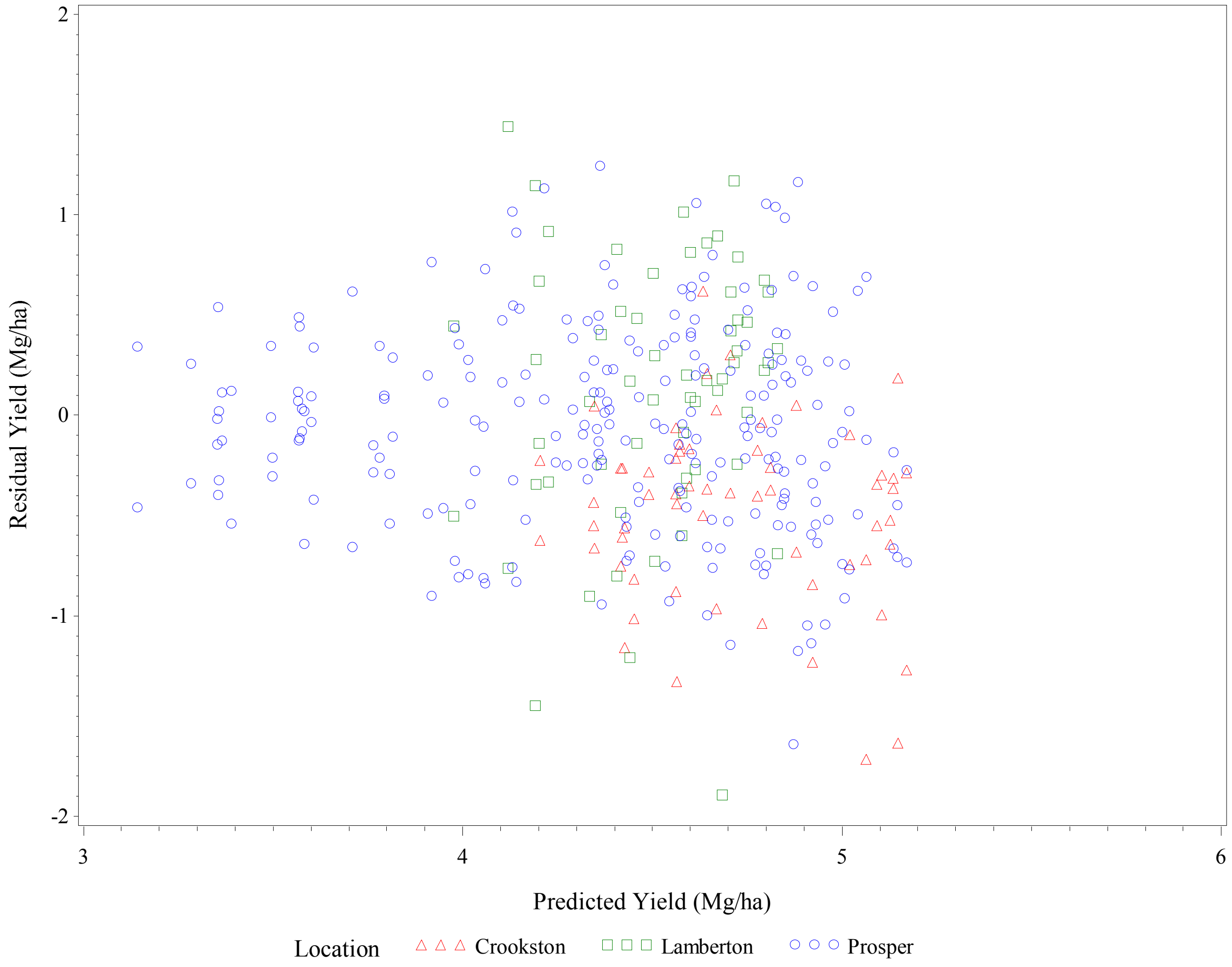

Figure 12. Validation dataset predictions plotted against actual observed yields combined over the six lowest yielding environments from the combined analysis, ND and MN, 2013-2015.

Figure 13. Validation dataset predictions plotted against actual observed yields combined over the six lowest yielding environments from the combined analysis, ND and MN, 2013-2015.

Model Predictions

Semi-dwarf plant stature from the *Rht-Bb* allele was beneficial for yield over the 12 cultivars (Figure 14). The semi-dwarf allele of *Rht-B* was represented by four cultivars in this study that yielded higher than the semi-dwarf allele for *Rht-D* or wild-type stature cultivars. The slopes between the three classes of cultivars for semi-dwarf genes differed slightly. Seeding rate for maximum yield of *Rht-Db* cultivars required almost a one million seeds ha^{-1} more than either *Rht-Bb* or wild-type stature cultivars.

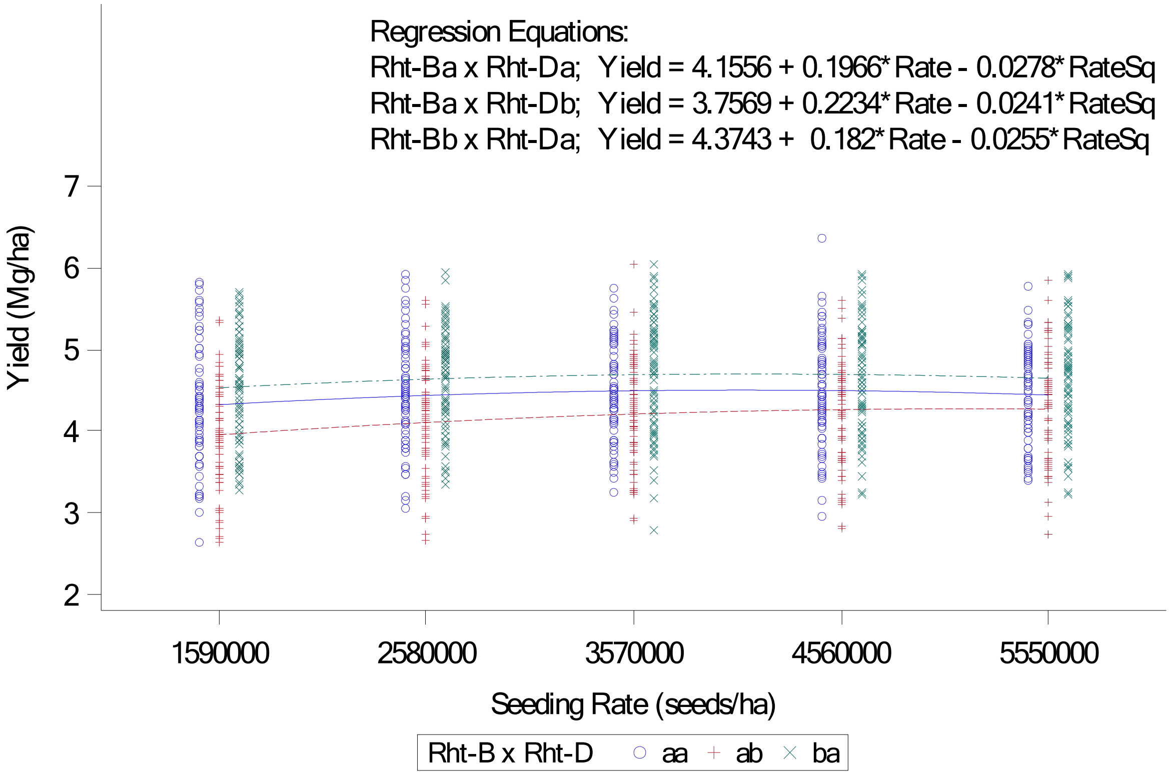

Figure 14. Influence of *Rht-Bb*, *Rht-Db*, and *Rht-a* (wild-type stature) alleles on seeding rate response for yield combined over the six lowest yielding environments from the combined analysis, ND and MN, 2013-2015.

† Seeding rate for the peak of the curve: aa = 3.68, ab = 4.65, and ba = 3.75 million seeds ha^{-1}.

Photoperiod had an impact on the relative yield and yield response curve across the six lowest yielding environments in the trial (Figure 15). PI cultivars yielded consistently higher than PS cultivars across all five seeding rates. The seeding rate for maximum yield was half a million seeds higher for PI cultivars at 4.21, compared to 3.71 million seeds ha^{-1} for PS cultivars. These results are a contrast from Figure 4 where PS and PI cultivars had nearly identical seeding rate response curves for yield. The middle third and top third yielding environments had no effect from the *Ppd-D1* gene for photoperiod sensitivity.

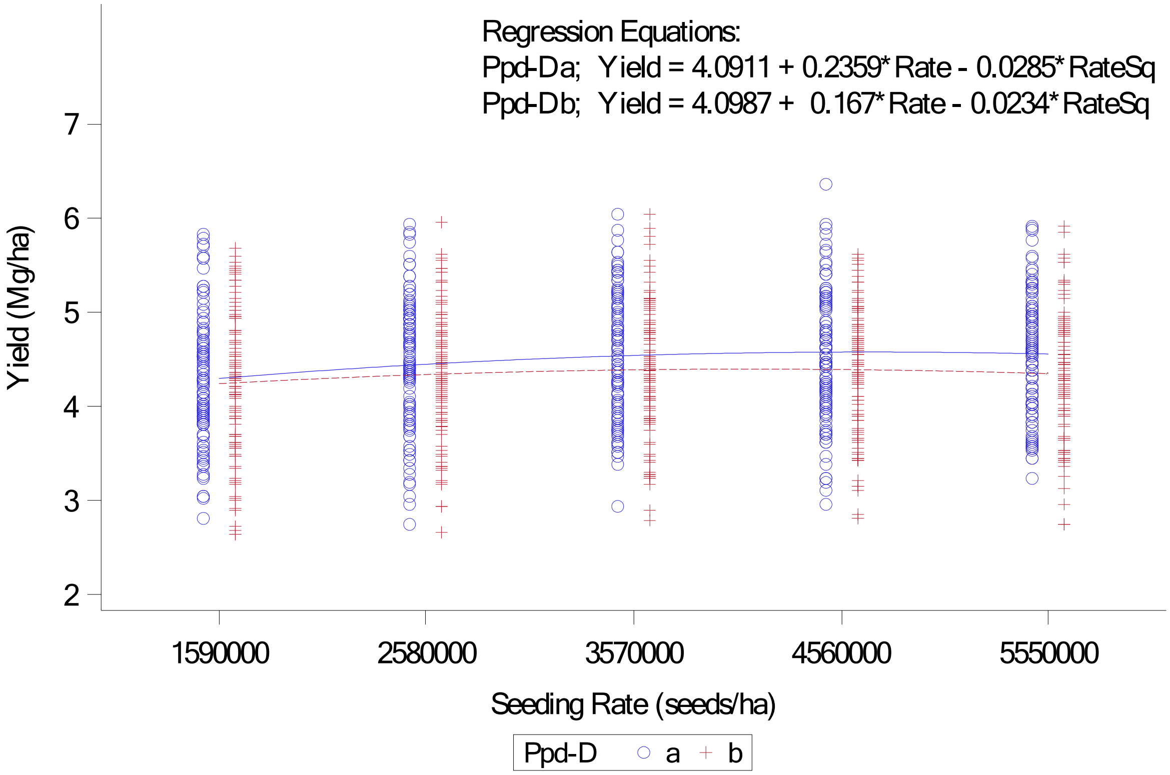

Figure 15. Influence of *Ppd-D* alleles on seeding rate response for yield combined over the six lowest yielding environments from the combined analysis, ND and MN, 2013-2015.
† Seeding rate for the peak of the curve: a = 4.21 and b = 3.71 million seeds ha^{-1}.

