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Genetic Variability Studies in Bread Wheat (*Triticum aestivum* L.) under Multi-Environment Trials in Northern Hills Zone

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ABSTRACT: Wheat (*Triticum aestivum* L.) is one of the most important cereal crop among the prime cereals at the global level. The possibility of a successful crop improvement depends considerably on the extent of genetic variability in a crop species. Accordingly, in the present investigation, thirty five bread wheat genotypes were evaluated in randomized complete block design with three replications at seven different agro-ecological zones of Himachal Pradesh to estimate the extent of genetic diversity. Phenotypic data was recorded for eight characters namely days to 50% flowering, days to 75% maturity, plant height (cm), tillers per plant (No.), peduncle length (cm), grain yield per plant (g), biological yield per plant (g) and thousand kernel weight (g). The analysis of variance revealed significant difference in all environments for all the investigated traits. The highest value for GCV and PCV was observed for peduncle length (29.44 and 26.71 respectively). Moderate to high GCV, PCV, heritability and genetic advance as % of mean showed by two traits *viz.* peduncle length and thousand kernel weight; heritability broad sense (h^2_{bs}) and GA (%) of mean was observed moderate to high for days to 50% flowering, days to 75% maturity, plant height, peduncle length and thousand kernel weight. Showing crucial involvement of additive gene action and selection will be efficient for these characters.

Keywords: Wheat, multi-environment trials, variability parameters, heritability, genetic advance.

INTRODUCTION

Wheat (*Triticum aestivum* L. 2n = 42) is an important cereal crop and is the staple food for more than 2.5 billion people all over the world (CRP, 2018). Globally it provides 20% of dietary calories and protein, thus contributing considerably to food security (Shiferaw *et al.*, 2013). Worldwide wheat is the most widely cultivated than any other crop (Curtis and Halford, 2014) on an area of 219 million hectares with an annual production of 760.92 million metric tons (FAO, 2020). However, the key challenges to wheat production which leads to a decreased yield are the low annual rate (0.9%) of yield increase (Ray *et al.*, 2013), stagnating yields (Ray *et al.*, 2012) and the impacts of biotic stresses, abiotic stresses and climate change (Wheeler and von Braun 2013). Hence, to accelerate wheat breeding for higher yield potential, lesser genetic vulnerable, stress resistance and climate resilience, it is important to diversify the wheat germplasm resources.

Determination of genetic variability is useful for crop improvement to boost productivity in more efficient way along with enhanced resistance under different stress conditions (Khodadadi *et al.*, 2011). Thus, genetic improvement of crops including wheat relies on the availability of diverse and superior genotypes. It has, however, been frequently asserted that modern and intensive monoculture of prominent cultivars led to narrowing of genetic variability in crops. In recent years, this possibly led to a genetic vulnerability of crops to biotic and abiotic stresses (Vellve 1993; Russell *et al.*, 2000; Fu *et al.*, 2005). Thus, it is vital in plant breeding programs to broaden its genetic background of crops to maintain sufficient genetic diversity to allow production of new and diverse varieties suitable for cultivation under a variety of biotic and abiotic stress conditions (Singh *et al.*, 2016; Zampieri *et al.*, 2017).

Grain yield is a complex trait, highly influenced by many environmental factors and genotype and environment interactions. In plant breeding programme, direct selection for yield could be misleading. A successful selection depends upon the knowledge on the genetic variability and association of agro-morphological traits with grain yield. So there is an acute need to assess the variability amongst various germplasm resources in different environments.

Adaptation of variable wheat genotypes at diverse agro-ecological conditions of the northern hills zone under Multi-environment Trials (METs) is useful, as performance of genotypes over range of environments are considered to measure the criteria for genetic stability. The main objective of breeders is to develop varieties that give stable productivity under variable environmental conditions. The alteration in yield is the result of genotype × environment interaction. Thus, testing is done by assessing the variable wheat genotypes under different environmental conditions, to analyse the stability of a genotype, which gives the clear cut picture of the performance by variable genotypes at different locations.

