Table 3.The 2010 Southern Regional Performance Nursery (SRPN) growth chamber entries.

Entry	Line	**Class**	Pedigree	Program Source
1	Kharkof	HRW	Kharkof	check
2	Scout 66	HRW	Scout 66	check
3	TAM-107	HRW	TAM-107	check
4	Fuller	HRW	Fuller	check
5	KS07HW52-5	HWW	KS025580(TREGO/CO960293)/KS02HW25(TGO/JGR 8W)	KSU-HAYS
6	OK05526	HRW	KS94U275/OK94P549 F4:12	OSU
7	OK05204	HRW	SWM866442/OK95548 F4:12	OSU
8	OK07231	HRW	OK92P577-(RMH 3099)/OK93P656-(RMH 3299) F4:10	OSU
9	NE07444	HRW	KS96HW10-3=(KS91HW29// RIO BLANCO/KS91H184)/WAHOO/NE99585	UNL
10	NI07703	HRW	R-148 (G97343) =(919021/B725//K92)/NI00436 =(WI89-273-13/NE93427 (=BEZ 1/CTK78//ARTHUR/CTK78/3/BENNET/4/NORKAN)	UNL
11	NI08708	HRW	CO980829 (=Yuma/T-57//CO850034/3/4*Yuma/4/NEWS1)/Wesley	UNL
12	CO050270	HRW	Hatcher/NW97S295	CSU
13	CO050303-2	HRW	CO980829/TAM 111	CSU
14	KS010990M~8	HRW	Trego/Ventnor//KS940786-6-4	KSU-Manhattan
15	KS06O3A~50-3	HRW	OVERLEY*3/AMADINA	KSU-Manhattan
16	KS011327M~2	HRW	KS940748-2-4/TX97V4311//Overley	KSU-Manhattan
17	TX06A001281	HRW	TX98VR8422/U3704A-7-7	TAMU
18	TX06A001386	HRW	TX99A6030/CUSTER	TAMU
19	TX05V7259	HRW	T107//TX78V3620/Ctk78/3/TX87V1233/4/Arap//TX86V1540/T200	TAMU
20	TX05V7269	HRW	HBG0358/4/T107//TX78V3620/Ctk78/3/TX87V1233	TAMU

Entry number used in growth chamber experiment, not the same entry number as original 2010 Southern Regional Performance list. Pedigrees according to USDA-ARS 2010 Southern Regional Performance nursery Graybosh (2010). HRW-hard red winter wheat, Programs for which source seed was provide.

Experimental design

Three growth chamber cycles were conducted in this study. In the first (2010) and second (2011) growth chamber cycle, seeds from the selected lines were vernalized in petri dishes by germinating twenty seeds at room temperature for 30 hr, then continuing the growing cycle in a refrigerator at 1-2° C. The sprouted seeds were left under dark refrigeration for six weeks according to Davidson et al. (1985). Three seeds were planted per six-inch, pot with two pots per variety into a soil medium. Each pot per variety represented a replication. A parallel set was planted without exposure to vernalizing temperatures to represent the non-vernalized set according to Darapuneni et al., 2013. Both sets of pots were then placed in a split-split plot arrangement in two growth chambers and rotated weekly to equalize temperature and light fluctuation within the chamber. The chambers were set for 12 and 16 hour day-lengths. Data was taken on flowering and heading dates of all lines. The same experiment was repeated in 2011. The 2012 growth chamber experiment included two vernalization treatments (3 and 6 weeks) and two photoperiod lengths (10hr and 14hr).

Data collection

Flowering dates were recorded when 50% of the tillers in the pot showed visible anther extrusion and or when trapped anthers changed from green to yellow. Data compiled by the USDA-ARS on the remaining 30 field locations were utilized including; grain yield, heading date, yield stability and height. Genotyping was conducted at the USDA-ARS genotyping lab in Manhattan, KS, using KASP chemistry in a K-Biosciences SNP pipeline to assess marker data of the lines used in this experiment. The

markers considered for this experiment were photoperiod marker PPD-D1 LD and markers for the three vernalization genes *Vrn-A1, Vrn-A1b* and *Vrn-D3.*

Basal Vegetative period (BVP), i.e. intrinsic earliness, was measured as time for vernalized seedling (6 week) to grow to anthesis in the longer photoperiod (16 hour), based on testing conducted in the 2010 and 2011 growth chamber evaluations. Furthermore, the main effect of vernalization (ΔV) was measured as the difference in anthesis date between vernalized (6 wk) and moderately vernalized (3 wk) seedlings under medium long day (14 h) conditions, based on testing conducted in the 2012 growth chamber evaluation. The main effects of photoperiod (ΔP) were measured as difference in days to anthesis between 16 and 12 h treatments in the vernalized seedlings (6 wk vernalization) measurements from growth chamber experiment evaluations done in 2011 and 2012.

Statistical analysis

Growth chamber data were analyzed as a split-split plot design using SAS 9.3. The ANOVA tables of the 2010 and 2011 growth chamber experiments showed the main plot being photoperiod (16 hour vs. 12 hour), the sub-plot being vernalization treatment (6 week vs. 0 week), and the sub-sub plot being genotype (Table 4). Furthermore, the ANOVA table of the 2012 growth chamber experiment shows the main plot representing photoperiod (14 hour vs. 10 hour), the sub-plot representing vernalization treatment (6 week vs. 3 week), and the sub-sub plot represented by genotype, and can be seen on the second table on page 28.

