Tillering Response in HRSW Cultivars as Influenced by Planting Date, Plant Population, and Genetic Background

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Introduction

Tillering in hard red spring wheat (HRSW) is dependent on many genetic, biotic, and abiotic factors. Space planted trials show the full genetic potential for tillering capacity.

Objectives

This research explores the relationship between known genes for plant stature and photoperiod sensitivity with space planted trials to predict tillering in HRSW. It is a small part of a larger set of trials with the objective to predict seeding rate responses in solid-seeded wheat production at different planting dates with known genes for plant stature and photoperiod sensitivity.

Materials and Methods

Field experiments were conducted from 2014-2015 at the Northwest Research and Outreach Center in Crookston, Minnesota, USA. Factors in the trials were twelve cultivars and five planting dates. HRSW cultivars were chosen in pairs from the alleles for genes *Ppd-D1*, *Rht-B1*, and *Rht-D1* (Table 1). The experimental design for the trials was a RCBD with a split-plot restriction, with the whole-plot as planting date and split-plot as HRSW cultivar. Data collected for tillering was head counts at Feekes 11.3.

Table 1. Genetic identity of the HRSW cultivars.

Group	Cultivar	*Ppd-D1*[z]	*Rht-B1*[y]	*Rht-D1*[x]
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

[Z] *Ppd-D1b* is photoperiod sensitive, *Ppd-D1a* is photoperiod insensitive
[Y] *Rht-B1b* is semi-dwarf, *Rht-B1a* is the tall allele
[X] *Rht-D1b* is semi-dwarf, *Rht-D1a* is the tall allele

Table 2. Stems per plant for the five linear contrasts used to compare genes *Rht-B1*, *Rht-D1* and *Ppd-D1* in 12 cultivars of HRSW at Crookston, MN, 2014.

| Contrast group	Treatment	5/23/14	5/30/14	6/6/14	6/23/14	6/27/14	Regression Equation	*R²*
		------------stems plant⁻¹------------						
1	*Rht-B1b* or *D1b*	18.3	16.6	12.4	6.9	5.6	y= -0.49x + 20596	0.95
1	All other combinations	21.1	21.5	14.0	7.9	4.5	y= -0.37x + 15554	0.99
2	*Rht-B1b* only	21.3	17.7	14.2	7.6	5.6	y= -0.44x + 18236	0.99
2	All other combinations	20.0	20.3	13.3	7.5	4.7	y= -0.45x + 19051	0.95
3	*Ppd-D1b* only	20.1	17.4	12.4	5.3	4.3	y= -0.46x + 19440	0.99
3	All other combinations	20.2	20.3	13.7	8.0	5.0	y= -0.45x + 18810	0.96
4	*Rht-B1b* and *Ppd-D1b*	32.4	26.0	12.3	9.8	3.3	y= -0.75x + 31212	0.88
4	All other combinations	16.2	18.6	13.7	7.1	5.2	y= -0.36x + 15248	0.90
5	*Rht-D1b* and *Ppd-D1b*	11.7	22.0	13.4	6.9	3.6	y= -0.35x + 14589	0.56
5	All other combinations	21.9	19.4	13.5	7.7	5.1	y= -0.47x + 19780	0.98
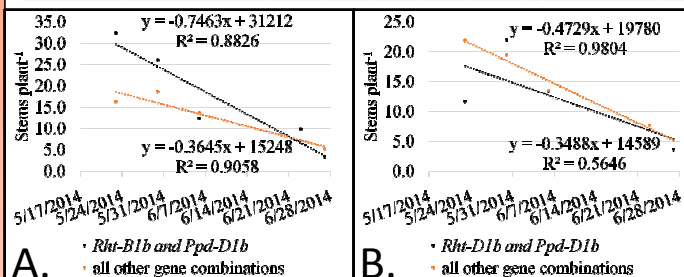
Figure 1. Stems per plant for two selected linear contrasts used to compare genes *Rht-B1b*, *Rht-D1b* and *Ppd-D1b* in 12 cultivars and five planting dates at Crookston, MN, 2014.

Table 3. Stems per plant for the five linear contrasts used to compare genes *Rht-B1*, *Rht-D1* and *Ppd-D1* in 12 cultivars of HRSW at Crookston, MN, 2015.

| Contrast group	Treatment	5/4/15	5/11/15	5/18/15	5/25/15	6/1/15	Regression Equation	*R²*
		------------stems plant⁻¹------------						
1	*Rht-B1b* or *D1b*	16.3	13.8	12.8	10.2	3.7	y= -0.41x + 17332	0.90
1	All other combinations	18.8	18.8	13.0	10.1	2.5	y= -0.59x + 24954	0.92
2	*Rht-B1b* only	14.9	14.6	13.0	10.1	3.8	y= -0.38x + 16065	0.93
2	All other combinations	18.6	17.7	12.9	10.2	2.7	y= -0.56x + 23683	0.84
3	*Ppd-D1b* only	15.0	16.0	11.6	7.5	1.8	y= -0.50x + 22705	0.93
3	All other combinations	18.6	17.4	13.2	10.7	3.1	y= -0.53x + 20956	0.90
4	*Rht-B1b* and *Ppd-D1b*	21.6	23.9	14.9	12.4	1.4	y= -0.74x + 31315	0.86
4	All other combinations	15.9	14.6	11.8	9.3	3.4	y= -0.43x + 18211	0.94
5	*Rht-D1b* and *Ppd-D1b*	17.9	17.3	13.7	8.4	2.9	y= -0.53x + 22214	0.92
5	All other combinations	18.0	17.1	12.8	10.5	2.9	y= -0.56x + 23411	0.94
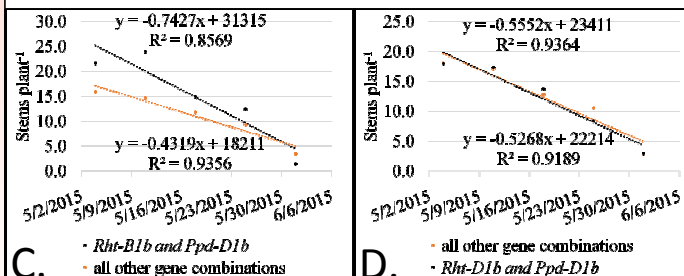
Figure 2. Stems per plant for two selected linear contrasts used to compare genes *Rht-B1b*, *Rht-D1b* and *Ppd-D1b* in 12 cultivars and five planting dates at Crookston, MN, 2015.

Results

Genetic influence was evident in both years. In 2015, presence of *Ppd-D1b*, *Rht-B1b*, or *Rht-D1b* alone did not increase the number of stems (Table 2). However, when *Rht-B1b* was in combination with *Ppd-D1b* stem numbers were significantly increased at all dates besides the last planting on 6/1/2015. For the first two dates in 2014, the combination of *Rht-B1b* and *Ppd-D1b* resulted in greater stem numbers than the rest of the gene combinations. The linear regression equations show the much steeper slope in contrast group 4 for both years, for *Rht-B1b* and *Ppd-D1b* compared to all other gene combinations (Figure 1A and 2C).

Conclusion

Rht-B1b in combination with *Ppd-D1b* was the only positive allele for either semi-dwarf or photoperiod sensitivity. The combination consistently decreased the regression slope and decreased tillering more rapidly than either *Rht-B1b* or *Ppd-D1b* alone. Solid-seeded yield trials will verify if these traits simply increase tillering or allow more tillers to reach maturity.

Acknowledgments