MATERIAL AND METHODS

The experimental materials comprised of 35 diverse wheat genotypes including elite cultivars, advance lines, released varieties and three checks HS 542, HS 490 and HS 562. The experiments were carried out in randomized complete block design (RCBD) having three replications, at seven environments in five locations across different agroclimatic conditions of Northern Hills Zone *viz*., Research Sub Station Akrot (Una); Krishi Vigyan Kendra (KVK), Sundernagar; Hill Agricultural Research and Extension Centre (HAREC), Bajaura; Department of Organic Agriculture, College of Agriculture, CSKHPKV Palampur and Rice and Wheat Research Centre, Malan (RWRC Malan) during *Rabi* 2019-20.

Table 1: List of locations/environments used in the study.

Sr. No.	Code	Location	Date of Sowing	Altitude (a.m.s.l)	Latitude	Longitude	Annual Rainfall (mm.)
1.	E_1	Akrot	Timely Sown (Rainfed)	425	31.4°N	76.1° E	1100
2.	E_2	Sundernagar	Late sown (Rainfed)	914	22.7° N	71.6° E	1431
3.	E_3	Bajaura	Late sown (Rainfed)	1090	$31^0$8’N	$77^0$0’E	873
4.	E_4	Palampur	Late Sown (Rainfed/organic)	1290.8	32°80' N	76°33' E	2500
5.	E_5	Malan I	Timely sown (Rainfed)	950	$32^0$1’N	$76^0$1’E	1800
6.	E_6	Malan II	Timely sown (Irrigated)	950	$32^0$1’N	$76^0$1’E	1800
7.	E_7	Malan III	Timely sown (Irrigated)	950	$32^0$1’N	$76^0$1’E	1800

Each genotype was sown in three rows with plot size of 2.0 × 0.6 m^2 with row to row spacing of 20 cm. The observations were recorded on five randomly selected competitive plants in each replication on various phonological and morpho-physiological traits namely: days to 50% flowering (DTF), days to 75% maturity (DTM), plant height (cm) (PH), tillers per plant (No.) (TPP), peduncle length (cm) (PL), grain yield per plant (g) (GY), biological yield per plant (g) (BY) and thousand kernel weight (g) (TKW).

Statistical analysis. The Statistical analysis of the data for variability over the seven locations (environments) was done with the help of software WINDOSTAT Version 9.2 from Indostat Services, Hyderabad. Scott-Knott clustering algorithm was used to make comparison between treatment means (Scott and Knott, 1974).

Analysis of variance was done as per Panse and Sukhatme (1984). The analysis of variance (ANOVA) was constructed based on the linear model given by Fisher (1954):

$$Y_{ij} = m + g_i + r_j + e_{ij}$$

Where, Y_{ij} is phenotypic observation of i^{th} genotype grown in the j^{th} replication; m is General population mean; g_i is Effect of i^{th} genotype; r_j is the effect of j^{th} replication and e_{ij} is error associated with i^{th} genotype in j^{th} replication.

The phenotypic & genotypic components of variance (PCV & GCV), heritability in broad sense (h²bs) and Genetic advance as (%) of mean were computed as suggested by Burton and De Vane (1953); Johnson *et al.* (1955).

$$\text{Phenotypic coefficient of variation (PCV \%)} = (\sigma_p / x) \times 100$$

$$\text{Genotypic coefficient of variation (GCV \%)} = (\sigma_g / x) \times 100$$

Where, σ_p is the phenotypic standard deviation; σ_g is the genotypic standard deviation; σ_e is environmental standard deviation and x is the population mean.

$$\text{Heritability } [h^2_{bs}\%] = \sigma^2_g / (\sigma^2_g + \sigma^2_e) \times 100$$

Where, σ^2_g is genotypic variance and σ^2_e is phenotypic variance

$$\text{Genetic advance (GA)} = K \times \sigma_p \times h^2_{(bs)}$$

$$\text{GA\% of mean} = (GA/ x) \times 100$$

Where, K is the selection differential at 5% selection intensity *i.e.* 2.06.

RESULTS AND DISCUSSIONS

Analysis of variance and mean comparison. The analysis of variance revealed (Table 1) significant difference in all the investigated traits in all environments.