The main effect yield advantage of *Rht-Bb* cultivars over *Rht-Ba* cultivars is evident in the interaction figure between *Rht-B* and *Ppd-D* (Figure 16). For wild-type stature cultivars a yield advantage was found with PS cultivars compared to PI and there was no interaction between the two groups. However, when *Rht-Bb* cultivars were coupled with PS, the seeding rate for maximum yield was an unrealistic 0.62 million seeds ha^{-1}, compared to 4.26 million seeds ha-1 for *Rht-Bb* and PI combination cultivars. The crossover interaction occurred just above the second lowest seeding rate. The cultivars Albany and Faller that make up the *bb* group can both be planted at much lower seeding rates in low yielding environments, though the exact reasons are not readily apparent (Table 10).

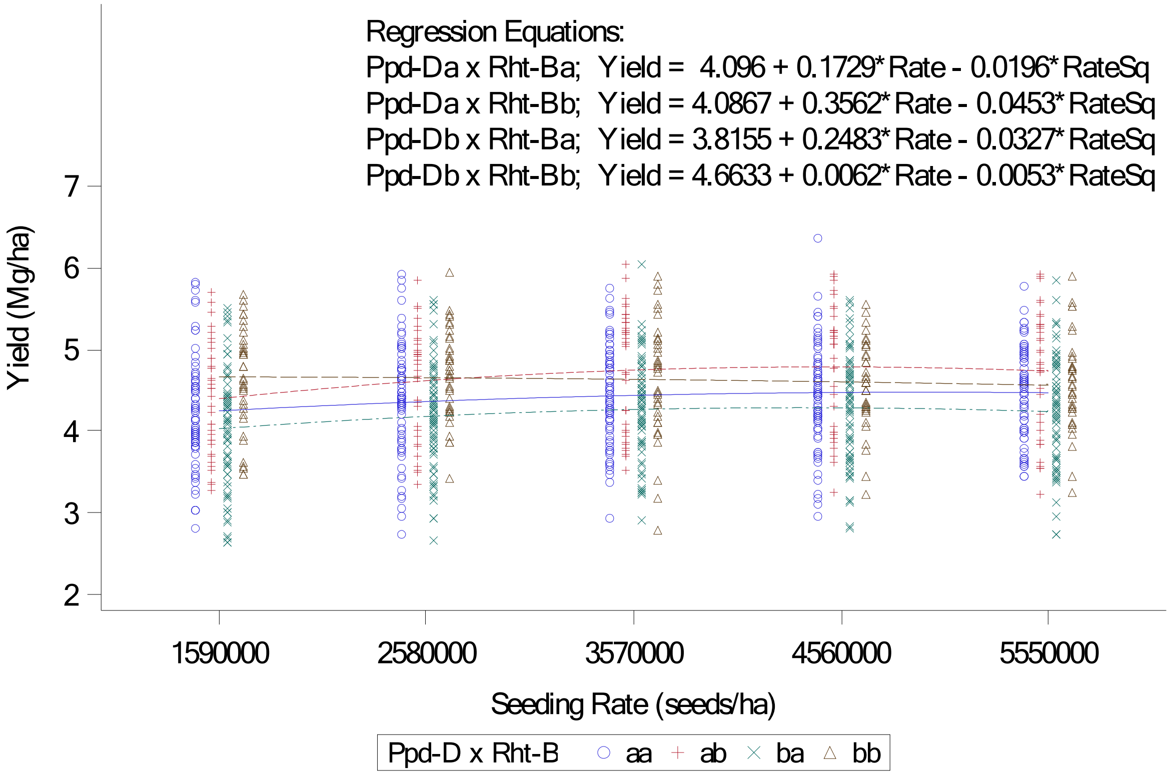

Figure 16. Yield response curves to seeding rate for the interaction between *Rht-B* and *Ppd-D* alleles combined over the six lowest yielding environments from the combined analysis, ND and MN, 2013-2015.

† Seeding rate for the peak of the curve: aa = 4.16, ab = 4.26, ba = 3.98, and bb = 0.62 million seeds ha^{-1}.

The interaction between *Rht-D* and *Ppd-D* breaks out first into main effects, with *Rht-Db* cultivars needing much higher seeding rates for maximum yield and having lower relative yield across the six lowest yielding environments than wild-type stature cultivars (Figure 17). Photoperiod insensitive cultivars also had higher relative yield than PS cultivars, though this main effect was explained above. Both interactions between the subgroups were diverging as the seeding rates increased.

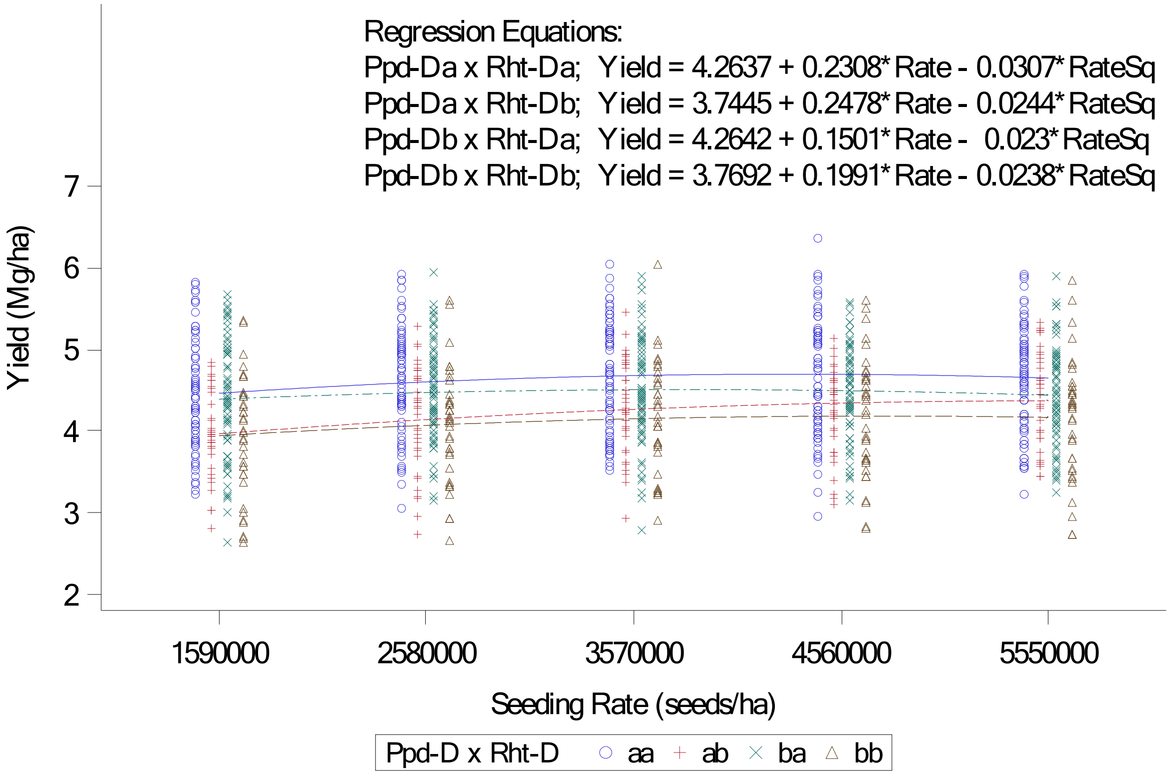

Figure 17. Yield response curves to seeding rate for the interaction between *Rht-D* and *Ppd-D* alleles combined over the six lowest yielding environments from the combined analysis, ND and MN, 2013-2015.

† Seeding rate for the peak of the curve: aa = 3.83, ab = 5.16, ba = 3.36, and bb = 4.15 million seeds ha^{-1}.

The latitude response for the bottom third yielding environments was variable as four environments averaged into the Prosper seeding rate response curve, but just one envionment averaged into both Lamberton and Crookston seeding rate response curves (Figure 18). The range in yield of the 21 environments across all seeding rates and cultivars was from a lowest average yield of 3.62 Mg ha^{-1} to a highest average yield of 7.27 Mg ha^{-1}. If split into thirds there were six environments in the bottom third from 3.62-4.83 Mg ha^{-1}, ten locations in the middle third from 4.84-6.05 Mg ha^{-1}, and five locations in the top third from 6.06-7.27 Mg ha^{-1} with the bottom third grouping shown in Figure 18.

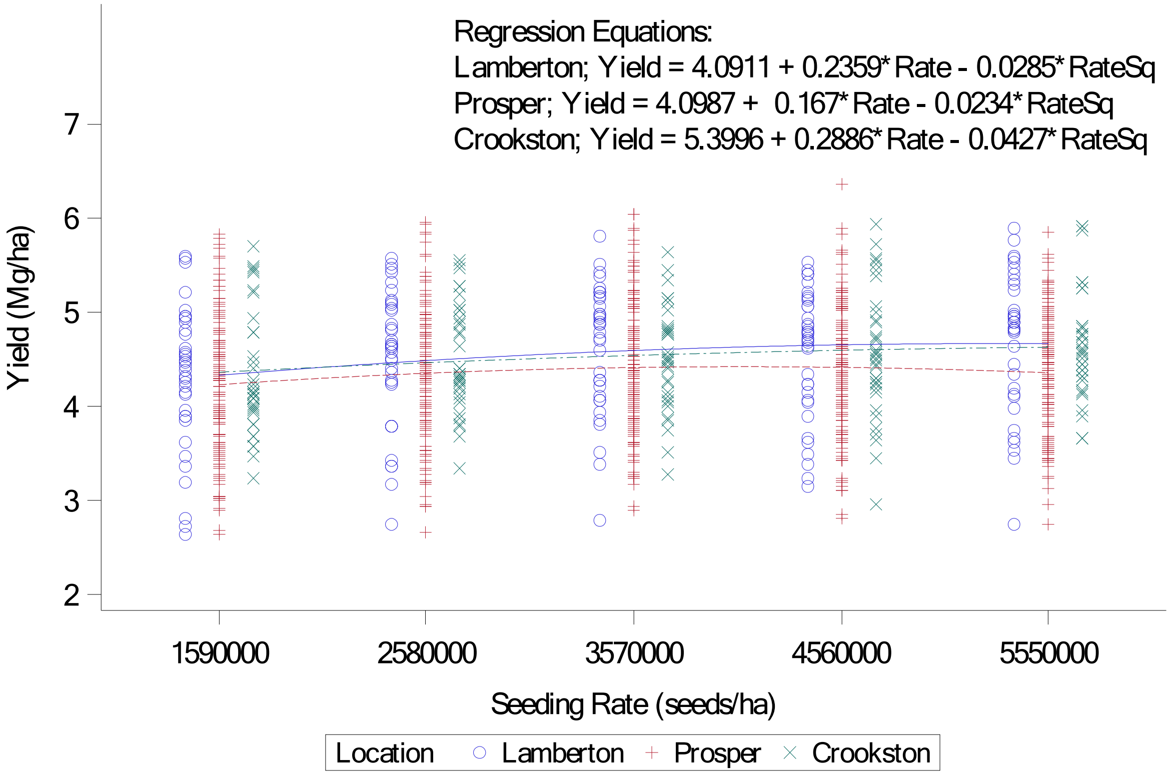

Figure 18. Yield response curves to seeding rate of the bottom six yielding environments for latitude with each location averaged over between 1-4 environments, ND and MN, 2013-2015. † Seeding rate for the peak of the curve: Lamberton = 4.76, Prosper = 3.53, and Crookston = 5.91 million seeds ha^{-1}.

Discussion

Original Yield Model

Latitude was significantly influencing the predicted values and skewing residuals in the original yield model that used all 21 environments. The validation environments at Kimball, MN are approximately 275 km away (1.77 degrees S) from the environments at Perley, MN, and Perley is approximately 179 km away (1.65 degrees S) from Hallock, MN. The yield trends from a limited dataset of 13 training environments did not accurately predict yields at eight nearby though distant out-of-sample validation environments. One reason for the inaccurate predictions was that there were not enough environments to accurately represent the large geographic reference area to allow for a complete understanding of how environments yield moving around the reference area. Additionally, there were so many other stresses to the HRSW crop such as lodging, disease, and water availability that were not included as covariates in the model. However, regardless of the problems that latitude presented, the predictive power and R^2 of the training model decreased greatly if latitude was not included as a covariate in the model and residuals were even more randomly distributed.

