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-D1z	Rht-B1y	Rht-D1x
1	Albany	b	b	а
	Faller	b	b	a
2	Knudson	a	b	а
	Samson	a	b	a
3	Briggs	b	а	a
	Vantage	b	а	a
4	Sabin	a	a	a
	Oklee	a	а	а
5	Kelby	а	а	b
	Kuntz	a	a	b
6	Marshall	b	а	b
	Rollag	b	а	b

 $^{^{\}rm Z}\,Ppd\text{-}D1b$ is photoperiod sensitive, Ppd-D1a is photoperiod insensitive

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	R^2	
				st	ems plai	nt-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	
ı	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	
l	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	
Т	35.0	y = -0.7463x + 31	212	1	25.0			0.4500 1.10500		
	30.0 R ² =0.8826				y = -0.4/29X = 19/60					
_ 50.0			_ 1:	20.0 R ² =0.9804						
-	□ \				15.0 R=0.9804					
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ď	E 15.0 10.0			- 1	§ 10.0 5.0 v = -0 3488x + 14580					
	5.0	y = -0.3645x + 15	248	**	5.0		У	= -0.3488x + 14589		
	0.0	$R^2 = 0.9058$		-	0.0			$R^2 = 0.5646$		
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5	11 ⁷¹ /5/24/5/31	1126/116/14/16/2X/14	6/28/20		31177	2A14513	VIMPU	16114161211612810		
1										
	. Plat.	B1b and Ppd-D1b				. Rht.	Dilh on	d Ppd-D1b		

Figure 1. Stems per plant for two selected linear contrasts used to compare genes Rht-Blb, Rht-Dlb and Ppd-Dlb in 12 cultivars and five planting dates at Crookston, MN, 2014.

all other gene combinations

all other gene combinations

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	R^2	
	s	stems plant1							
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	
25.0 R=0.8569 20.0 15.0 10.0				20.0 Just 15.0 10.0					
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0.0	$R^2 = 0.9356$	•	_	0.0		R	² = 0.9189		
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· Rht-	· Rht-B1b and Ppd-D1b				- all other gene combinations				
all or ر	ther gene combination	ns		. Rht-D1b and Ppd-D1b					
igure 2. Stem	s per plant for two se	lected	linear	contrast	s used t	o com	nare genes Rht_R1h	Rht.	

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.

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Y Rht-B1b is semi-dwarf, Rht-B1a is the tall allele X Rht-D1b is semi-dwarf, Rht-D1a is the tall allele