The seed yield per plant in pooled environments ranged from 4.59-5.84 with a mean value of 5.27 g and it is minimum in E_4 (2.40g) and maximum in E_6 (7.80g). In E_2 seven genotypes *viz.*, TAW 164, HPW 376, HPW 439, HPW 373, HPW 314 and BW 272 were significantly superior to the best check *i.e.*, HS 542; in all other environments none of the genotype was significantly superior to the best check.

Table 2: Analysis of variance for different traits in wheat genotypes over seven environments and pooled over environment.

Sr. No.	Characters	Mean sum of squares			
		Source	**Replication**	**Genotypes**	**Error**
		df	**2**	**34**	**68**
1.	**Days to flowering**	E_1	6.43	26.87*	2.47
		E_2	3.47	31.98*	2.94
		E_3	3.47	31.98*	2.94
		E_4	81.38*	163.78*	0.00
		E_5	58.66*	42.41*	2.66
		E_6	21.61*	66.53*	4.85
		E_7	15.89*	92.91*	3.08
		Pooled	**76.84***	**2228.76***	**15.23**
2.	**Days to maturity**	E_1	1.27	40.0*	1.36
		E_2	0.87	29.21*	1.88
		E_3	119.47*	31.98*	2.94
		E_4	82.31*	159.6*	0.00
		E_5	90.24*	181.49*	1.48
		E_6	13.87*	160.41*	1.06
		E_7	8.87*	152.49*	0.44
		Pooled	**18.16**	**8413.77***	**17.02**
3.	**Plant height**	E_1	13.98	127.24*	48.09
		E_2	116.31	320.36*	3.69
		E_3	85.27	145.20*	33.45
		E_4	44.41	71.31*	14.71
		E_5	0.47	226.77*	12.69
		E_6	20.18	271.42*	24.32
		E_7	7.97	219.42*	12.63
		Pooled	**26.19**	**3541.56***	**48.27**
4.	**Tillers per plant**	E_1	0.82*	0.76*	0.12
		E_2	3.19*	0.55*	0.34
		E_3	4.50	0.48*	0.11
		E_4	1.04*	0.38*	0.13
		E_5	4.33*	0.81*	0.21
		E_6	0.42	1.21*	0.25
		E_7	6.87*	0.77*	0.30
		Pooled	**2.12***	**73.73***	**0.26**
5.	**Peduncle length**	E_1	8.53*	72.1*	1.43
		E_2	37.2	59.39*	1.24
		E_3	181.70*	61.84*	2.96
		E_4	21.72*	54.18*	1.28
		E_5	0.55	71.77*	1.42
		E_6	33.69*	55.78*	1.24
		E_7	32.85*	55.17*	1.32
		Pooled	**135.23***	**836.53***	**4.06**
6.	**Biological yield per plant**	E_1	3.65	9.53*	1.81
		E_2	2.30	5.06*	1.31
		E_3	3.14	6.91*	3.46
		E_4	4.89*	1.82*	0.69
		E_5	13.16*	9.18*	2.60
		E_6	4.85	9.47*	2.14
		E_7	9.03*	7.79*	1.47
		Pooled	**33.68***	**1739.97***	**2.96**
7.	**Grain yield per plant**	E_1	0.33	0.88*	0.16
		E_2	5.80	1.77*	0.46
		E_3	0.25	0.66*	0.33
		E_4	0.65*	0.24*	0.09

		E_5	1.60*	1.09*	0.22
		E_6	0.75	0.95*	0.25
		E_7	0.94*	0.81*	0.15
		Pooled	**6.04***	**139.61***	**0.39**
8.	**Thousand kernel weight**	E_1	25.60*	54.70*	0.96
		E_2	25.60*	54.70*	0.96
		E_3	23.77*	97.67*	1.13
		E_4	8.97*	54.70*	0.96
		E_5	111.40*	54.70*	0.96
		E_6	22.90	26.87*	14.64
		E_7	1.45*	53.26*	0.42
		Pooled	**124.69***	**1238.77***	**12.11**
*Significant at 5% level (P<0.05)					

Parameters of variability. The various parameters of variability *viz*., mean, range, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) along with heritability in broad sense (h^2_{bs}) and genetic advance (GA) expressed as percentage of mean for different traits are presented in Table 2.