Twenty-one environments across three years provided a diversity of environments, where six early maturing, PI cultivars were balanced by six late maturing, PS cultivars (Figure 4). This current research found no yield advantage for either PI or PS cultivars, while Busch et al. (1984) who found a 9% yield advantage from PI near isogenic lines (NILs) compared to PS NIL's, and Marshall et al. (1989) who found that yield for PI NIL's were always equal to or greater than PS lines in similar geographies to this study.

Future research using this approach over a wide geographic reference area would likely benefit from including more environments spaced evenly and/or more closely together, or shrinking the overall size of the reference area. The conclusion for this first model for yield was that the training environments were not predictive of the validation environments.

Tillering Model

Predicting tillering can be useful as tillering gives HRSW adaptability to diverse geographies. *Rht-Bb* cultivars had more tillers than either *Rht-Db* or wild-type stature cultivars at the lowest two seeding rates of the trial (Figure 9). This result is in line with Sial et al. (2002) who found the two cultivars with *Rht-Bb* to have significantly more stems per plant than *Rht-Db* cultivars in field experiments in Pakistan. Contrary to both these results, Pinthus and Levy

(1983) found no difference between wild-type stature, and semi-dwarf HRSW cultivars for stems per plant.

Latitude was a major factor in tillering when combined over all cultivars and future analysis on the latitude by cultivar interaction for stems per plant should be done with this data. There were no weather covariates taken for the environments, so the overall tillering capacity for each latitude cannot be fully explained. The trend for less tillers as environments moved northward in the geographic area could be useful to producers trying to predict the tillers they will have in their production region.

Yield Model Reworked

Photoperiod sensitivity did not affect HRSW yield over 21 diverse geographies in eastern ND and MN. However, similar to prior research by Marshall et al. (1989) in a similar geography, environments with below average yields had a yield increase with PI compared to PS due to earlier heading and maturity to beat stresses in the growing season. The increase in yield with PI cultivars was 0.05 Mg ha^{-1} at the lowest seeding rate, but was between 0.15 and 0.25 Mg ha^{-1} higher at the highest three seeding rate treatments. Photoperiod insensitive cultivars yielded 3.2% higher than PS cultivars when averaged over all five seeding rates. The sample of cultivars used in this research provided a lower increase for PI over PS cultivars than the 9% increase from PI lines found by Busch et al. (1984) in MN. Prior research on photoperiod in HRSW for this geography of ND and MN had used 10 (Busch et al., 1984) and 11 (Marshall et al., 1989) pairs of NILs for *Ppd-D1*. This current research used six cultivars with each allele for *Ppd-D1*, instead of NILs, which is a slightly lower sample size and different methodology. However, the cultivars in this research were still a random sampling of cultivars available. Lower yielding environments are subject to greater stresses, especially increased temperature that is detrimental to a cool season cereal crop. This current research found that the earlier maturing PI cultivars were advantageous in stressed environments and could be planted 0.5 million seeds ha^{-1} higher for maximum yield than PS cultivars in these environments.

With regards to the semi-dwarf genes as main effects, it was clear that *Rht-Db* semi-dwarfs needed higher seeding rates to reach maximum yield than wild-type stature or *Rht-Bb* semi-dwarfs (Figures 14 and 16-17). The relative yield in this trial of *Rht-Bb* cultivars was higher than either *Rht-Db* or wild-type stature cultivars, however this could have been a function of a small sample size and particularly high yielding cultivars, Faller and Albany, making up two of the four *Rht-Bb* cultivars.

Predictive models have been attempted with varying success in a wide array of agricultural research, from QTL impacts, to water use yield response curves and more. As far as we know this is the first undertaking to try and use a rigorous experimental design and statistical approach to predict optimum seeding rates for maximum yield in HRSW using genetic traits. The problem of latitude and relative yield differences between environments was hard to overcome for the predictive model, though it was somewhat resolved by looking at the lowest yielding environments.

Conclusions

Predicting the yield of plots in 9 validation environments with a model built from 13 training environments proved difficult to do given the requirements of creating a truly predictive model. The training model R^2 was 0.46, however the validation model predictions had an R^2 of just 0.01. Relative yield levels and yield response curves were difficult to predict for validation data due to geographic separation, not enough environments within a very large geographic reference area, stresses not included as covariates, and a relative lack of a true seeding rate response curve for many environments where the curve was much flatter than would be expected due to favorable growing conditions.

A tillering model was developed and found to be predictive. Tillering is an important trait contributing to yield in wheat and it may be useful for a producer to know about this characteristic when planting a specific HRSW cultivar. The tillering model had an R^2 of 0.63 for the training dataset and 0.71 for the validation dataset. Photoperiod sensitive cultivars had more stems per plant than PI cultivars across the entire seeding rate response curve. Latitude was predictive of stems per plant, with more southern environments having more stems per plant and higher yielding environments having less stems per plant.

The predictive power of a yield model for only the six bottom yielding environments was tested and substantiated. An R^2 of 0.42 for the training dataset and 0.44 for the validation dataset was more predictive than the original yield model with 13 environments in the training population. Photoperiod insensitive cultivars yielded higher than PS cultivars and required a seeding rate of about 0.5 million more seeds ha^{-1} for maximum yield. Cultivars with *Rht-Db* semi-dwarf stature required about 1.0 million more seeds ha^{-1} for maximum yield compared with either wild-type stature or *Rht-Bb* semi-dwarfs.

The objective of this research to mesh genetic knowledge of a HRSW cultivar with agronomic practices in order to predict an optimum seeding rate for maximum yield was rigorously tested. There did prove to be predictive power especially for tillering and lesser so for yield, by having genetic knowledge of a cultivar coupled with known geographic and planting date information. The results are an important first step in developing predictive models for seeding rate decisions in HRSW with regards to genetic and location characteristics as covariates. For future research, more environments might be added more closely together.

However, the unpredictable nature of weather and growing seasons will continue to provide a challenge.

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APPENDIX

Table A 1. Type 1 analysis of covariance for the final yield model built from the entire training dataset of 13 environments, ND and MN, 2013-2015.

Source	df	Mean Square	F
Intercept	-	-	-
Rep	2	6.2***	11.4
Ppd-D	1	3.4*	6.3
Rht-B	1	105.4***	192.9
Rht-D	1	2.7*	4.9
Seeding Rate (Rate)	1	19.3***	35.3
Calendar Day (CD)	1	56.8***	103.9
Latitude	1	226.6***	413.9
Rate*Rate	1	8.2***	15.1
CD*CD	1	5.0**	9.1
Latitude*Latitude	1	645.1***	1180.0
Ppd-D*Rht-B	1	8.2***	15.0
Ppd-D*Rht-D	1	4.5**	8.2
Residual	2322	0.5	-

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 2. Type 1 analysis of covariance for the final tillering model built from the entire training dataset of 13 environments, ND and MN, 2013-2015.

Source	df	Mean Square	F
Intercept	-	-	-
Rep	2	0.5	0.9
Ppd-D	1	20.5***	38.1
Rht-B	1	17.8***	33.1
Seeding Rate (Rate)	1	1265.0***	2353.5
Day Length (DL)	1	631.8***	1175.5
Calendar Day (CD)	1	18.1***	33.6
Latitude	1	136.1***	253.2
Rate*Rate	1	115.7***	215.2
Latitude*Latitude	1	23.1***	43.1
Rate*Latitude	1	38.1***	71.0
Residual	2326	0.5	-

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 3. Type 1 analysis of covariance for the final yield model built from only the bottom six yielding environments out of the 21 total environments, ND and MN, 2013-2015.

Source	df	Mean Square	F
Intercept	-	-	-
Rep	1	0.9	3.5
Ppd-D	1	4.5***	16.9
Rht-B	1	19.2***	71.9
Rht-D	1	9.2***	34.3
Seeding Rate (Rate)	1	4.1***	15.3
Day Length (DL)	1	10.0***	37.5
Calendar Day (CD)	1	3.0***	11.3
Latitude	1	8.0***	29.9
Rate*Rate	1	1.7*	6.5
CD*CD	1	63.0***	235.0
Latitude*Latitude	1	17.8***	66.2
Ppd-D*Rht-B	1	1.2*	4.5
Rht-B*DL	1	4.0***	14.9
Rht-D*DL	1	1.8***	6.7
Residual	705	0.3	-

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 4. Means squares and significance levels for the ANOVA for agronomic traits, Prosper, ND, 2013.

Source	DF	Population	Spikes ha^{-1}	Stems Plant^{-1}	Protein	Mg ha^{-1}
Rep	2	8.6×10^{-9}	9.2×10^{-12}***	1.7*	5.9	0.2
A [Cultivar]	11	1.1×10^{-12}***	2.5×10^{-12}*	1.1*	6.1*	1.4*
Error (a)	22	2.1×10^{-11}	8.3×10^{-11}	0.4	2.6	0.4***
B [Seeding Rate]	4	4.7×10^{-13}***	3.0×10^{-12}**	28.2***	1.0	1.5***
A * B	44	2.2×10^{-11}	6.8×10^{-11}	0.3	1.9	0.2***
Error (b)	96	2.0×10^{-11}	7.7×10^{-11}	0.2	2.1	0.0

*** Significant at the 0.001 probability level.
** Significant at the 0.01 probability level.
* Significant at the 0.05 probability level.

Table A 5. Means squares and significance levels for the ANOVA for agronomic traits, Perley, MN, 2013.

Source	DF	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	1.4×10^{-11}	3.0×10^{-10}	0.0	74.3	0.7	8.8*	0.4
A [Cultivar]	11	1.6×10^{-11}	2.6×10^{-12}***	0.4	139.1**	2.3***	6.7*	0.9*
Error (a)	22	2.6×10^{-11}	6.2×10^{-11}	0.2	31.4***	0.3***	2.5***	0.4***
B [Seeding Rate]	4	5.2×10^{-13}***	3.1×10^{-12}**	23.7***	15.8*	2.1***	0.5*	0.4***
A * B	44	2.3×10^{-11}	6.1×10^{-11}	0.2	10.3*	0.7***	0.2	0.1
Error (b)	96	2.5×10^{-11}	7.4×10^{-11}	0.3	5.8	0.1	0.2	0.1

*** Significant at the 0.001 probability level.
** Significant at the 0.01 probability level.
* Significant at the 0.05 probability level.

Table A 6. Means squares and significance levels for the ANOVA for agronomic traits in the optimum planting date, Crookston, MN, 2013.

Source	DF	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	6.3 x 10^{-11}*	2.2 x 10^{-12}*	0.4	235.4***	2.2	6.8***	0.9
A [Cultivar]	11	7.9 x 10^{-11}**	2.4 x 10^{-12}**	0.6**	153.2***	9.8***	10.0***	2.7***
Error (a)	22	1.8 x 10^{-11}	6.3 x 10^{-11}	0.2	14.6*	1.1***	0.6***	0.4***
B [Seeding Rate]	4	3.4 x 10^{-13}***	3.0 x 10^{-12}**	13.6***	7.3	4.4***	0.9***	0.5*8*
A * B	44	3.1 x 10^{-11}	7.1 x 10^{-11}	0.2	13.4**	1.8***	0.5***	0.1
Error (b)	96	3.4 x 10^{-11}	6.9 x 10^{-11}	0.2	7.3	0.3	0.2	0.1

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 7. Means squares and significance levels for the ANOVA for agronomic traits in the late planting date, Crookston, MN, 2013.

