Himachal Journal of Agricultural Research 49(2): 155-162 (2023)

Studies on genetic variability in bread wheat (*Triticum aestivum* L.) under multiple environments in Northern western Himalayas

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Manuscript Received: 04.07.2023; Accepted: 06.10.2023

Abstract

One of the most significant cereal crops in world is wheat (*Triticum aestivum* L.) which accounts for one-third of all cereal crops. The level of genetic variability in a crop species has a significant impact on the potential of successful crop improvement program. In order to assess the level of genetic variation, sixty-six bread wheat genotypes were examined in α- RBD with three replications at three different agro-ecological zones of Himachal Pradesh. 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 found that there were significant differences in all environments for all of the characters studied. For peduncle length, the highest value for GCV and PCV was observed (29.23 and 25.11% respectively). GCV, PCV, heritability, and genetic advance as % of mean were found to be moderate to high for two traits, peduncle length and thousand kernel weight; heritability broad sense (h^2bs) and GA (%) of mean were found to be 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.

Key words: Wheat, multi-location trials, variability, heritability and genetic advance

Wheat is one of the vital cereal crops after rice to meet the food requirements of the world. It ranks first in terms of acreage while second in terms of production globally. Bread wheat (*Triticum aestivum* L.) is a hexaploid (2n=6x=42; AABBDD genome), self-pollinated and annual cereal crop. It belongs to tribe Triticeae and family Poaceae. It provides over 20% of calories and protein for human nutrition for about 35% of world's population in more than 40 countries. Globally, it occupies 220.89-million-hectare area with the production of 778.90 million tonnes and 3.5 tonnes per ha of productivity (USDA 2020-21), while in India, the wheat crop is grown over 31.35-million-hectare area with total production of 109.59 million tonnes and productivity 34.9 q/ha (Anonymous 2022).

India is one of the principal wheat producing and consuming countries in the world. It is grown over a wide range of climatic conditions in India and its importance in Indian agriculture is second only to rice. In Himachal Pradesh, wheat occupies an area of about 0.33 million hectares with total production of 0.57 million tonnes and productivity of 17.12 q/ha (Anonymous 2021). The main challenges in wheat production that lead to yield loss are low annual yield growth (0.9%) (Ray *et al*. 2013), yield stagnation (Ray *et al*. 2012), and the effects of biotic stress, abiotic stress 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.

Therefore, it is important to diversify wheat germplasm resources to accelerate wheat breeding towards higher yield potential, lower genetic susceptibility, stress tolerance and climate resilience.

Due to the narrow genetic background, improved strains are less tolerant to biotic and biotic stresses (Maqbool *et al.* 2010).

Declining genetic diversity makes crops increasingly vulnerable to disease and adverse climate change (Ranjana *et al.* 2013). Accurate information about the type and degree of genetic diversity and divergence present in wheat is therefore useful in parent selection for the development of superior cultivars. The presence of genetic diversity plays an important role in the success of breeding programs. Indeed, the higher the plant diversity (Mohammadi and Prasanna 2003), the greater the potential for producing productive recombinants and the greater the variability of generational segregation during genetic improvement. Rauf *et al.* (2012) state that accurate knowledge of genetic diversity and genetic relationships between breeding lines is a prerequisite for crop improvement programs, as it aids in the development of superior recombinants.

Different wheat genotypes were tested in different agroecological conditions in the Northern Hill Zone in the context of a multiple-environment trial (MET), as genotype performance in different environments is considered as a criterion measure of genetic stability (Kalimullah *et al.* 2012). It is useful to adapt to The main goal of breeders is to develop varieties that provide stable productivity under changing environmental conditions. Changes in yield are the result of interactions between genotype and environment. Therefore, to analyze genotypic stability, trials were conducted by evaluating different wheat genotypes under different environmental conditions, giving a clear picture of the performance of different genotypes in different locations.

Materials and Methods

The experimental materials comprised of 66 diverse wheat genotypes including elite cultivars, advance lines, released varieties and four checks HPW251, HS 240, HS 562 and PBW 723. The experiments were carried out in alpha-RBD design having three replications at CSKHPKV Palampur, Rice and Wheat Research Centre, Malan (RWRC Malan) during *Rabi* 2019-20, Rabi 2020-21 and *Rabi* 2021-22.

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 (DT50%F), days to 75% maturity (DT75% M), tillers per plant (No.) (TPP), plant height (cm) (PH), peduncle length (cm) (PL), grain yield per plant (g) (GY), biological yield per plant (g) (BY) and thousand grain weight (g) (TGW).