High PCV (>25%) was observed for peduncle length; moderate (15-25%) for tillers per plant**,** Thousand kernel weight whereas, it was low (<15%) for days to 50% flowering, days to 75% maturity, plant height, biological yield per plant and grain yield per plant. High GCV (>25%) was observed for peduncle length; whereas, it was low (<15%) for days to 50% flowering, days to 75% maturity, plant height, tillers per plant, thousand kernel weight, biological yield per plant and grain yield per plant. The lower value of GCV as compared to PCV for all the traits indicated that the effect of environment was negligible on the development of plants.

The experiments revealed that broad sense heritability (h^2_{bs}) was high (>70%) for days to 50% flowering, days to 75% maturity and peduncle length; moderate (50-70%) for plant height whereas, it was low (<50%) for number of tillers, thousand kernel weight, biological yield per plant and grain yield per plant. Genetic advance expressed as percentage of mean was not observed to be high (>50%) for none of the trait; moderate (25-50%) for peduncle length and thousand kernel weight and low (>25%) for days to 50% flowering, days to 70% maturity, plant height, tillers per plant, biological yield per plant and grain yield per plant.

The traits *viz*. peduncle length and thousand kernel weight showed moderate to high GCV, PCV, heritability and genetic advance as % of mean, showing crucial involvement of additive gene action in the expression of these traits.

Scott-Knot Test Grouping have revealed that the eight genotypes 25, 31, 7, 16, 18, 19, 9 and 29 (*i.e*., HPW 314, HPW349, TAW 164, HPW 442, PW 1076, MT 19-18, TAW 172 and MLW 1449) are at par to each other and to the check varieties HS 542 HS 490 HS 562 and were significantly superior in pooled grain yield per plant over seven environments to the rest of genotypes.

Table 2: Variability parameters for various traits in wheat genotypes under seven environments and pooled over environment.

Sr. No.	Traits		Mean± S.E.(m)	Range	PCV (%)	GCV (%)	h^2_{bs} (%)	GA (%) of mean
1.	**Days to 50 % Flowering**	E_1	88.64±0.91	82.00-92.67	3.67	3.21	76.62	5.80
		E_2	88.86±0.98	82.00-92.66	3.99	3.50	76.43	6.31
		E_3	95.86±0.98	89.00-99.66	3.70	3.24	76.34	5.85
		E_4	120.48±0.02	103.33-128.33	6.12	6.08	95.32	12.62
		E_5	114.54±0.94	103.33-122.67	3.48	3.17	83.12	5.97
		E_6	123.92±1.27	112.33-129.66	4.06	3.65	80.12	6.77
		E_7	126.19±1.01	108.33-132.33	4.55	4.33	90.32	8.50
		Pooled	**108.35±0.85**	**98.71-111.95**	**4.47**	**2.65**	**83.27**	**3.24**
2.	**Days to 75% maturity**	E_1	159.90±0.61	153.00-166.00	2.35	2.24	90.65	4.39
		E_2	159.46±0.79	152.00-163.00	2.07	1.89	82.58	3.55
		E_3	164.86±0.98	158.00-168.66	2.15	1.88	76.14	3.40
		E_4	184.71±0.54	167.28-192.28	3.94	3.65	93.89	8.12
		E_5	172.47±0.70	153.67-181.33	4.54	4.49	97.64	9.14
		E_6	166.24±0.59	148.87-173.83	4.42	4.38	98.10	8.94
		E_7	173.90±0.91	157.33-181-33	4.11	4.09	94.01	8.39
		Pooled	**168.79±0.90**	**157.06-173.54**	**3.59**	**2.63**	**87.77**	**3.98**
3.	**Plant height (cm)**	E_1	87.70±4.00	77.00-103.00	9.84	5.85	35.99	7.18
		E_2	91.68±1.10	74.83-120.38	11.40	11.20	96.14	22.69
		E_3	92.63±3.33	81.00-111.33	9.01	6.58	52.87	9.85