Source	DF	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	7.7 x 10^{-11}	7.3 x 10^{-11}	0.2	164.8***	0.1	8.5***	2.8**
A [Cultivar]	11	5.7 x 10^{-11}*	1.5 x 10^{-12}**	0.3**	258.2***	0.8***	6.7***	2.6***
Error (a)	22	1.8 x 10^{-11}	3.3 x 10^{-11}	0.1	12.6**	0.1**	0.4***	0.3***
B [Seeding Rate]	4	7.7 x 10^{-13}***	6.3 x 10^{-12}***	14.9***	4.5	0.6***	0.1	0.9***
A * B	44	3.7 x 10^{-11}	1.0 x 10^{-12}	0.1	8.4*	0.3***	0.2	0.1*
Error (b)	96	2.8 x 10^{-11}	7.8 x 10^{-11}	0.1	5.2	0.1	0.2	0.1

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 8. Means squares and significance levels for the ANOVA for agronomic traits, Hallock, MN, 2013.

Source	DF	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	4.3 x 10^{-11}	1.0 x 10^{-12}	0.2	230.8**	4.3	5.2*	1.1
A [Cultivar]	11	2.1 x 10^{-12}***	9.1 x 10^{-12}**	1.9***	310.4***	29.9***	17.2***	5.6***
Error (a)	22	3.7 x 10^{-11}***	2.3 x 10^{-12}***	0.4***	31.8***	3.3***	1.3***	0.6***
B [Seeding Rate]	4	1.1 x 10^{-14}***	6.6 x 10^{-12}***	68.7***	38.4***	17.3***	1.0***	0.6***
A * B	44	4.1 x 10^{-11}***	2.3 x 10^{-12}***	0.5***	30.5***	4.1***	1.2***	0.5***
Error (b)	96	1.2 x 10^{-11}	6.7 x 10^{-11}	0.2	5.7	0.4	0.1	0.1

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 9. Means squares and significance levels for the ANOVA for agronomic traits in the optimum planting date, Lamberton, MN, 2014.

Source	DF	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Protein	Mg ha^{-1}
Rep	2	8.1 x 10^{-11}*	6.0 x 10^{-12}*	4.0***	2.0	3.5*	0.3
A [Cultivar]	11	4.8 x 10^{-11}	8.2 x 10^{-12}***	1.4**	273.1***	9.0***	3.8***
Error (a)	22	2.2 x 10^{-11}	1.5 x 10^{-12}**	0.4	38.5***	0.6***	0.5***
B [Seeding Rate]	4	3.4 x 10^{-13}***	3.0 x 10^{-13}***	17.7***	10.4	0.0	1.7***
A * B	44	2.4 x 10^{-11}	5.8 x 10^{-11}	0.3	5.4	0.1	0.1
Error (b)	96	2.3 x 10^{-11}	6.3 x 10^{-11}	0.3	5.7	0.1	0.1

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 10. Means squares and significance levels for the ANOVA for agronomic traits in the late planting date, Lamberton, MN, 2014.

Source	DF	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Protein	Mg ha^{-1}
Rep	2	8.0 x 10^{-11}	1.5 x 10^{-12}	2.7	145.2	0.7	0.8
A [Cultivar]	11	6.8 x 10^{-11}	7.7 x 10^{-12}*	4.0	241.5**	9.1***	3.0
Error (a)	22	5.0 x 10^{-11}	3.0 x 10^{-12}***	2.6*	58.1***	0.4***	1.8***
B [Seeding Rate]	4	2.1 x 10^{-13}***	1.0 x 10^{-13}***	61.6***	118.1***	0.8***	1.3***
A * B	44	2.9 x 10^{-11}	5.0 x 10^{-11}	1.3	22.7***	0.2	0.2
Error (b)	96	3.5 x 10^{-11}	5.0 x 10^{-11}	1.5	10.1	0.1	0.2

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 11. Means squares and significance levels for the ANOVA for agronomic traits, Kimball, MN, 2014.

Source	DF	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	3.3 x 10^{-11}	5.2 x 10^{-10}	0.1	9.7	3.1	3.7	1.4
A [Cultivar]	11	7.9 x 10^{-11}**	3.0 x 10^{-12}***	0.5	310.5***	47.4***	13.2***	5.8***
Error (a)	22	2.4 x 10^{-11}	4.4 x 10^{-11}	0.3*	21.6***	2.5***	1.8***	1.0***
B [Seeding Rate]	4	4.9 x 10^{-13}***	4.1 x 10^{-12}***	32.1***	9.2*	10.7***	0.1	0.3
A * B	44	3.1 x 10^{-11}**	3.3 x 10^{-11}	0.2	3.9	2.0***	0.1	0.5**
Error (b)	96	1.6 x 10^{-11}	3.4 x 10^{-11}	0.2	3.7	0.2	0.1	0.3

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 12. Means squares and significance levels for the ANOVA for agronomic traits in the optimum planting date, Prosper, ND, 2014.

Source	DF	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	1.4 x 10^{-12}*	9.6 x 10^{-11}	0.3	90.1**	30.2**	61.6**	0.2
A [Cultivar]	11	1.1 x 10^{-12}*	7.8 x 10^{-12}***	1.2***	213.8***	31.2***	5.7	3.7***
Error (a)	22	4.1 x 10^{-11}	4.5 x 10^{-11}	0.2	8.3*	4.2***	4.8***	0.2***
B [Seeding Rate]	4	4.5 x 10^{-13}***	1.3 x 10-12	37.9***	9.6	2.8***	0.2	0.1
A * B	44	2.2 x 10^{-11}	5.4 x 10^{-11}	0.2	6.7	0.8**	0.2	0.1*
Error (b)	96	3.0 x 10^{-11}	5.7 x 10^{-11}	0.2	4.5	0.4	0.2	0.0

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 13. Means squares and significance levels for the ANOVA for agronomic traits in the late planting date, Prosper, ND, 2014.

Source	DF	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	2.9 x 10^{-12}**	1.2 x 10^{-11}	4.2	120.3*	3.9	26.4**	0.0
A [Cultivar]	11	1.6 x 10^{-12}**	3.3 x 10^{-12}**	6.1**	425.9***	31.3***	5.5	5.1***
Error (a)	22	3.6 x 10^{-11}	7.2 x 10^{-11}	1.5*	25.4***	2.8***	4.3**	0.1*
B [Seeding Rate]	4	3.0 x 10^{-13}***	4.9 x 10^{-12}***	88.2***	38.0***	22.4***	0.1	0.8***
A * B	44	3.1 x 10^{-11}	7.2 x 10^{-11}	0.7	5.5	2.6***	0.1	0.1
Error (b)	96	2.5 x 10^{-11}	5.9 x 10^{-11}	0.8	4.7	0.7	0.1	0.1

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 14. Means squares and significance levels for the ANOVA for agronomic traits, Perley, MN, 2014.

Source	DF	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	7.4 x 10^{-10}	1.4 x 10^{-12}	0.4	26.6	5.4	0.4	1.8
A [Cultivar]	11	4.9 x 10^{-11}	5.7 x 10^{-12}***	0.8***	361.2***	18.6***	15.9***	5.1***
Error (a)	22	3.1 x 10^{-11}	5.5 x 10^{-11}	0.2	22.2***	1.7***	2.2***	0.9***
B [Seeding Rate]	4	5.7 x 10^{-13}***	4.8 x 10^{-12}***	21.7***	6.9	3.0***	0.0	0.2
A * B	44	2.9 x 10^{-11}	3.3 x 10^{-11}	0.2*	8.5***	0.9*	0.1	0.1*
Error (b)	96	2.3 x 10^{-11}	3.5 x 10^{-11}	0.1	3.7	0.5	0.1	0.1

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 15. Means squares and significance levels for the ANOVA for agronomic traits in the optimum planting date, Crookston, MN, 2014.

Source	DF	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	2.2 x 10^{-11}	6.2 x 10^{-12}***	0.4*	49.7	1.5	7.2***	12.6***
A [Cultivar]	11	1.1 x 10^{-12}***	5.3 x 10^{-12}***	0.4**	255.2*	7.8*	13.5***	4.8***
Error (a)	22	1.5 x 10^{-11}	5.8 x 10^{-11}	0.1	108.4***	2.8***	0.6**	0.9***
B [Seeding Rate]	4	5.5 x 10^{-13}***	8.9 x 10^{-12}***	20.0***	9.0	0.2	0.5	0.3
A * B	44	2.7 x 10^{-11}	4.7 x 10^{-11}	0.1*	8.4	0.2	0.2	0.2
Error (b)	96	2.2 x 10^{-11}	5.3 x 10^{-11}	0.1	7.5	0.2	0.3	0.2

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 16. Means squares and significance levels for the ANOVA for agronomic traits in the late planting date, Crookston, MN, 2014.

Source	DF	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	7.2 x 10^{-11}*	4.0 x 10^{-12}*	0.2	576.1***	3.4	0.4	6.6**
A [Cultivar]	11	7.4 x 10^{-11}**	2.8 x 10^{-12}**	0.3**	320.6***	4.0	4.7***	1.1
Error (a)	22	1.6 x 10^{-11}	8.0 x 10^{-11}*	0.1	36.5***	2.3***	0.8**	0.9***
B [Seeding Rate]	4	7.3 x 10^{-13}***	6.9 x 10^{-12}***	12.2***	14.7	0.9**	0.6	0.7***
A * B	44	4.6 x 10^{-11}	9.5 x 10^{-11}**	0.1	10.3*	0.3	0.3	0.2*
Error (b)	96	4.0 x 10^{-11}	4.5 x 10^{-11}	0.1	6.8	0.2	0.3	0.1

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 17. Means squares and significance levels for the ANOVA for agronomic traits, Hallock, MN, 2014.

Source	DF	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	8.7 x 10^{-11}	3.0 x 10^{-11}	0.8*	2.0	0.5	0.4	0.2
A [Cultivar]	11	7.9 x 10^{-11}*	3.7 x 10^{-12}***	1.3***	557.1***	1.3	5.6	3.6*
Error (a)	22	3.4 x 10^{-11}	5.5 x 10^{-11}	0.2	31.3***	0.9***	7.4***	1.4***
B [Seeding Rate]	4	5.7 x 10^{-13}***	3.7 x 10^{-12}***	34.6***	6.5	0.3	0.1	0.8***
A * B	44	4.3 x 10^{-11}	5.3 x 10^{-11}*	0.2	5.0	0.3***	0.1	0.1*
Error (b)	96	3.1 x 10^{-11}	3.3 x 10^{-11}	0.3	5.8	0.1	0.1	0.0

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 18. Means squares and significance levels for the ANOVA for agronomic traits in the optimum planting date, Lamberton, MN, 2015.

Source	DF	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Mg ha^{-1}
Rep	2	5.9 x 10^{-11}	3.4 x 10^{-11}	1.7	87	0.0	3.9***
A [Cultivar]	11	3.2 x 10^{-11}	4.3 x 10^{-12}	2.6*	278.4***	5.4***	7.8***
Error (a)	22	2.3 x 10^{-11}	3.2 x 10^{-12}*	0.9	26.4*	1.1***	0.4***
B [Seeding Rate]	4	2.8 x 10^{-13}***	2.1 x 10^{-13}***	42.0***	34.3***	0.8**	3.7***
A * B	44	2.0 x 10^{-11}	1.7 x 10^{-12}	0.7	4.6	0.3**	0.1
Error (b)	96	2.3 x 10^{-11}	1.9 x 10^{-12}	0.7	4.9	0.2	0.1

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 19. Means squares and significance levels for the ANOVA for agronomic traits in the late planting date, Lamberton, MN, 2015.

Source	DF	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Mg ha^{-1}
Rep	2	6.0 x 10^{-11}*	8.3 x 10^{-12}	9.2***	158.8***	4.2***	4.7***
A [Cultivar]	11	4.6 x 10^{-13}***	2.4 x 10^{-13}***	98.0***	11.2	3.4***	0.8**
Error (a)	22	2.6 x 10^{-11}	2.8 x 10^{-12}	2.1**	8.7	0.8***	0.2
B [Seeding Rate]	4	4.9 x 10^{-11}	5.1 x 10^{-12}	2.5	4.8	0.6	0.3
A * B	44	2.5 x 10^{-11}	5.3 x 10^{-12}*	1.4	13.4**	0.3***	0.5***
Error (b)	96	3.5 x 10^{-11}	5.6 x 10^{-12}	1.1	6.0	0.1	0.2

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 20. Means squares and significance levels for the ANOVA for agronomic traits, Kimball, MN, 2015.