Statistical analysis: Statistical analysis of data on variability among the three sites (environments) was performed using WINDOSTAT version 9.2 software from Indostat Services, Hyderabad.

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, Yij is phenotypic observation of ith genotype grown in the jth replication; m is General population mean; gi is Effect of ith genotype; rj is the effect of jth replication and eij is error associated with ith genotype in jth replication.

The phenotypic & genotypic components of variance (PCV & GCV), heritability in broad sense (h^2bs) and Genetic advance as (%) of mean were computed as suggested by Burton and De Vane (1953); Johnson *et al.* (1955).

Phenotypic coefficient of variation (PCV %) = (σp/ x) × 100 Genotypic coefficient of variation (GCV %) = (σg/ x) × 100 Where, σp is the phenotypic standard deviation; σg is the genotypic standard deviation; σe is environmental standard deviation and x is the population mean.

Heritability [h^2bs%] = σ^2g / (σ^2g + σ^2e) × 100

Where, σ^2g is genotypic variance and σ^2e is phenotypic variance

Genetic advance (GA) = K × σp × h^2 (bs)

GA% of mean = (GA/ x) × 100

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

Results and Discussion

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 4.23-5.44 with a mean value of 5.07 g and it is minimum in E_3 (2.40 g) and maximum in E_2 (7.80 g). In E_2 seven genotypes *viz*., HD 2967, HPW 376, HPW 439, HPW 373, HPW 314 and BW 272 were significantly superior to the best check i.e., HS 562; in all other environments none of the genotype was significantly superior to the best check.

Parameters of variability: The different parameters of variability *viz*., range, mean, 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.

Table1.List of locations/environments used in the study

Sr. No.	Code	Location	Date of Sowing	Altitude (amsl)	Latitude	Longitude	Annual Rainfall (mm)
1.	E1	Malan I (Rabi 2019-20)	Timely sown (Irrigated)	950	$32^0$1'N	$76^0$1'E	1800
2.	E2	Malan II (Rabi 2020-21)	Timely sown (Irrigated)	950	$32^0$1'N	$76^0$1'E	1800
3.	E3	Malan III (Rabi 2021-22)	Timely sown (Irrigated)	950	$32^0$1'N	$76^0$1'E	1800

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

		Mean sum of squares			
Sr.No.	**Traits**	**Source**	**Replication**	**Genotypes**	**Error**
		df	2	34	68
1	**Days to 50% flowering**	E1	5.42	26.87*	2.47
		E2	3.47	31.98*	2.94
		E3	3.65	31.98*	3.56
		Pooled	6.84*	28.76*	3.23
2	**Days to 75% maturity**	E1	1.27	40.0*	1.36
		E2	0.87	29.21*	1.88
		E3	1.47*	31.98*	2.94
		Pooled	1.16	33.77*	2.02
3	**Plant height**	E1	13.98	127.24*	48.09
		E2	16.31	320.36*	43.69
		E3	15.27	145.20*	33.45
		Pooled	16.19	141.56*	38.26
4	**Tillers per plant**	E1	0.82*	0.76*	0.12
		E2	3.19*	0.55*	0.34
		E3	4.50	0.48*	0.11
		Pooled	2.12*	0.73*	0.26
5	**Peduncle length**	E1	8.53*	72.1*	1.43
		E2	37.2	59.39*	1.24
		E3	3.70*	61.84*	2.96
		Pooled	3.23*	56.53*	2.06
6	**Biological yield per plant**	E1	3.65	9.53*	1.81
		E2	2.30	5.06*	1.31
		E3	3.14	6.91*	3.46
		Pooled	2.68*	7.97*	2.96
7	**Grain yield per plant**	E1	0.33	0.88*	0.16
		E2	5.80	1.77*	0.46
		E3	0.25	0.66*	0.33
		Pooled	5.04*	0.61*	0.39*
8	**Thousand grain weight**	E1	25.60*	54.70*	0.96
		E2	23.77*	97.67*	1.13
		E3	8.97*	54.70*	0.96
		Pooled	**14.69***	**68.77***	**1.11**

PCV was found to be high (>25%) for peduncle length, moderate (15-25%) for tillers per plant, thousand kernel weight, low (15%) for days to 50% flowering, days to 75% maturity, plant height, biological yield per plant, and grain yield per plant. There was a high GCV (>25%) noted for peduncle length; however, the GCV 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. For all traits, GCV was lower than PCV, indicating that environment had little effect on plant development. The experiments revealed that broad sense heritability (h^2bs) 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*., thousand kernel weight and peduncle length 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.