Biplot analysis

The GGEbiplot software of Yan and Kang (2003), was used to generate the biplots illustrated in the results section . A two-way matrix of genotypes as entries and traits as testers was generated from mean values for genotypes. Rows and columns were treated as entries and testers, respectively. The biplot model was as follows:

$$Y_{ij} - \mu - \beta_j = \lambda_1 \xi_{i1} \eta_{j1} + \lambda_2 \xi_{i2} \eta_{j2} + \in_{ij}$$

where = Y_{ij} expected value of entry i and tester j, μ = grand mean, β_j = mean of all crosses to j, λ_1= PC1, ξ_{i1}= PC1 eigenvector of entry i, η_{j1}= PC1 eigenvector of tester j, λ_2= PC2, ξ_{i2}= PC2 eigenvector of entry i, η_{j2}= PC2 eigenvector of tester j, and $\in_{ij}$= residual of model associated with combinations of entry i and tester j.

According to Yan and Tinker (2006) traits with acute angles are positively associated while obtuse angles indicated a negative association. Traits with near right angles are independent. Entries close to one another signify similar trait profiles and entries opposite one another relative to the origin signify opposite trait profiles. Performance of an entry with regard to a trait is better than average if the angle between its vector and the trait's vector is less than 90°; lower than average if greater than 90°; and near average if the angle is near 90°.

For genotype-by-environment or genotype-by-trait interactions, it is necessary to establish whether or not there are relevant rank changes of a specific genotype across a given environment or for a given trait. For example, HRW is expected to have longer days to heading in the northern Great Plains as opposed to South Texas. If there are not relevant rank changes, a particular line(s) may be identified as early across all environments. A biplot allows a breeder to determine whether or not a single environment should be divided into multiple mega-environments to exploit or avoid any potential genotype-by-environment interactions. A biplot can also assist a breeder in identifying the sources of these interactions. The most ideal test environments and superior genotypes can be identified through the use of biplot analysis (Yan and Tinker, 2006).

Two types of biplot views were generated for analysis of the HRW set in this study. These views include a mean performance and stability view of genotypes and a which-won-where view.

Table 4. Split-split plot analysis of 2010 and 2011data with the main plot being photoperiod (16 vs. 12 hour), the sub-plot being vernalization (6 vs. 0 week), and the sub-sub plot being genotype.

Source	DF	SS	MS	F value	P value
Year	1	2514.4031	2514.4031**	32184.4	0.0035
Error a = rep(year)	2	0.0813	0.0406	0.00	0.9966
P	1	7097.0281	7097.0281*	3115.29	0.0114
year*P	1	100.1281	100.1281NS	43.95	0.0953
Error b = rep*P	1	2.2781	2.2781	0.19	0.6637
V	1	317079.1531	317079.1531**	277987	<.0001
year*V	1	2514.4031	2514.4031**	2204.41	0.0005
P*V	1	7097.0281	7097.0281**	6222.05	0.0002
year*P*V	1	100.1281	100.1281*	87.78	0.0112
Error c = rep*P*V	2	2.2813	1.1406	0.10	0.9094
Genotype	19	5900.2844	310.5413**	25.87	<.0001
P*Genotype	19	1525.9094	80.3110**	6.69	<.0001
V*Genotype	19	5900.2844	310.5413**	25.87	<.0001
P*V*Genotype	19	1525.9094	80.3110**	6.69	<.0001
year*Genotype	19	1609.0344	84.6860**	7.05	<.0001
year*P*V*Genotype	57	2872.6531	50.3974**	4.20	<.0001
Error d = residual	155	1860.8594	12.0055		

Coefficient of variation (CV%) = 11.00
NS, *, and ** = Significant at 5% and 1% respectively; P=photoperiod, V=vernalization

Table 5. Main effects and interaction of photoperiod and vernalization for days to anthesis of 20 hard red winter wheat lines tested in the growth chamber in 2010 and 2011.

	2010			2011		
Photoperiod (h)	**HV**	**NV**	**Mean**	**HV**	**NV**	**Mean**
12	**65.65**	**0.00**	**32.83**	**79.1**	**0.0**	**39.6**
16	**49.05**	**0.00**	**24.53**	**58.0**	**0.0**	**29.0**
Mean	**57.35**	**0.00**	**28.7**	**68.6**	**0.0**	**34.3**
CV%			**7.9%**			**12.8%**
LSD 0.05 (P)			**0.95**			**5.24**
LSD 0.05 (V)			**0.24**			**1.26**

Photoperiod 12 hr and 16 hr, HV 6 weeks of vernalization, NV 0 weeks of vernalization.

Table 6. Split-split plot analysis of 2012 data with the main plot being photoperiod (14 vs. 10 hour), the sub-plot representing vernalization (6 vs. 3 week), and the sub-sub plot representing genotype.