Source	DF	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	1.4×10^{-11}	1.0×10^{-12}	0.5	71.4	17.1**	1.6*	4.6***
A [Cultivar]	11	6.0×10^{-11}	6.7×10^{-12}**	1.6*	762.0***	43.6***	7.7***	3.0***
Error (a)	22	3.8×10^{-11}*	1.6×10^{-12}***	0.7*	21.7***	2.8**	0.4	0.2**
B [Seeding Rate]	4	3.2×10^{-13}***	5.8×10^{-12}***	30.5***	27.8**	36.9***	1.4***	2.7***
A * B	44	2.1×10^{-11}	9.0×10^{-11}	0.4	6.6	3.6***	0.3	0.2***
Error (b)	96	1.9×10^{-11}	6.4×10^{-11}	0.4	6.5	1.3	0.3	0.1

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 21. Means squares and significance levels for the ANOVA for agronomic traits in the optimum planting date, Prosper, ND, 2015.

Source	DF	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	4.6×10^{-11}	2.2×10^{-12}	0.2	27.6	4.8	2.4**	1.4
A [Cultivar]	11	1.8×10^{-11}	4.9×10^{-12}**	1.4**	77.1***	34.4***	10.0***	3.4***
Error (a)	22	1.8×10^{-11}	1.2×10^{-12}	0.4	13.3***	2.8***	0.3***	0.5***
B [Seeding Rate]	4	2.2×10^{-13}***	9.1×10^{-12}***	29.7***	13.1*	26.0***	0.1	0.6***
A * B	44	2.1×10^{-11}	7.1×10^{-11}	0.4	5.6	1.1*	0.1*	0.2*
Error (b)	96	1.7×10^{-11}	7.7×10^{-11}	0.3	5.2	0.7	0.1	0.1

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 22. Means squares and significance levels for the ANOVA for agronomic traits in the late planting date, Prosper, ND, 2015.

Source	DF	Population	Spikes ha^{-1}	Stems $Plant^{-1}$	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	2.2 x 10^{-12}*	2.0 x 10^{-12}	0.7	6.2	0.7	0.1	0.1
A [Cultivar]	11	6.8 x 10^{-11}	5.5 x 10^{-12}***	1.2**	413.1***	29.2***	5.9***	1.4***
Error (a)	22	5.2 x 10^{-11}	8.4 x 10^{-11}	0.3	30.0***	1.0**	0.1*	0.1***
B [Seeding Rate]	4	5.0 x 10^{-13}***	7.1 x 10^{-12}***	26.2***	18.6*	8.3***	0.0	0.4***
A * B	44	3.0 x 10^{-11}	8.5 x 10^{-11}	0.5	9.8	1.0**	0.1	0.1*
Error (b)	96	6.6 x 10^{-11}	5.8 x 10^{-11}	0.3	7.5	0.5	0.0	0.0

*** Significant at the 0.001 probability level.
** Significant at the 0.01 probability level.
* Significant at the 0.05 probability level.

Table A 23. Means squares and significance levels for the ANOVA for agronomic traits, Perley, MN, 2015.

Source	DF	Population	Spikes ha^{-1}	Stems $Plant^{-1}$	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	3.3 x 10^{-11}	6.0 x 10^{-12}	0.5	40.7	2.6	0.4	1.2
A [Cultivar]	11	3.4 x 10^{-11}*	6.6 x 10^{-12}*	2.2***	435.0***	19.1***	7.9***	2.0**
Error (a)	22	1.3 x 10^{-11}	2.7 x 10^{-12}**	0.4*	21.5***	1.9***	0.4***	0.6***
B [Seeding Rate]	4	5.7 x 10^{-13}***	2.2 x 10^{-13}***	36.1***	2.4	14.5***	0.1	0.7*
A * B	44	1.7 x 10^{-11}	1.2 x 10^{-12}	0.3	10.5***	2.8***	0.1	0.4*
Error (b)	96	2.0 x 10^{-11}	1.2 x 10^{-12}	0.2	4.4	0.6	0.1	0.2

*** Significant at the 0.001 probability level.
** Significant at the 0.01 probability level.
* Significant at the 0.05 probability level.

Table A 24. Means squares and significance levels for the ANOVA for agronomic traits in the optimum planting date, Crookston, MN, 2015.

Source	DF	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	7.0×10^{-10}	1.0×10^{-12}	0.4	205.4**	7.6	1.2	0.6
A [Cultivar]	11	1.3×10^{-11}	9.5×10^{-12}***	1.6**	296.5***	29.5***	6.0***	1.1***
Error (a)	22	2.2×10^{-11}	1.6×10^{-12}	0.4	26.2***	4.0***	0.4***	0.2
B [Seeding Rate]	4	4.3×10^{-13}***	1.5×10^{-13}***	32.2***	2.0	3.9*	0.0	0.4*
A * B	44	2.2×10^{-11}	1.4×10^{-12}	0.6	5.7	1.5	0.1	0.2*
Error (b)	96	1.7×10^{-11}	1.0×10^{-12}	0.4	5.2	1.4	0.1	0.1

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 25. Means squares and significance levels for the ANOVA for agronomic traits in the late planting date, Crookston, MN, 2015.

Source	DF	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	2.1×10^{-11}	2.4×10^{-12}	0.3	22.6	5.9*	1.2*	0.6
A [Cultivar]	11	2.2×10^{-11}	3.8×10^{-12}**	0.8*	277.4***	11.9***	5.9***	1.2**
Error (a)	22	4.9×10^{-11}	1.1×10^{-12}	0.3	16.0*	1.5**	0.2*	0.3*
B [Seeding Rate]	4	3.9×10^{-13}***	6.8×10^{-12}***	21.2***	15.8	3.9***	0.0	0.6**
A * B	44	6.9×10^{-11}	9.4×10^{-11}	0.5	6.8	2.0***	0.1	0.2
Error (b)	96	7.3×10^{-11}	8.4×10^{-11}	0.4	8.6	0.6	0.1	0.1

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 26. Means squares and significance levels for the ANOVA for agronomic traits, Hallock, MN, 2015.

Source	DF	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	2.6 x 10^{-11}	7.8 x 10^{-12}***	1.0**	1.2	7.0*	8.9***	7.1***
A [Cultivar]	11	4.4 x 10^{-11}**	7.1 x 10^{-12}***	1.1***	635.0***	19.6***	10.4***	1.6**
Error (a)	22	1.3 x 10^{-11}	5.6 x 10^{-11}	0.1	14.1***	1.4***	0.9***	0.5***
B [Seeding Rate]	4	5.9 x 10^{-13}***	1.6 x 10^{-13}***	29.0***	27.5***	3.0***	0.3*	0.2
A * B	44	1.8 x 10^{-11}	5.4 x 10^{-11}	0.1	5.5**	1.3***	0.1	0.2**
Error (b)	96	2.9 x 10^{-11}	5.8 x 10^{-11}	0.1	3.5	0.3	0.1	0.1

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 27. Means squares and significance levels for the ANOVA for agronomic traits, combined over 21 environments, ND and MN, 2013-2015.

Source	DF	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Protein	Mg ha^{-1}
Trial	20	1.6 x 10^{-13}***	1.6 x 10^{-14}***	59.1***	5299.7***	146.4***	58.5***	173.0***
Rep(Trial)	42	5.3 x 10^{-11}*	2.9 x 10^{-12}***	0.8*	96.5**	4.8	6.8***	2.3***
A [Cultivar]	11	3.2 x 10^{-12}***	7.1 x 10^{-13}***	14.8***	4413.7***	159.4***	106.0***	22.5***
Error (a)	682	3.5 x 10^{-11}*	1.5 x 10^{-12}***	0.5***	53.7***	4.4***	2.1***	1.1***
B [Seeding Rate]	4	1.1 x 10^{-15}***	1.6 x 10^{-14}***	630.5***	15.0	88.1***	1.3***	6.8***
A * B	44	3.7 x 10^{-11}	1.5 x 10^{-12}**	1.2***	24.7***	8.2***	0.6***	0.7***
Error (b)	3153	3.0 x 10^{-11}	8.7 x 10^{-11}***	0.4	6.5	0.6	0.3	0.1

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 28. Means squares and significance levels for the ANOVA for agronomic traits, Crookston, MN, 2013.

Source	df	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	2.9 x 10^{-11}	2.4 x 10^{-12}	0.0	373.1	0.6	5.2	3.4
A [Planting Date]	1	3.1 x 10^{-12}*	1.9 x 10^{-12}	3.4	104.5	6.9	2.8	5.5*
Error (a)	2	1.1 x 10^{-11}***	5.0 x 10^{-11}	0.5*	27.1	1.7	10.0***	0.3
B [Cultivar]	11	1.1 x 10^{-14}***	2.9 x 10^{-12}***	0.8***	349.0***	7.7***	15.4***	5.0***
A * B	11	2.1 x 10^{-12}	1.0 x 10^{-12}*	0.1	62.3***	3.0***	1.3*	0.3
Error (b)	44	1.8 x 10^{-11}	4.8 x 10^{-11}	0.1	13.6***	0.6***	0.5***	0.4***
C [Seeding Rate]	4	1.1 x 10^{-11}***	8.8 x 10^{-12}***	28.5***	6.3	4.0***	0.6***	1.2***
A * C	4	4.8 x 10^{-11}***	5.8 x 10^{-11}	0.0	5.6	1.0***	0.5*	0.1
B * C	44	3.8 x 10^{-12}	1.0 x 10^{-12}	0.2	16.8***	1.4***	0.5***	0.1***
A * B * C	44	3.0 x 10^{-11}	6.7 x 10^{-11}	0.1	5.1	0.7***	0.2	0.1
Error (c)	191	3.1 x 10^{-11}	7.4 x 10^{-11}	0.2	6.2	0.2***	0.2	0.1

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

*   Significant at the 0.05 probability level.

Table A 29. Means squares and significance levels for the ANOVA for agronomic traits, Lamberton, MN, 2014.

Source	df	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Protein	Mg ha^{-1}
Rep	2	8.2 x 10^{-14}	5.3 x 10^{-14}	0.9	79.5	3.5	0.1
A [Planting Date]	1	1.0 x 10^{-11}*	6.3 x 10^{-13}**	15.7	1.1	1.7	77.6*
Error (a)	2	1.5 x 10^{-11}*	2.2 x 10^{-12}	5.8*	67.7	0.6	1.0
B [Cultivar]	11	8.1 x 10^{-13}*	1.4 x 10^{-13}***	4.6**	352.6***	17.2***	5***
A * B	11	3.5 x 10^{-12}	1.9 x 10^{-12}	0.8	162.0**	0.9	1.9
Error (b)	44	3.6 x 10^{-11}	2.3 x 10^{-11}***	1.5*	48.3***	0.5***	1.1***
C [Seeding Rate]	4	5.4 x 10^{-11}***	3.7 x 10^{-11}***	71.3***	47.7***	0.3*	2.8***
A * C	4	1.0 x 10^{-10}**	2.9 x 10^{-12}***	8.0***	80.8***	0.5***	0.1
B * C	44	2.1 x 10^{-12}	4.6 x 10^{-12}	0.8	14.0**	0.1	0.2
A * B * C	44	3.2 x 10^{-11}	6.3 x 10^{-12}	0.7	14.1**	0.1	0.1
Error (c)	191	2.9 x 10^{-11}	5.7 x 10^{-11}	0.9	7.9	0.1	0.2

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 30. Means squares and significance levels for the ANOVA for agronomic traits, Prosper, ND, 2014.