Table 3. Variability parameters for various traits in wheat genotypes under three environments and pooled over environment

Sr. No.	Traits		Mean ± S.E. (m)	Range	PCV (%)	GCV (%)	h^2bs (%)	GA (%) of mean
1	**Days to flowering**	E1	88.64±0.91	82.00-92.67	3.67	3.21	76.62	5.80
		E2	88.86±0.98	82.00-92.66	3.99	3.50	76.43	6.31
		E3	95.86±0.98	89.00-99.66	3.70	3.24	76.34	5.34
		Pooled	**107.34±0.75**	**93.71-108.93**	**3.43**	**2.56**	**83.15**	**3.43**
2	**Days to maturity**	E1	159.90±0.61	153.00-166.00	2.35	2.24	90.65	4.39
		E2	159.46±0.79	152.00-163.00	2.07	1.89	82.58	3.55
		E3	164.86±0.98	158.00-168.66	2.15	1.88	76.14	3.40
		Pooled	**168.79±0.90**	**134.06-134.54**	**3.39**	**2.63**	**87.77**	**3.78**
3	**Plant height**	E1	87.70±4.00	77.00-103.00	9.84	5.85	35.99	7.18
		E2	91.68±1.10	74.83-120.38	11.40	11.20	96.14	22.69
		E3	92.63±3.33	81.00-111.33	9.01	6.58	52.87	9.85
		Pooled	**92.86±2.05**	**71.33-113.33**	**10.24**	**9.87**	**71.24**	**16.58**
4	**Tillers per plant**	E1	3.23±0.26	2.24-4.84	19.78	13.91	49.56	20.15
		E2	4.09±0.28	2.93-6.13	18.40	13.85	56.63	21.48
		E3	3.45±0.32	2.25-4.22	19.58	11.43	34.64	13.74
		Pooled	**3.09±0.11**	**2.88-4.21**	**18.58**	**10.16**	**29.85**	**17.41**
5	**Peduncle length (cm)**	E1	16.75±0.69	9.11-25.60	29.77	28.90	94.59	57.87
		E2	15.22±0.64	8.10-25.10	28.76	28.00	93.03	55.34
		E3	13.14±0.66	6.03-23.10	33.41	33.24	93.08	64.10
		Pooled	**13.45±0.44**	**7.52-24.88**	**29.44**	**26.71**	**81.18**	**55.10**
6	**Biological yield per plant (g)**	E1	19.60±0.78	15.67-23.13	10.69	8.18	58.78	12.90
		E2	19.86±0.84	16.40-22.90	7.78	7.86	53.69	11.89
		E3	15.66±0.76	12.23-19.67	12.07	9.27	58.70	14.66
		Pooled	**17.17±0.37**	**14.80-18.73**	**11.13**	**4.84**	**34.54**	**12.34**
7	**Grain yield per plant (g)**	E1	5.96±0.23	4.75-7.01	10.63	8.21	59.18	13.06
		E2	9.53±0.39	3.39-6.50	20.78	14.55	48.67	20.91
		E3	5.92±0.33	5.09-7.12	11.22	5.58	24.25	5.73
		Pooled	**4.27±0.13**	**4.29-5.84**	**12.91**	**5.32**	**43.32**	**11.52**
8	**Thousand grain weight (g)**	E1	30.82±0.57	22.77-40.97	14.09	13.73	94.93	53.21
		E2	22.28±0.57	14.23-32.43	39.40	38.05	93.69	75.70
		E3	32.05±0.57	23.99-42.19	29.97	28.90	94.95	57.85
		Pooled	**26.85±0.67**	**21.32-36.76**	**13.27**	**9.86**	**41.78**	**59.14**

Supplementary mean table for pooled over 3 enviroments [E_1: Rabi 2019-20, E_2: *Rabi* 2020-21, E_3: *Rabi* 2021-22]