Source	DF	Type I SS	Mean Square	F Value	Pr > F
Rep	1	212.7198	212.7198	0.24	0.6269
P	1	303055.1555	303055.1555	6.68E7	<.0001
Error a = REP*P	1	0.0002	0.0002	0.00	0.9996
V	1	4305.0156	4305.0156	12.73	0.0703
P*V	1	34727.0582	34727.0582	102.40	0.0096
Error b = REP*P*V	2	804.0872	402.0436	0.45	0.6391
Name	18	27367.9625	1520.4424	1.70	0.0588
P*Name	18	38718.9917	2151.0551	2.41	0.0046
V*Name	18	26166.2202	1453.6789	1.63	0.0758
P*V*Name	18	21431.5903	1190.6439	1.33	0.1940
Error c = residual	71	63360.9868	892.4083		
Corrected total	150	520149.7881			

CV% = 55.1

Table 7. Main effects and interaction of photoperiod and vernalization for days to anthesis of 20 hard red winter wheat lines tested in the growth chamber in 2012.

	2012		
Photoperiod (h)	**HV**	**MV**	**Mean**
10	**19.5**	**0.00**	**9.7**
14	**78.4**	**119.7**	**99.3**
Mean	**48.5**	**59.8**	**55.0**
CV%			**55.1**
LSD 0.05 (P)			**00.14**
LSD 0.05 (V)			**12.7**

Photoperiod 10 hr and 14 hr, HV 6 weeks of vernalization, MV 3 weeks of vernalization

Results and discussion

Analysis of variance

In the 2010-2011 growth chamber analysis all effects and first-order and second-order interactions were significant at the 5% level of probability. We had a significant photoperiod-by-vernalization-by-genotype interaction, indicating that genotypes responded differently across different day lengths and vernalization treatments (Table 4) Table 5 shows the main effects and interaction of photoperiod and vernalization for the 2010-2011 growth chamber experiments. Days to anthesis decreased significantly ($P < 0.005$) as day-length increased.

In the 2012 growth chamber analysis a significant photoperiod-by-vernalization interaction was observed, indicating that the averaged flowering date for all 20 genotypes varied significantly across different vernalization and photoperiod treatments (Table 6). Table 7 shows the main effects and interaction of photoperiod and vernalization, based on days to anthesis, for the 2012 growth chamber experiment. The results showed that fully vernalized (6 weeks) plants flowered earlier than partially

vernalized ones (3 weeks).This indicates that it will be difficult to predict line performance without testing under varying photoperiod and vernalization conditions, which concurs with Ortiz-Ferrara et al. (1995), in which they concluded that without simple screening of these traits, adaptation of wheat to broad growing regions would be limited.

A summary of the means of the lines for BVP, the main effects of photoperiod (ΔP) and vernalization (ΔV) from the growth chamber flowering date results, as well as the four markers associated with photoperiod and vernalization, plant height, days to heading, yield and yield stability across the 2010 SRPN locations are compiled in Table 8. The BVP of the genotypes varied greatly as they did in other studies (Ortiz-Ferrara et al., 1995) and ranged from 42.3 to 76.5 day in this study.

The ΔP, the difference in flowering dates from the longer day photoperiod at 16 hours verses the shorter day photoperiod at 12 hours ranged from 6.8 days to anthesis (DTA) to 43 DTA. There were eight lines that tested photoperiod insensitive, nine sensitive, two unknown and 1 heterogeneous for the PPD-D1 gene. The ΔP for lines that tested photoperiod insensitive based on PPD-1 ranged from 6.8 to 21 DTA. The ΔP for lines that tested photoperiod sensitive based on PPD-1 ranged from 10.3 to 43 DTA. As noted in Ortiz-Ferrara et al., 1995, the long day requirement in photoperiod sensitive wheat is not overcome by prolonged vernalization. The longest ΔP of 43 DTA was observed in old cultivar Scout66. The photoperiod insensitive wheat with the lowest DTA (6.8) was OK07231, which could confirm that the PPD-D1 insensitivity gene was expressed in this un-released advanced line. However, the genotype NI07703, which

tested PPD-D1 insensitive but with growth chamber measured ΔP of 21.3 could point to a false negative PPD-D1 data point or interaction between photoperiod sensitivity and vernalization requirement. This could confirm statements made by other researchers that a complex interaction between vernalization and photoperiod exists (Stefany, 1993). Not specific to the photoperiod sensitivity of a particular HRW cultivar, other studies have noted that with an increase in photoperiod length there is a decrease in the vegetative phase of wheat (Gonzalez et al., 2001).

The ΔV, the difference in flowering dates from the (6 wk) vernalization to the moderately vernalized (3 wk), under a medium long day (14hr), ranged from 0 to 100 DTA. There were three genes evaluated in this study; vrn-A1, vrn-A1b and vrn-D3. HRW can be classified into three distinct groups based on response to the low temperature requirement needed to reach vernalization saturation point. According to Li et al., (2013) a weak winter type would need less than 2 weeks, a semi winter type would need between 2-4 weeks and a strong winter type would require more than 4 weeks of vernalization. In this study there were 14, 3, and 3 lines that tested weak winter, intermediate, and heterogeneous, respectively based on the vrn-A1 gene. The ΔV values for lines that tested weak winter based on vrn-A1 ranged from 0 to 91 DTA. On the other hand, the ΔV values for lines that tested intermediate winter, based on vrn-A1 marker, ranged from 26 to 100 DTA. Furthermore, the ΔV values for the lines that tested heterogeneous winter based on vrn-A1 were 0 to 47.5 DTA. It is worth noting that Kharkof has a ΔV of 91 DTA but tested vrn-A1 weak winter, whereas TX06A1281 has a ΔV of 26 DTA and tested vrn-A1 intermediate winter. The discrepancy could be

explained by genotyping error, an interaction with other vernalization genes in this study, or of most interest, additional unreported genes that condition it's unique response.