Source	df	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	2.2 x 10^{-13}	8.0 x 10^{-14}	1.9	200.5*	17.9	5.4	0.1
A [Planting Date]	1	8.6 x 10^{-12}*	1.4 x 10^{-12}**	57.8*	650.7*	2088.0**	61.6	237.2***
Error (a)	2	2.1 x 10^{-12}*	2.8 x 10^{-12}	2.5	10.0	16.2*	82.9***	0.1
B [Cultivar]	11	1.4 x 10^{-13}**	8.9 x 10^{-12}***	5.2***	583.9***	28.9***	7.7	7.4***
A * B	11	1.4 x 10^{-11}**	2.2 x 10^{-12}***	2.0*	55.9**	33.6***	3.5	1.4***
Error (b)	44	3.9 x 10^{-11}	5.8 x 10^{-11}	0.8**	16.9***	3.5***	4.5***	0.1***
C [Seeding Rate]	4	7.4 x 10^{-11}***	4.2 x 10^{-11}***	120.4***	32.9***	20.0***	0.2	0.6***
A * C	4	9.6 x 10^{-12}**	2.0 x 10^{-11}**	5.7***	14.8*	5.2***	0.1	0.2**
B * C	44	2.7 x 10^{-12}	6.0 x 10^{-11}	0.6	7.0*	2.2***	0.2	0.1
A * B * C	44	2.6 x 10^{-11}	6.6 x 10^{-11}	0.3	5.2	1.2***	0.1	0.8*
Error (c)	191	2.7 x 10^{-11}	5.8 x 10^{-11}	0.5	4.6	0.6	0.1	0.1

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

*   Significant at the 0.05 probability level.

Table A 31. Means squares and significance levels for the ANOVA for agronomic traits, Crookston, MN, 2014.

Source	df	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	5.7×10^{-13}	2.8×10^{-12}	0.2	471.2	4.7*	5.5	18.2
A [Planting Date]	1	1.9×10^{-12}*	9.2×10^{-12}	10.5*	3.2	18.7**	1.7	3.5
Error (a)	2	3.7×10^{-11}	7.4×10^{-12}***	0.4*	154.5	0.2	2.3*	1.0
B [Cultivar]	11	1.6×10^{-14}***	6.3×10^{-13}***	0.5***	469.2***	6.6*	16.1***	3.5***
A * B	11	2.4×10^{-11}	1.7×10^{-11}*	0.2*	106.6	5.2	2.1**	2.4*
Error (b)	44	1.6×10^{-11}	6.9×10^{-11}	0.1	72.5***	2.6***	0.7***	0.9***
C [Seeding Rate]	4	1.3×10^{-11}***	1.5×10^{-11}***	31.6***	19.0*	0.7**	0.3	0.8***
A * C	4	8.9×10^{-11}*	8.9×10^{-12}	0.6***	4.7	0.4	0.5	0.2
B * C	44	3.9×10^{-11}	7.6×10^{-12}*	0.2*	9.3	0.2	0.3	0.2
A * B * C	44	3.4×10^{-11}	6.6×10^{-11}	0.1	9.4	0.2	0.2	0.2*
Error (c)	191	3.1×10^{-11}	4.9×10^{-11}	0.1	7.1	0.2	0.3	0.2

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 32. Means squares and significance levels for the ANOVA for agronomic traits, Lamberton, MN, 2015.

Source	df	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Mg ha^{-1}
Rep	2	8.7 x 10^{-10}	1.9 x 10^{-12}	0.1	33.1	0.3	1.1
A [Planting Date]	1	9.9 x 10^{-11}	1.2 x 10^{-14}*	34.4	780.3	2.5	102.4*
Error (a)	2	9.9 x 10^{-11}*	3.5 x 10^{-12}	4.1*	58.8	0.4	3.2**
B [Cultivar]	11	6.3 x 10^{-11}*	1.0 x 10^{-13}*	9.1***	374.6***	9.3***	11.7***
A * B	11	2.9 x 10^{-11}	2.6 x 10^{-12}	2.7*	62.6**	0.4	0.7
Error (b)	44	2.4 x 10^{-11}	3.8 x 10^{-12}*	1.2	19.9***	0.7***	0.4***
C [Seeding Rate]	4	7.2 x 10^{-13}***	4.5 x 10^{-13}***	133.6***	36.4***	3.5***	3.8***
A * C	4	1.6 x 10^{-12}***	4.7 x 10^{-11}	6.4***	9.1	0.7***	0.7**
B * C	44	1.7 x 10^{-11}	2.5 x 10^{-12}	1.8***	5.8	0.8***	0.2
A * B * C	44	2.8 x 10^{-11}	1.9 x 10^{-12}	1.0	7.5	0.3***	0.1
Error (c)	191	2.9 x 10^{-11}	2.2 x 10^{-12}	0.9	5.4	0.1	0.2

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

*   Significant at the 0.05 probability level.

Table A 33. Means squares and significance levels for the ANOVA for agronomic traits, Prosper, ND, 2015.

Source	df	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	1.8×10^{-12}	2.8×10^{-12}	0.3	21.3	1.0	0.9	1.1
A [Planting Date]	1	4.0×10^{-13}	2.1×10^{-12}	31.7*	195.3	555.0**	382.3**	100.0**
Error (a)	2	8.1×10^{-11}	1.5×10^{-12}	0.6	12.5	4.4	1.6***	0.3
B [Cultivar]	11	5.7×10^{-11}	9.5×10^{-12}***	2.4***	333.8***	48.7***	15.1***	3.6***
A * B	11	2.8×10^{-11}	8.4×10^{-11}	0.1	156.7***	14.9***	0.9***	1.3***
Error (b)	44	3.5×10^{-11}	1.0×10^{-12}*	0.4	21.6***	1.9***	0.2***	0.3***
C [Seeding Rate]	4	6.9×10^{-13}***	1.6×10^{-13}***	55.8***	24.6**	30.7***	0.0	0.2**
A * C	4	3.1×10^{-12}***	7.6×10^{-10}	0.1	7.3	3.5***	0.1	0.7***
B * C	44	2.9×10^{-11}	2.4×10^{-11}	0.4	7.7	1.2	0.1	0.1**
A * B * C	44	2.2×10^{-11}	1.1×10^{-12}*	0.5*	7.8	0.8	0.1*	0.1**
Error (c)	191	4.2×10^{-11}	6.7×10^{-11}	0.3	6.4	0.6	0.1	0.1

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

Table A 34. Means squares and significance levels for the ANOVA for agronomic traits, Crookston, MN, 2015.

Source	df	Population	Spikes ha^{-1}	Stems Plant^{-1}	Height	Lodging	Protein	Mg ha^{-1}
Rep	2	3.1 x 10^{-10}	9.0 x 10^{-11}	0.3	172.2	2.2	1.4	1.0
A [Planting Date]	1	4.3 x 10^{-12}	2.6 x 10^{-13}	11.3*	58.1	8.9	23.4*	84.6**
Error (a)	2	2.5 x 10^{-11}	2.5 x 10^{-12}	0.3	54.6	11.4*	1.0*	0.2
B [Cultivar]	11	2.4 x 10^{-11}	1.2 x 10^{-13}***	2.2***	428.7***	31.9***	11.3***	1.7***
A * B	11	1.1 x 10^{-11}	8.1 x 10^{-11}	0.2	145.2***	9.5***	0.5	0.6*
Error (b)	44	3.5 x 10^{-11}	1.3 x 10^{-12}	0.3	21.1***	2.8***	0.3***	0.2*
C [Seeding Rate]	4	8.2 x 10^{-13}***	2.1 x 10^{-13}***	52.7***	7.0	7.5***	0.0	1.0***
A * C	4	4.2 x 10^{-11}	1.0 x 10^{-12}	0.6	11.0	0.2	0.0	0.0
B * C	44	4.5 x 10^{-11}	9.7 x 10^{-11}	0.7*	8.1	1.8**	0.2*	0.3**
A * B * C	44	4.6 x 10^{-11}	1.4 x 10^{-12}	0.5	4.4	1.7**	0.1	0.1
Error (c)	191	4.5 x 10^{-11}	9.4 x 10^{-11}	0.4	6.9	1.0	0.1	0.1

*** Significant at the 0.001 probability level.

** Significant at the 0.01 probability level.

* Significant at the 0.05 probability level.

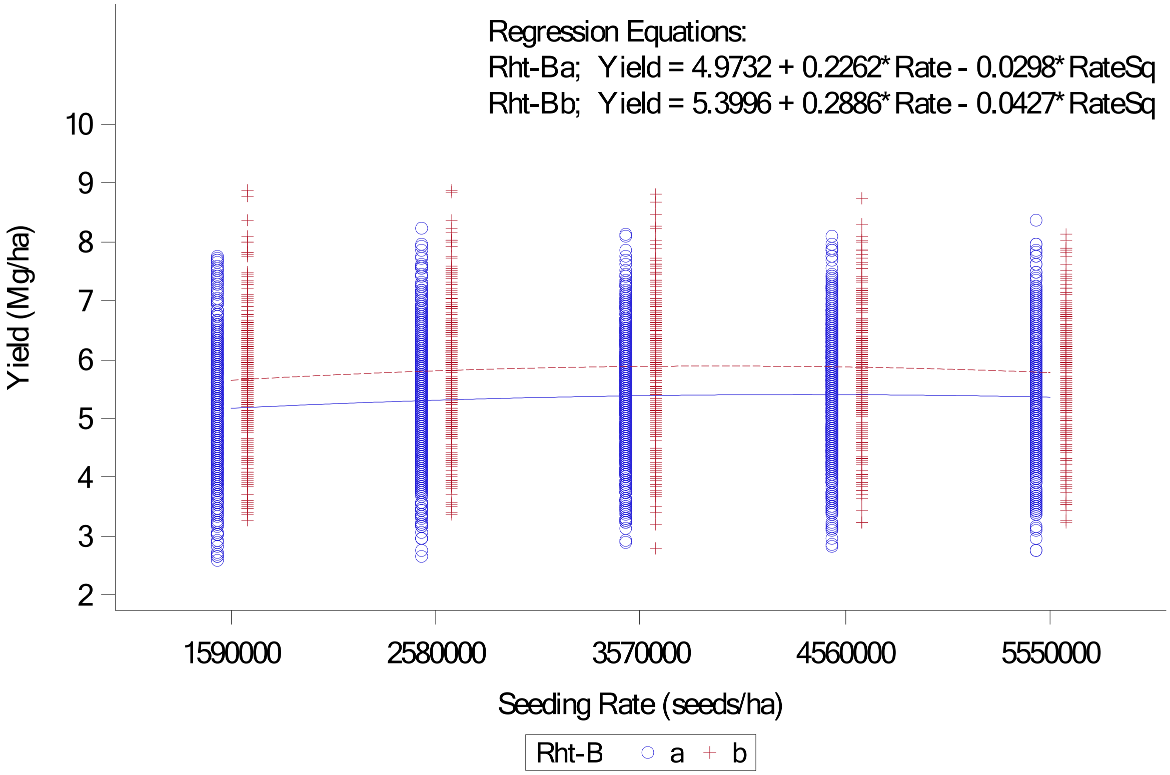

Figure A 1. Yield response curves to seeding rate for *Rht-B* alleles combined over 21 environments, ND and MN, 2013-2015.