S. No.	Genotype	Days to 50% flowering	Days to maturity	Plant Height	Tiller per plant	Peduncle length	Biological yield per plant	Grain yield per plant	1000-grain weight
1	Agra Local	88.33	163.00	88.00	3.45	12.91	20.30	6.15	35.17
2	BRW 3273	90.33	159.00	90.33	3.77	17.03	18.90	5.73	29.03
3	DBW107	85.33	157.33	83.33	3.87	22.89	19.07	5.78	31.17
4	DBW179	86.67	161.67	82.67	2.86	14.46	16.17	4.90	28.37
5	DBW24	89.33	155.33	85.00	4.14	12.83	15.67	4.75	34.63
6	DBW39	91.33	166.00	80.00	3.42	15.12	19.07	5.80	35.10
7	Desi Mundla	82.67	165.67	91.67	3.42	18.52	18.43	5.59	28.70
8	FLW16	89.00	160.67	77.00	3.63	13.87	18.00	5.46	34.57
9	GRU 2010 1817	86.67	158.00	91.67	3.76	13.74	21.47	6.51	31.63
10	HD2967	85.67	159.00	84.00	4.65	20.30	21.53	6.53	29.70
11	HD3086	91.00	159.00	82.33	3.63	27.10	18.47	5.62	33.77
12	HD3237	90.33	163.33	92.67	2.85	20.54	19.57	5.94	29.53
13	HD3271	92.67	166.00	78.00	3.72	11.37	18.93	5.73	31.20
14	HI1620	91.67	164.00	91.00	3.55	25.27	17.90	5.43	29.87
15	HI8173	87.67	163.67	84.33	3.03	10.61	20.57	6.27	28.77
16	HIKK 05	90.67	165.33	95.33	2.87	17.16	23.13	7.01	23.27
17	HPW368	89.33	159.33	88.33	4.25	18.31	17.37	5.33	34.63
18	HPW376	85.67	160.33	89.33	3.72	25.27	22.23	6.70	33.43
19	HPW469	86.33	153.00	101.67	3.43	17.85	19.63	6.00	34.40
20	HPW470	92.00	158.00	82.33	2.73	18.72	18.37	5.56	25.13
21	HPW472	90.33	154.00	85.00	2.37	24.34	19.73	5.98	40.97
22	HPW473	90.00	162.33	89.67	3.69	21.37	22.50	6.81	31.03
23	HPW474	90.67	159.00	89.67	3.84	14.62	19.93	6.10	33.17
24	HS295	86.00	154.00	77.33	3.86	14.43	17.97	5.44	24.47
25	HS627	90.33	154.00	83.00	4.20	24.34	21.13	6.47	28.73
26	HTW9	92.33	159.67	89.00	3.81	22.67	20.53	6.19	28.83
27	HW3631	89.33	158.33	84.33	4.24	21.71	20.80	6.31	31.17
28	Kanku	85.00	157.00	102.33	3.64	25.97	22.07	6.71	33.77
29	KBRL 79 2	91.33	158.33	103.00	3.47	15.13	18.70	5.67	25.13
30	PBW724	83.67	160.00	83.67	2.75	12.73	17.87	5.44	32.10
31	PBW725	84.33	156.67	81.00	4.23	12.87	21.27	6.45	24.43
32	PBW752	82.00	159.00	89.00	3.86	25.97	17.83	5.39	39.23
33	PBW756	90.67	158.33	89.67	3.28	20.78	19.77	6.37	33.87