		E_4	44.90±2.21	33.67-56.67	12.90	9.67	56.76	14.93
		E_5	90.81±2.05	72.67-111.67	10.09	9.30	84.10	17.65
		E_6	91.86±2.05	70.33-116.33	11.24	9.87	71.24	17.88
		E_7	88.20±2.05	70.67-107.00	10.23	9.41	83.56	17.82
		Pooled	**83.96±1.51**	**73.75-101.36**	**10.65**	**6.71**	**65.45**	**8.71**
4.	**Tillers per plant (no.)**	E_1	3.58±0.20	2.37-4.65	16.17	12.88	63.69	21.14
		E_2	3.75±0.33	2.48-4.78	17.02	7.18	67.5	6.75
		E_3	3.43±0.18	2.84-4.57	13.89	10.23	54.55	15.53
		E_4	1.50±0.21	0.99-2.93	30.99	19.43	39.54	25.09
		E_5	3.23±0.26	2.24-4.84	19.78	13.91	49.56	20.15
		E_6	4.09±0.28	2.93-6.13	18.40	13.85	56.63	21.48
		E_7	3.45±0.32	2.25-4.22	19.58	11.43	34.64	13.74
		Pooled	**3.29±0.11**	**2.69-4.21**	**18.58**	**10.16**	**29.85**	**11.43**
5.	**Peduncle Length (cm)**	E_1	19.60±0.78	10.61-27.10	27.40	26.60	94.59	53.21
		E_2	17.10±0.64	10.20-27.26	26.54	25.73	95.69	51.30
		E_3	18.81±0.99	11.46-27.76	23.25	23.54	86.78	45.20
		E_4	11.04±0.65	4.27-19.44	39.40	38.05	93.01	75.70
		E_5	16.75±0.69	9.11-25.60	29.77	28.90	94.59	57.87
		E_6	15.22±0.64	8.10-25.10	28.76	28.00	93.03	55.34
		E_7	13.14±0.66	6.03-23.10	33.41	33.24	93.08	64.10
		Pooled	**15.75±0.44**	**8.92-24.88**	**29.44**	**26.71**	**81.18**	**49.20**
6.	**Biological yield per plant (g)**	E_1	19.60±0.78	15.67-23.13	10.69	8.18	58.78	12.90
		E_2	19.53±0.66	16.74-22.90	8.18	5.72	48.76	8.25
		E_3	18.99±1.07	16.33-22.80	11.30	5.64	24.06	5.81
		E_4	8.55±0.48	6.60-10.03	12.05	7.18	35.18	8.80
		E_5	17.99±0.93	13.57-21.60	12.16	8.23	45.51	11.47
		E_6	19.86±0.84	16.40-22.90	7.78	7.86	53.69	11.89
		E_7	15.66±0.76	12.23-19.67	12.07	9.27	58.70	14.66
		Pooled	**17.17±0.37**	**15.10-18.73**	**11.13**	**4.84**	**34.54**	**4.34**
7.	**Grain Yield per plant (g)**	E_1	5.96±0.23	4.75-7.01	10.63	8.21	59.18	13.06
		E_2	9.53±0.39	3.39-6.50	20.78	14.55	48.67	20.91
		E_3	5.92±0.33	5.09-7.12	11.22	5.58	24.25	5.73
		E_4	3.11±0.17	2.40-3.65	12.09	7.17	35.67	8.77
		E_5	5.89±0.27	4.54-7.20	12.11	9.10	56.57	14.06
		E_6	6.45±0.28	5.47-7.30	10.78	7.49	48.84	10.73
		E_7	5.05±0.23	3.95-6.94	12.07	9.06	58.61	14.65
		Pooled	**5.27±0.13**	**4.59-5.84**	**12.91**	**5.32**	**43.32**	**4.52**
8.	**Thousand kernel weight (g)**	E_1	30.82±0.57	22.77-40.97	14.09	13.73	94.93	53.21
		E_2	31.39±0.56	23.33-41.13	26.54	25.73	94.53	51.40
		E_3	30.70±0.61	20.70-42.06	23.25	23.54	86.84	45.30
		E_4	22.28±0.57	14.23-32.43	39.40	38.05	93.69	75.70
		E_5	32.05±0.57	23.99-42.19	29.97	28.90	94.95	57.85
		E_6	32.00±2.20	25.79-39.49	28.96	28.00	93.70	55.85
		E_7	29.73±0.37	21.40-39.04	33.41	33.24	93.50	64.11
		Pooled	**29.85±0.76**	**23.52-36.76**	**15.27**	**9.86**	**41.78**	**34.14**