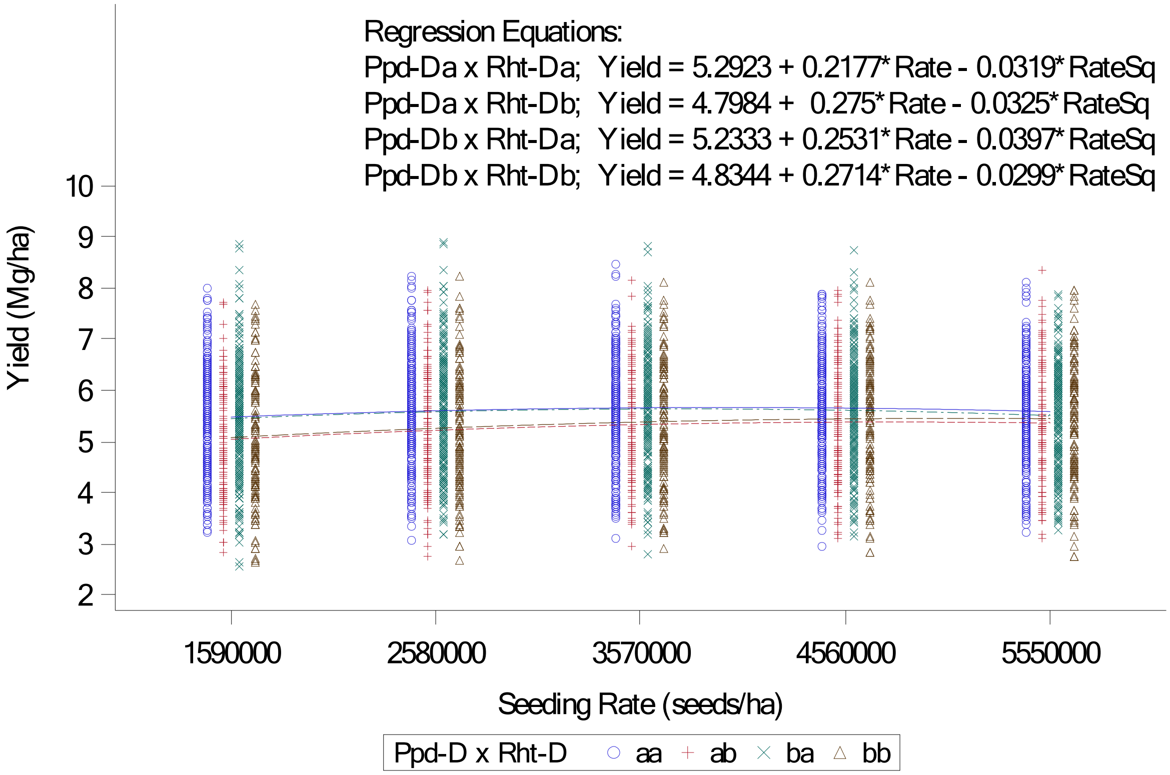

Figure A 2. Yield response curves to seeding rate for the interaction between *Rht-D* and *Ppd-D* alleles combined over 21 environments, ND and MN, 2013-2015.

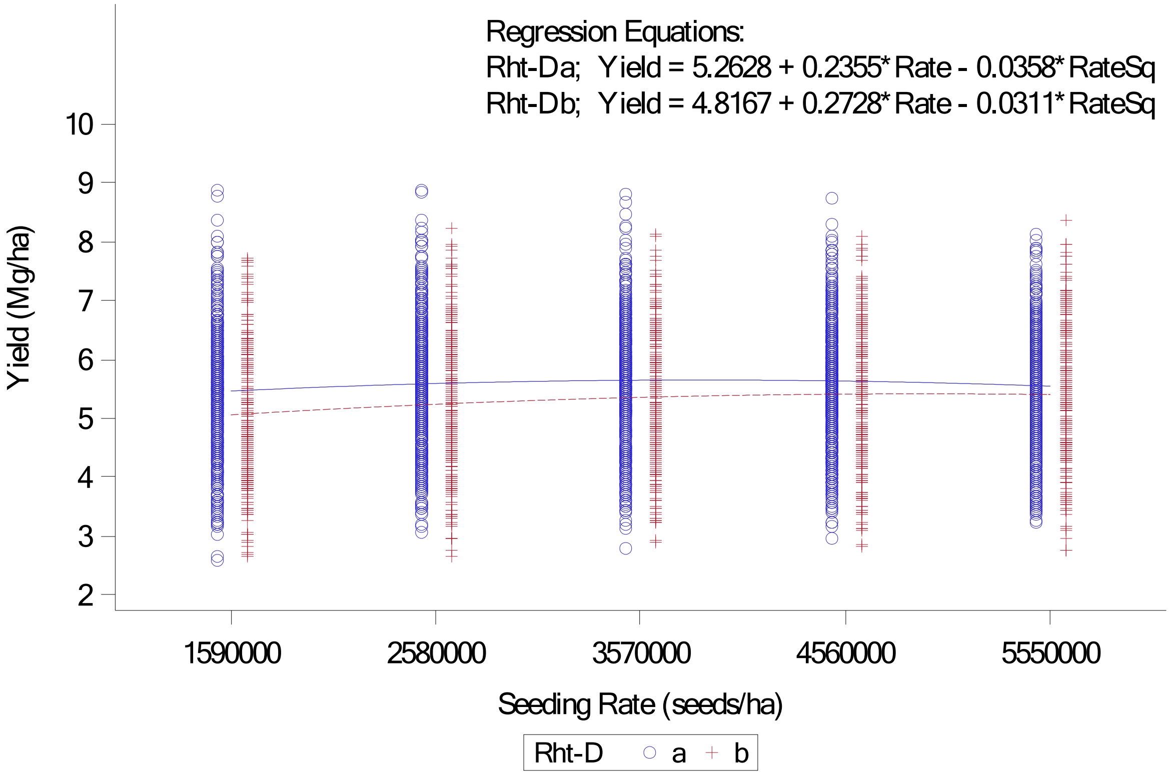

Figure A 3. Yield response curves to seeding rate for *Rht-D* alleles combined over 21 environments, ND and MN, 2013-2015.

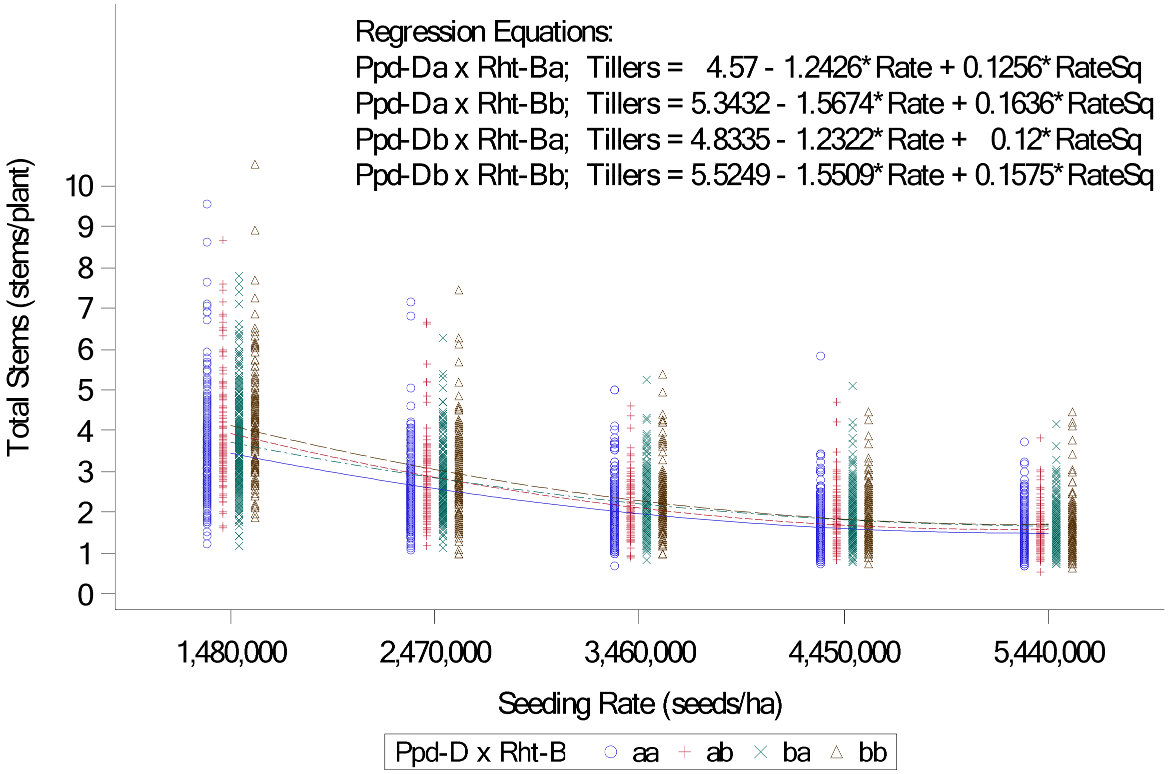

Figure A 4. Tillering response curves to seeding rate for the interaction between *Rht-B* and *Ppd-D* alleles combined over 21 environments, ND and MN, 2013-2015.

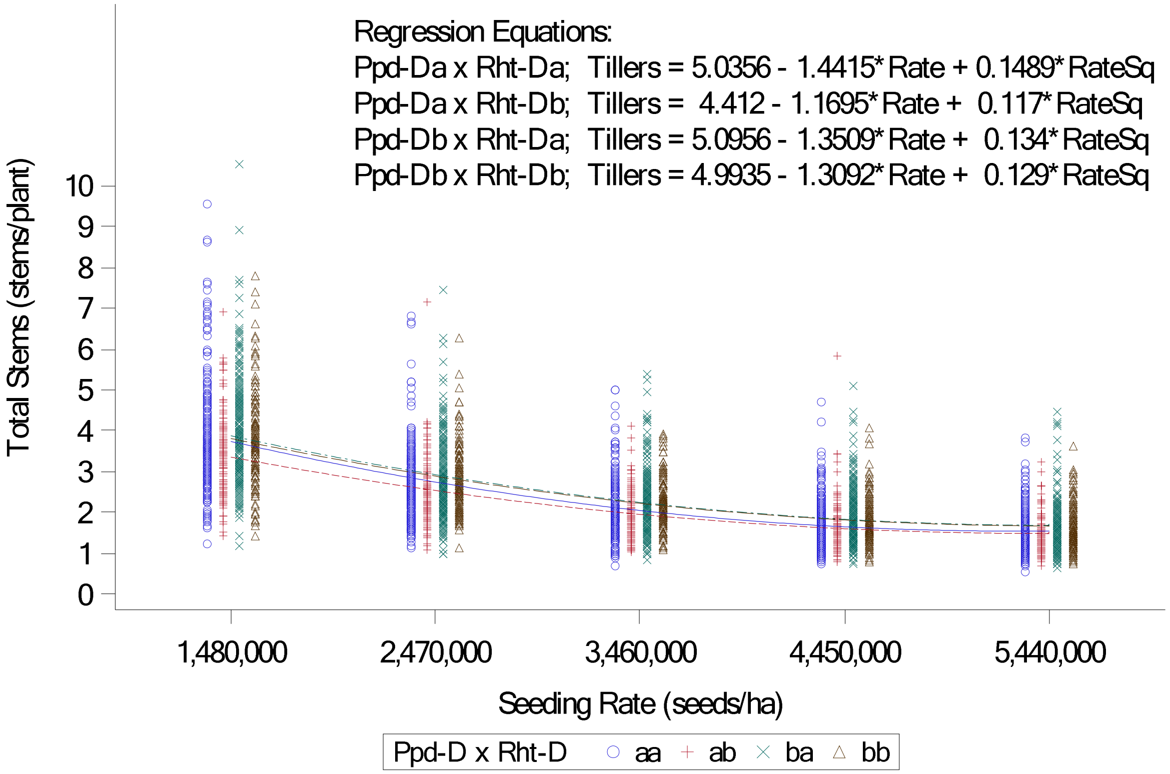

Figure A 5. Tillering response curves to seeding rate for the interaction between *Rht-D* and *Ppd-D* alleles combined over 21 environments, ND and MN, 2013-2015.