34	PBW757	91.33	164.00	93.00	3.48	14.83	21.80	6.59	22.77
35	PBW771	92.33	164.33	90.67	3.77	12.83	19.40	6.03	27.13
36	PBW812	85.83	160.5	85.5	2.37	11.83	19.22	5.07	34.09
37	PBW813	87.83	156.5	87.83	2.69	15.95	17.82	4.65	27.95
38	PW1903	82.83	154.83	80.83	2.79	21.81	17.99	4.7	30.09
39	PW1904	84.17	159.17	80.17	1.78	13.38	15.09	3.82	27.29
40	PW1905	86.83	152.83	82.5	3.06	11.75	14.59	3.67	33.55
41	PW1906	88.83	163.5	77.5	2.34	14.04	17.99	4.72	34.02
42	PW1908	80.17	163.17	89.17	2.34	17.44	17.35	4.51	27.62
43	PW1909	86.5	158.17	74.5	2.55	12.79	16.92	4.38	33.49
44	PW1910	84.17	155.5	89.17	2.68	12.66	20.39	5.43	30.55
45	PW1911	83.17	156.5	81.5	3.57	19.22	20.45	5.45	28.62
46	PW1912	88.5	156.5	79.83	2.55	26.02	17.39	4.54	32.69
47	Sonalika	87.83	160.83	90.17	1.77	19.46	18.49	4.86	28.45
48	Tarmori	90.17	163.5	75.5	2.64	10.29	17.85	4.65	30.12
49	TL3006	89.17	161.5	88.5	2.47	24.19	16.82	4.35	28.79
50	TYR1	85.17	161.17	81.83	1.95	9.53	19.49	5.19	27.69
51	TYR2	88.17	162.83	92.83	1.79	16.08	22.05	5.93	22.19
52	TYR3	86.83	156.83	85.83	3.17	17.23	16.29	4.25	33.55
53	TYR4	83.17	157.83	86.83	2.64	24.19	21.15	5.62	32.35
54	TYR5	83.83	150.5	99.17	2.35	16.77	18.55	4.92	33.32
55	Unnat PBW 550	89.5	155.5	79.83	1.65	17.64	17.29	4.48	24.05
56	WH1105	87.83	151.5	82.5	1.29	23.26	18.65	4.9	39.89
57	WH1124	87.5	159.83	87.17	2.61	20.29	21.42	5.73	29.95
58	WH1127	88.17	156.5	87.17	2.76	13.54	18.85	5.02	32.09
59	WH1142	83.5	151.5	74.83	2.78	13.35	16.89	4.36	23.39
60	WH1216	87.83	151.5	80.5	3.12	23.26	20.05	5.39	27.65
61	WH1264	89.83	157.17	86.5	2.73	21.59	19.45	5.11	27.75
62	WH1270	86.83	155.83	81.83	3.16	20.63	19.72	5.23	30.09
63	HPW251	82.5	154.5	99.83	2.56	24.89	20.99	5.63	32.69
64	HS240	88.83	155.83	100.5	2.39	14.05	17.62	4.59	24.05
65	HS562	81.17	157.5	81.17	1.67	11.65	16.79	4.36	31.02
66	PBW723	85.83	160.5	85.5	2.37	11.83	19.22	5.07	34.09
	Mean	87.50	158.73	86.45	3.06	17.71	19.07	5.44	30.48
	CD (P=0.05)	2.56	1.90	11.30	0.57	1.95	2.19	0.66	1.59
	CV	1.77	0.73	7.91	9.77	6.56	6.87	6.76	3.18

Results and Discussion

The analysis of variance conducted across various wheat genotypes in diverse agro-ecological zones of Himachal Pradesh indicated the presence of substantial genetic diversity for all the evaluated parameters. Jee *et al*. (2019) observed highly significant differences between the genotypes in their study, indicating that the germplasm selected for the study exhibited a wide range of variation, which is crucial for any breeding program. In terms of the Coefficient of Phenotypic Variation (PCV) and Coefficient of Genotypic Variation (GCV), it was noted that PCV values were slightly higher than GCV values. This finding is consistent with the results reported by Singh *et al*. (2018) in wheat, Gautam *et al*. (2021) in chickpea, and Shiva Kumar *et al*. (2021) in linseed. This suggests that environmental factors have a relatively minor influence on the expression of the evaluated traits. For traits such as peduncle length, tillers per plant, and thousand kernel weight, both PCV and GCV ranged from moderate to high. Similarly, Singh *et al*. (2019) and Morteza *et al*. (2018) reported high GCV and PCV values for biological yield per plot and harvest index. Heritability and genetic progress are key factors in selecting traits for the genetic improvement of wheat grain yield. For traits like days to 50% flowering, days to 75% maturity, plant height, peduncle length, and thousand kernel weight, the heritability in the broad sense (h2bs) and Genetic Advance (GA) as a percentage of the mean were found to be moderate to high. Singh *et al*. (2019) reported a 5% mean heritability and genetic advance for variables such as harvest index, number of grains per spike, and biological yield per plot. Singh *et al*. (2018) discovered high GCV and PCV, as well as high heritability and genetic progress, suggesting that additive gene action and selection could be effective for improving these traits. These findings provide valuable insights into the potential for genetic improvement of wheat and other crops.

Conclusion

In Multi-environment Trials (METs) conducted in the Northern Hills Zone, the assessed wheat genotypes exhibited significant diversity in the analysed variables. Among the genotypes tested, six of them, namely HPW 368, HPW 474, WH 1105, WH 1142, HD 2967, and PW 1909, demonstrated comparable performance to the check varieties PBW 723 and HS 562 in terms of pooled grain yield per plant across three different environments. This suggests that these genotypes have the potential to be further studied in future METs and could be valuable candidates for inclusion in breeding programs aimed at improving wheat varieties in the Northern Hills Zone.

Acknowledgement: The authors would like to express their gratitude to the Department of Science and Technology (DST, INSPIRE) for providing financial support, Department of Genetics and Plant Breeding, CSK HPKV, Palampur (H.P.) and Rice and Wheat Research Centre, Malan, Kangra (H.P.) for providing the research facilities.

Conflicts of Interest: The authors declare that there is no conflict of interest.

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