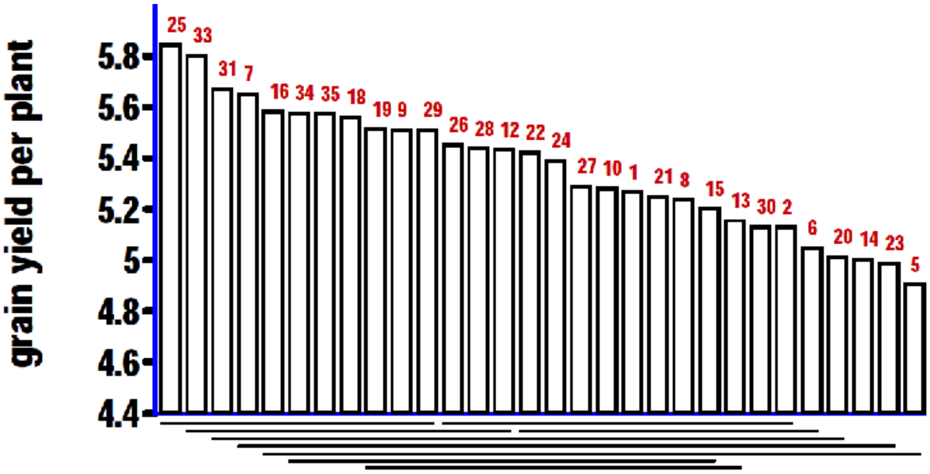

Fig. 1. Scott-Knot Test grouping for pooled grain yield per plant over seven environments.

DISCUSSION

The analysis of variance showed the existence of adequate genetic variation at various agro-ecological zones of Himachal Pradesh, among the various wheat genotypes for all the traits studied. Jee *et al*. (2019) also found that the analysis of variance was highly significant between the genotypes under their study. It shows that the germplasm selected for the study have significant variability which is required by any breeding program. It was observed that value of PCV was slightly higher than the value of GCV. Similar results were observed by Singh *et al.* (2018) in wheat, Gautam *et al*. (2021) in chickpea and Shiva Kumar *et al.* (2021) in linseed indicating less effect of environment on the expression of traits studied.

Moderate to high PCV and GCV was observed for peduncle length, tillers per plant, Thousand kernel weight. Singh *et al.* (2019); Morteza *et al.* (2018) recorded high GCV and PCV for biological yield per plot and harvest index.

Heritability and genetic advance are two important selection parameters, these are useful in selection for various traits for genetic improvement of grain yield in wheat. Heritability broad sense (h^2_{bs}) and GA (%) of mean was observed moderate to high for days to 50% flowering, days to 75% maturity, plant height, peduncle length and thousand kernel weight. Singh *et al.* (2019) observed high heritability and genetic advance as 5% mean for traits like harvest index, number of grains per spike and biological yield per plot. Singh *et al.* (2018) also found high GCV and PCV along with high heritability and high genetic advance which indicated considerable inclusion of additive gene action and selection would be effective for these traits.

FUTURE SCOPE

The evaluated genotypes showed considerable variability for the studied traits under Multi-environment Trials (METs) in Northern Hills Zone. Eight genotypes HPW 314, HPW349, TAW 164, HPW 442, PW 1076, MT 19-18, TAW 172 and MLW 1449, were at par to the check varieties HS 542 HS 490 HS 562 and were significantly superior to other genotypes in pooled grain yield per plant over seven environments. These genotypes can be further evaluated over the years under METs and can be utilized in future breeding programs.

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Conflicts of Interest. None.

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