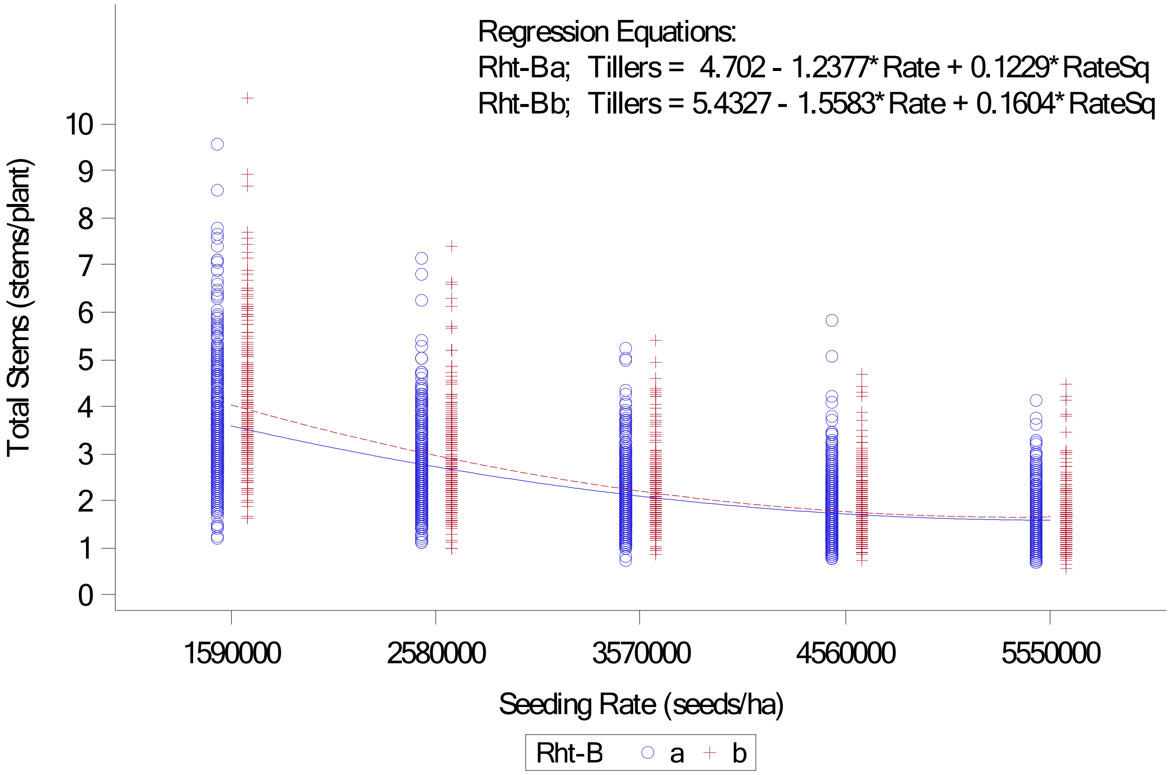

Figure A 6. Tillering response curves to seeding rate for *Rht-B* alleles combined over 21 environments, ND and MN, 2013-2015.

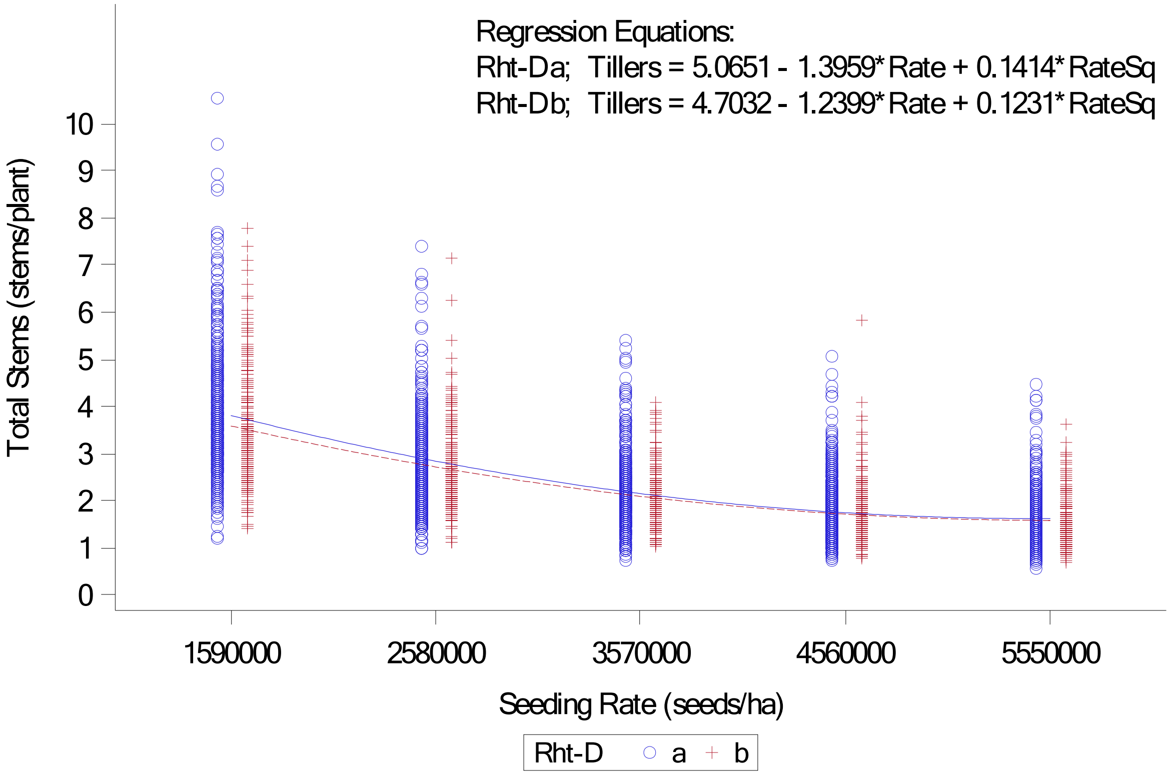

Figure A 7. Tillering response curves to seeding rate for *Rht-D* alleles combined over 21 environments, ND and MN, 2013-2015.

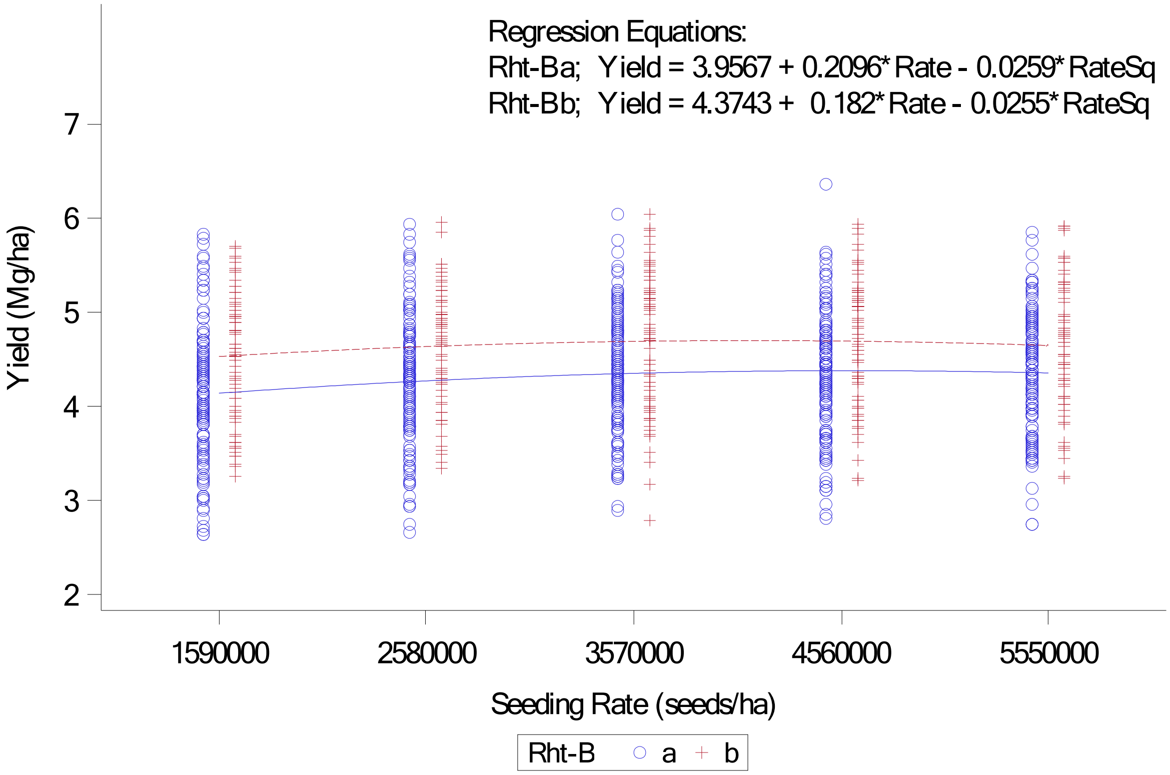

Figure A 8. Yield response curves to seeding rate for *Rht-B* alleles combined over the six lowest yielding environments, ND and MN, 2013-2015.

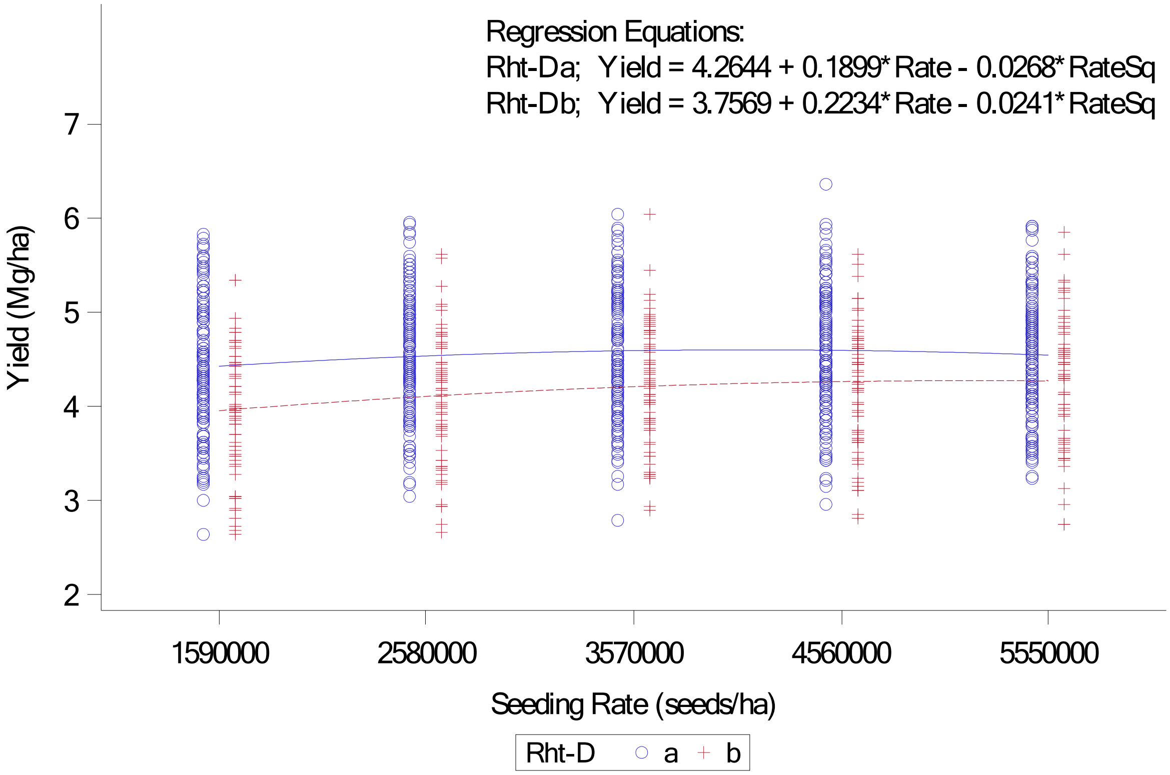

Figure A 9. Yield response curves to seeding rate for *Rht-D* alleles combined over the six lowest yielding environments, ND and MN, 2013-2015.