The Vrn-A1 marker was used to detect HRW alleles associated with early stem elongation, and it is associated with late stem elongation, according to the USDA's 2010 SRPN marker data. Seventeen of the 20 lines evaluated in this study tested as having vrn-A1b for late stem elongation, and the reaming three tested as having vrn-A1a for early stem elongation. In this study the vrn-D3 gene with alleles vrn-D3a, which is associated with earlier maturing HRW, had 12 lines, and vrn-D3b, which is associated with late maturing HRW was positive in eight lines. The two lines with the highest ΔV were TX05V7259 (100 DTA) and Kharkof (91 DTA). Both lines were photoperiod sensitive and vrn-A1b positive for late stem elongation; however, Kharkof which, on average across all location was 8 days later in the field trials than TX05V7259, tested as a weak winter vrn-A1 and late winter based on vrn-D3. Noted in a study conducted by Chen et al., (2010) in winter wheat cultivar Jagger, Vrn-A1 and Vrn-D3 alleles accelerated phonological development and PPD-1 decreased it due to Jagger photoperiod sensitivity.

In this study it is believed that a certain combination of genes would dictate the acceptable length of time a variety needs to be vernalized and receives the proper photoperiod length in order to complete its life cycle. As concluded in the study done by Chen et al., (2010), the correct combinations of alleles at loci Vrn-A1, Vrn-D1 and Ppd-1 would regulate the developmental phases in wheat and in turn could be customized to

fit various agricultural needs. A clear distinction can be made between lines that perform well in Texas and those that have underperformed. Newer lines such as TX06A1281, which is PPD-D1 LD insensitive, VRN-A1 inter-winter and VRN-D3 early winter, seem to outperform older lines Such as Kharkof which tested PPD-D1 LD sensitive, VRN-A1 weak winter and VRN-D3 late winter. Countries in the northern latitudes such as France and the UK would typically grow photoperiod sensitive wheat Worland et al. (1998). In contrast, in those countries in the southern latitudes of Europe, such as Italy and Yugoslavia, photoperiod insensitive wheat cultivars are more commonly grown. However some inconsistencies have been noted of older varieties and landraces being grown in some southern European areas as more photoperiod sensitive than newer lines Worland et al. (1998). Wheat breeders in southern Europe have improved adaptability by producing photoperiod insensitive wheat.

Table 8 Main effects of photoperiod and vernalization.

Name	BVP	ΔV	ΔP	PPD-D1	Vrn-A1	Vrn-A1b	Vrn-D3	Height (cm)	Heading (day)	Yield	Stability
Fuller	55.5		11.5	Sensitive	WeakWinter	Late	EarlyWinter	80	137	3512	1.1
NI07703	47.3	0	21.3	Insensitive	HeteroWinter	Late	EarlyWinter	81	139	3665	1.1
OK07231	54.3	0	6.8	Insensitive	WeakWinter	Late	Latewinter	80	141	3912	1.0
OK05526	46.8	12	15	Insensitive	HeteroWinter	Late	EarlyWinter	84	138	3876	1.0
KS010990M_	52.5	16.5	23.5	Unknown	WeakWinter	Early	Latewinter	82	141	3379	0.9
KS07HW525	53.3	20.1	13.3	Sensitive	WeakWinter	Late	EarlyWinter	75	139	3480	1.2
CO050270	47.8	23.5	19	Insensitive	WeakWinter	Late	EarlyWinter	79	136	3739	1.3
KS011327M_2	68.3	23.5	10.3	Sensitive	WeakWinter	Early	EarlyWinter	84	139	3556	1.0
TX06A1281	42.3	26	20.8	Insensitive	InterWinter	Late	EarlyWinter	75	136	3670	1.0
TX06A1386	51.3	29	12.8	Insensitive	WeakWinter	Late	EarlyWinter	83	139	3687	1.0
KS06O3A_50	49.5	32.5	19.3	Unknown	WeakWinter	Early	Latewinter	84	137	3426	0.9
NE07444	47.8	46	9.5	Insensitive	WeakWinter	Late	Latewinter	86	139	3451	0.8
NI08708	60	47.5	13	Insensitive	WeakWinter	Late	EarlyWinter	80	140	3881	1.0
TX05V7269	56.3	47.5	14.8	Sensitive	HeteroWinter	Late	Latewinter	80	140	3877	1.2
TAM107	45.8	57	33.8	Sensitive	WeakWinter	Late	EarlyWinter	75	137	3047	0.9
CO050303_	76.5	63	15.8	Sensitive	InterWinter	Late	Latewinter	85	142	3908	1.1
OK05204	51.3	68	19.8	Hetero	WeakWinter	Late	Latewinter	82	141	3736	1.0
Scout66	51.3	76.5	43	Sensitive	WeakWinter	Late	EarlyWinter	94	141	2861	0.6
Kharkof	65.5	91	32	Sensitive	WeakWinter	Late	Latewinter	102	146	2323	0.5
TX05V7259	48	100	22	Sensitive	InterWinter	Late	EarlyWinter	78	138	3839	1.0

Correlation analysis

The results of Pearson's correlation coefficients among grain yield, yield stability, days to heading, plant height, BVP, ΔV, and ΔP (Table 9) illustrate that the taller HRW lines in this study were generally late maturing, poor yielding and less stable across environments. The photoperiod-sensitive lines also proved to be lower yielding and unstable across locations. This is not a coincidence as a strongly positive relationship between plant height and photoperiod sensitivity has previously been noted Borojevic and Borojevic (2005). Both Rht8 (reduced height gene) and Ppd-D1 (daylight insensitivity gene) are both on chromosome 2D, and together they have been shown to decrease flowering by eight days, gave a ten cm reduction in plant height and increased spikelet fertility. According to our study, lines that required longer vernalization times and were more sensitive to photoperiods were unstable across environments.

There was a positive correlation between photoperiod sensitivity and vernalization requirements ($r=0.55$, $P < 0.05$) as determined by our growth chamber evaluations. Static genotypes will perform well across environments and is dynamic genotypes if its performance continually changes with environmental changes Mohammadi and Amir (2013). Davidson et al., (1985) noted that time to heading was longest in non-vernalized plants under natural photoperiods, but was accelerated by long photoperiods. Plants exposed to natural photoperiods had smaller responses to vernalization. However, under longer photoperiods conditions, vernalization effects were much greater. Their study concluded that flowering of wheat is accelerated by long photoperiods and vernalization.

Table 9. Correlations among agronomic traits and the main effect of photoperiod (ΔP) and main effect of vernalization (ΔV).

	Heading	Yield	Stability	ΔP	ΔV	BVP
Height	0.73***	-0.66**	-0.77***	0.41^{ns}	0.43ns	0.41^{ns}
Heading		-0.42^{ns}	-0.51*	0.22^{ns}	0.43ns	0.62**
Yield			0.79***	-0.71**	-0.39ns	-0.06^{ns}
Stability				-0.55*	-0.46*	-0.03^{ns}
ΔP					0.55*	-0.18^{ns}
ΔV						0.21^{ns}

(-) indicates a negative correlation, *** high level of significance, **intermediate level of significance, * low level of significance, ns- not significant.

GGE Biplot analysis

Genotype-by-trait biplot analysis provides a visual method for discerning the relationship among traits within a single or multitude of environments (Yang and Tinker, 2006). Furthermore, genotype-by-environment biplot analysis is a valuable visualization tool for evaluating multi-environment data, locations discriminating value and stability, and genotype-by-environment interaction. A biplot is a graphical display of a two-way table that breaks a product matrix into its column and row vectors (Yan and Tinker, 2006).

The "which-won-where" pattern of a GGE biplot dataset is considered one of its most attractive and illustrative views. In this view, a polygon is drawn on genotypes that are the farthest away from the biplot origin in order to encompass all other genotypes within the polygon's sides.

Genotypes located on the vertices of the polygon have the highest or lowest values for given traits in multiple environments (Yan and Tinker, 2006). Figures 2, 3, and 4 demonstrate which genotypes have the lowest or highest values for the main effect of photoperiod (ΔP), main effect for vernalization (ΔV), grain yield, height, and days to heading across the two growth chambers and all 30 field environments.

The Biplot for the relationships among photoperiod and vernalization explained 100% of total variation with 79.1% by PC1 and 20.9% by PC2 (Fig. 2). TX05V725 and Scout 66 were the vertex genotypes and the lines with the highest vernalization requirement and photoperiod sensitivity, respectfully. Kharkov was in the middle of the two, and had high ΔV and ΔP. On the other hand, genotypes Ok07231 and NI07703 had the lowest ΔV and ΔP, as they were the vertex genotypes located farthest from the ΔV and ΔP testers.

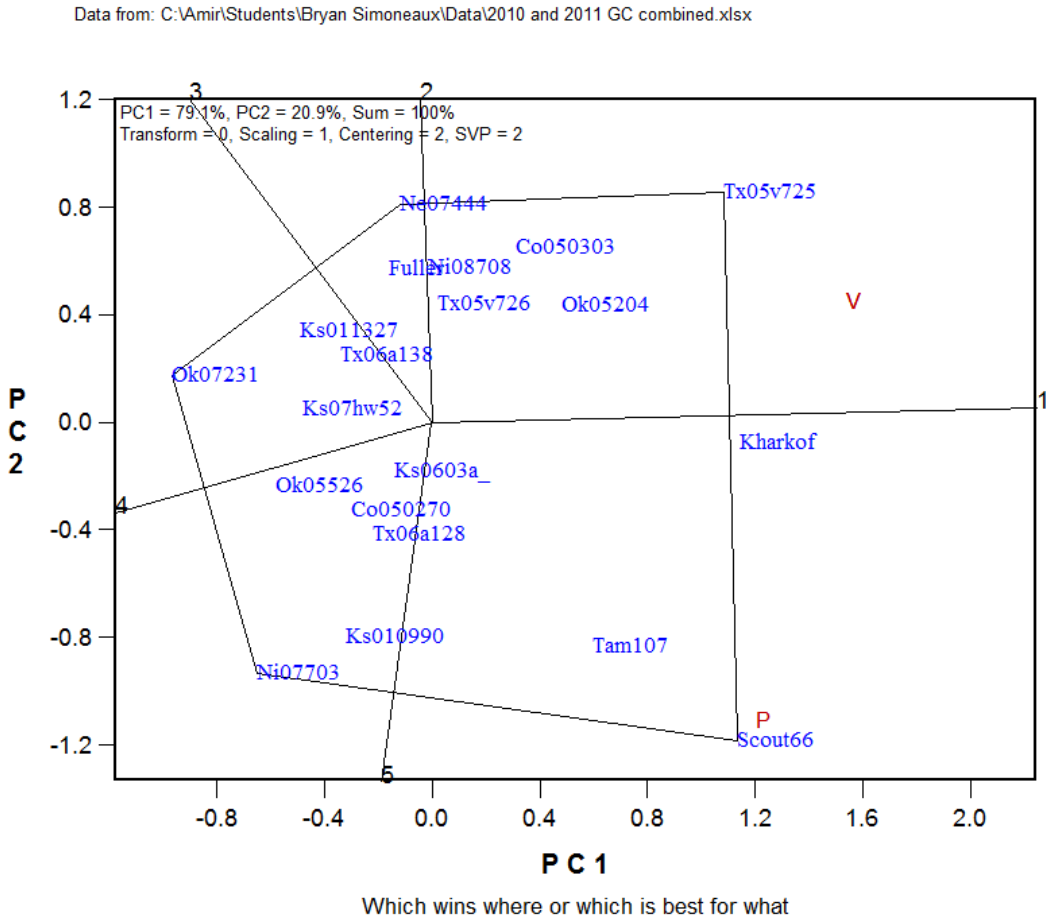

Fig. 2 Polygon view of biplot based on main effect of vernalization (V) and photoperiod (P) of 20 HRW lines tested in the growth chamber from 2010-2011. Genotypes that lie in the (V) quadrant have tested high for vernalization requirement and lines that lie in the (P) quadrant have tested to be photoperiod sensitive. Whereas lines that lie adjacent to the (P) quadrant have tested photoperiod in-sensitive. Lines that lie adjacent to the (V) quadrant have tested low in vernalization requirement.

The biplot for yield performance of the SRPN lines across all locations in the test (Table 10), explained 59.5% of the total variation with 49.9% by PC1 and 9.6% by PC2 (Fig.3). The biplot illustrates which lines performed well in terms of grain yield in which environments. TX05V7269 was the best overall genotype across all locations that fell within vectors 1 and 2. Genotypes TX06A1281, TX05V7259, KS07HW525 and CO050270 yielded higher in locations N1 and also performed well in locations C2, C3, K1, K2, K4, K5, N2, NE2, O1,O2, O4, T2, T4 and W1, which is illustrated by clusters 1 and 2 located between vectors 1 and 2. OK07231 was lower yielding than TXo5V7269 based on distance from the origin to the vertex of the biplot, but was the best entry for environments that fell within vectors 1 and 4. Genotype NI08708 did very well in location C4 and also along with NI07703, CO050303_2, and OK05204 did well in clusters 3, 4 and 5 located within vectors 1 and 4. These genotypes were closely associated with locations K3, NE1, NE4, S1, S2, T1, and T3 of vectors 1 and 4. Kharkov, Scout 66 and TAM 107 were the lowest yielders as they fell far from all location clusters.

Table 10. Locations, and their abbreviations, where the 2010 Southern Regional Performance Nursery (SRPN) was conducted.

Location	Abbreviations	Coordinates	Location	Abbreviations	Coordinates
Clovis Dryland	N1	34.4°N, 103.2°W	Hays	K1	38.8°N, 99.3°W
Clovis Irrigated	N2	34.4°N, 103.2°W	Hutchinson	K2	38.0°N, 97.9°W
Farmington	N3	36.7°N, 108.3°W	Salina	K3	38.8°N, 97.6°W
Bushland Dry	T1	35.1°N, 102.0°W	Colby	K4	39.3°N, 101.0°W
Bushland Irrigated	T2	35.1°N, 102.0°W	Garden City	K5	37.0°N, 100.0°W
Chilicothe	T3	34.2°N, 99.5°W	Wichita	K6	37.6°N, 97.3°W
Prosper	T4	33.0°N, 96.0°W	Winfield	K7	37.0°N,96.0°W
Stillwater	O1	36.0°N, 97.0°W	Lincoln	NE1	40.8°N, 96.6°W
Goodwell	O2	36.5°N, 101.6°W	Clay Center	NE2	40.5°N, 98.0°W
Lahoma	O3	36.3°N, 98.0°W	North Platte	NE3	41.1°N, 100.7°W
Granite	O4	34.9°N, 99.3°W	Sidney	NE4	41.1°N, 102.9°W
Akron	C1	40.1°N, 103.2°W	Alliance	NE5	42.0°N, 102.0°W
Burlington	C2	39.3°N, 102.2°W	Brookings	S1	44.3°N, 96.7°W
Fort Collins	C3	40.5°N, 105.0°W	Dakota Lakes	S2	44.1°N, 100.0°W
Walsh	C4	37.3°N, 102.2°W	Pine Bluffs	W1	41.1°N, 104.0°W

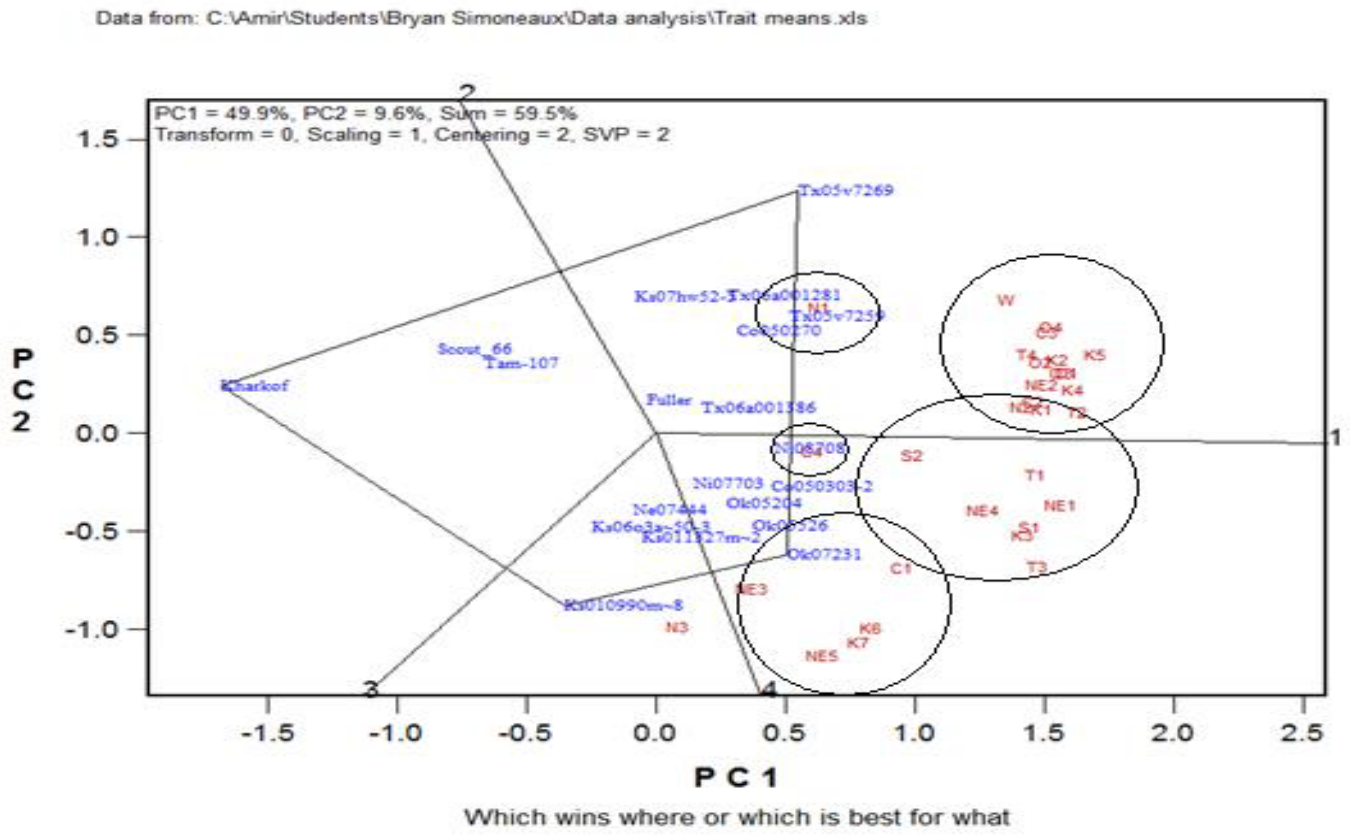

Fig. 3 Yield performance of the Southern Regional Performance Nursery (SRPN) lines done in 2010 across 30 U.S. Locations. (Abbreviations: Clovis Dryland-N1, Clovis Irrigated-N2, Farmington-N3, Bushland dryland-T1, Bushland Irrigated-N2, Chilicothe-T3, Prosper T-4, Stillwater-O1, Goodwell-O2, Lahoma O-3, Granite O-4, Akron C-1, Burlington C-2, Fort Collins C-3, Walsh C-4, Hays K-1, Hutchinson K-2, Salina K-3, Colby K-4, Garden City K-5, Wichita K-6, Winfield K-7, Lincoln NE-1, Clay Center NE-2, North Platte NE-3, Sidney NE-4, Alliance NE-5, Brookings S-1, Dakota Lakes S-2, Pine Bluffs W-1).

The Biplot below for association of ΔP and ΔV with agronomic traits, such as yield, plant height, and days to heading, explained 79.3% of the total variation with 60.8% by PC1 and 18.5% by PC2 (Fig. 4). The biplot shows that Kharkof was the tallest and latest as it is the vertex genotype farthest to the right of the biplot. Scout 66 and TAM 107 were also negatively associated with yield and were among the tallest and latest genotypes. In other studies, early genotypes were shorter and had a reduction in spikelets per head but had a net increase in grains per head due to higher spike fertility (Worland et al., 1998). Genotype OK07231 was the vertex genotype for grain yield based on its position between vertex 3 and 4.

Figures 5 and 6 depict the mean performance and stability of the HRW genotypes for ΔP, and ΔV as well as grain yield, plant height, and days to heading. The genotypes were evaluated for both yield performance and stability across environments. The red arrow points to the values for the different traits; while the blue arrows indicate variability or decreased stability in either direction. The genotypes located to the right of the blue vertical line indicate consistently higher values for traits across all locations.

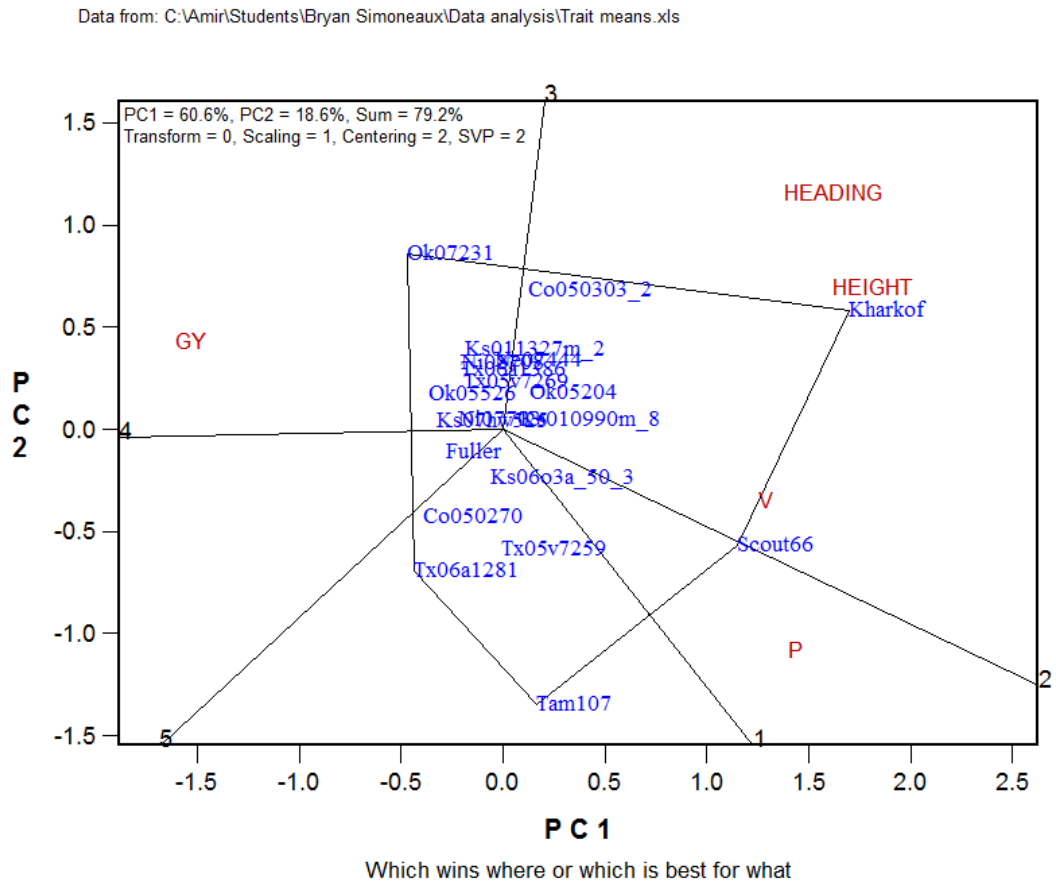

Figure 4 Association of the main effect of photoperiod (P) and vernalization (V) with yield, height, and heading date for 20 lines representing the 2010 Southern Regional Performance Nursery (SRPN).

Worland, A. J., Börner, A., Korzun, V., Li, W. M., Petrovic, S., & Sayers, E. J. (1998). The influence of photoperiod genes on the adaptability of European winter wheats. *Euphytica*, *100*:385-394.

Yan B.W., Kang M.S. (2003) *GGE Biplot Analysis*: A Graphical Tool for Breeders, Geneticists, and Agronomists, CRC Press, New York.

Yan, L., Fu, D., Li, C., Blechl, A., Tranquilli, G., Bonafede, M., ... & Dubcovsky, J. (2006). The wheat and barley vernalization gene VRN3 is an orthologue of FT. *Proceedings of the National Academy of Sciences*, *103*:19581-19586.

Yan W., Tinker N.A. (2006) Biplot analysis of multi-environment trial data: Principles and applications. *Canadian Journal of Plant Science* 86:623-645.

Yan, L., Loukoianov, A., Tranquilli, G., Helguera, M., Fahima, T., & Dubcovsky, J. (2003). Positional cloning of the wheat vernalization gene VRN1. *Proceedings of the National Academy of Sciences*, *100*:6263-6268.

.