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Assessment of genetic variability, heritability and genetic advance for yield and physiological traits under normal sown condition in bread wheat (*Triticum aestivum* L. em. Thell.)

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Abstract

The present investigation was carried out with 32 diverse genotypes of bread wheat in completely randomized block design with 3 replications at GBPUAT, Pantnagar under normal sown condition. The observations were recorded on 15 agronomic traits and 3 physiological traits. The statistical analysis for genetic variability was done using ANOVA, h^2 , GCV, PCV and GA. The analysis of variance revealed significant difference among the genotypes. The results of the present study indicated that high heritability values were observed in all the characters studied except grain filling duration. High GCV and PCV were observed for the characters plot yield, canopy temperature depression-I, -II, -III and SPAD value. Moderate GCV and PCV were found for the characters 1000 grain weight, harvest index, relative water content, grain weight per spike and biological yield per plant whereas low GCV and PCV were observed for the characters days to 75% heading, days to 75% anthesis, days to 75% maturity and grain filling duration. The genetic advance was observed moderate for the character like SPAD, harvest index and days to 75% heading while low genetic advance was estimated for the rest of the characters. High genetic advance was observed for none.

Keywords: variability, SPAD, GCV, PCV, GA and h^2 .

Introduction

Wheat is one of the most important and widely grown crops in the world having the area of 224.82 million hectare with the production of about 732.98 million tonnes and productivity of 3.26 tonnes per hectare globally (Anonymous, 2015a) [3]. India is second largest producer of wheat in the world. The area, production, and productivity of wheat in India in 2017-18 was 29.58 million ha, 99.7 million ton and 3.37 ton/ha, respectively (ICAR-IIWBR, 2018) [11]. It is grown in all the regions of the country and the states, and Uttar Pradesh, Punjab, Haryana, Madhya Pradesh, Rajasthan, Bihar, Maharashtra, Gujarat, West Bengal, Uttarakhand and Himanchal Pradesh together contribute about 98% to the total wheat production of the country and play an important role of supplying carbohydrate and protein (Tewari *et al.*, 2015) [26].

To overcome the problem of different biotic and abiotic stresses genetic variability analysis is one of the best ways to screen out the best donors for in any crop improvement breeding programme. Genetic variability and relationship among genotypes is a prerequisite for any successful breeding programme. Genetic variability of plants determines their potential for improved efficiency and hence their use for breeding, which eventually may result in enhanced food production. Evaluation of genetic variability levels among adapted, elite germplasm can provide predictive estimates of genetic variation among segregating progeny for pure-line cultivar development. Genetic variability explains the genetic differences between different populations within a species or between species. Genetic variability can be estimated by assessing the different genetic parameters like analysis of variance, heritability and genetic advance etc. The parents having more genetic variability result into higher heterotic expression in F1 and greater amount of genetic variability in segregating populations (Shekhawat *et al.*, 2001) [23].

Precise information on nature and degree of genetic variability helps the plant breeder in selecting the genetically diverse parents for the purposeful hybridization. (Arunachalam, 1981) [4]. Genetic improvement of yield especially in self-pollinated crops depends on nature and amount of genetic variability (Joshi and Dhawan, 1966) [13]. One of the important approaches to wheat breeding is hybridization and subsequent selection. Parents' choice is the

first step in plant breeding program through hybridization. In order to obtain transgressive segregants, genetic variability between parents is necessary (Joshi *et al.*, 2004) [14]. The higher genetic variability between parents, the higher heterosis in progeny can be observed (Joshi and Dhawan, 1966) [13]. Estimation of genetic variability is one of appropriate tools for parental selection in wheat hybridization programs. Appropriate selection of the parents is essential to be used in crossing nurseries to enhance the genetic recombination for potential yield increase. In view of the above, there is need to screen the variability of bread wheat genotypes based on morphological and physiological parameters to find out their suitability in different breeding programmes.

Materials and Methods

The initial research related to screening was carried out in the experimental area of N.E. Borlaug Crop Research Centre (NEBCRC), G.B. Pant University of Agriculture and Technology, Pantnagar, District U.S. Nagar, Uttarakhand during *rabi*, 2014-15. The experimental material consists of 32 genotypes of bread wheat including 3 checks (Table-1), namely, HD-2967, PBW-343 and C-306. The experiment was

laid out in randomized complete block design (RBD) with three replications under normal sown condition on 15 November, 2014. All the thirty two genotypes were evaluated during Rabi 2014-15. Each entry was planted in 5 meter long four rows plot. The rows were spaced 20 cm apart. All the recommended package of practices for wheat was followed to raise a healthy crop.

All the yield attributing and physiological observations on most of the characters were recorded on single plant basis except for days to 75 per cent heading, maturity and canopy temperature depression (CTD). Five representative plants from each plot were randomly selected and tagged for recording the observations on single plant basis. Average data from selected plants in respect of different character were used for statistical analysis. The observations were recorded for the sixteen yield attributing traits like days to 75% heading (DH), days to 75% anthesis (DA), days to 75% maturity (DM), plant height (PH), number of tillers per plant (NTP), grain filling duration (GFD), spike length (SL), number of spikelets per spike (NSS), number of grains per spike (NGS), grain weight per spike (GWS), 1000 grain weight (TGW), biological yield per

Table 1: List of Genotypes/Varieties

S. No.	Genotype	S. No.	Genotype	S. No.	Genotype	S. No.	Genotype
1.	PBN-51	9.	IC-532653	17.	HI-1563	25.	SONORA-64
2.	BWL-1793	10.	DHARWAR DRY	18.	HD-2864	26.	BACANORA-88
3.	BWL-0814	11.	GIZA-155	19.	RAJ-3765	27.	SALEMBO
4.	HD-2967 (check)	12.	ARIANA-66	20.	RAJ-4083	28.	CHIRYA-3
5.	BWL-1771	13.	PBW-343 (check)	21.	DBW-14	29.	BWL-9022
6.	BWL-0924	14.	BABAX	22.	WH-730	30.	CUS/79/PRULLA
7.	C-306 (check)	15.	IEPACA RABE	23.	RAJ-4037	31.	K-9465
8.	IC-11873	16.	OTHERY EGYPT	24.	SERI-82	32.	TEPOKO

Plant (BY), grain yield per plot (GY), harvest index (HI) and three physiological traits, canopy temperature depression (CTD), relative water content percent (RWC%) and chlorophyll content (SPAD value) of leaf. Canopy temperature was recorded 3 times at the interval of 10 days at different growth stages of the crop from the start of flowering (GS 61) to early dough stage (GS 83 as per Zodoks *et al.*, 1974) [28] and it was mentioned as canopy temperature -I (CT -I), canopy temperature-II (CT-II), canopy temperature-III (CT-III), and difference between canopy temperature and ambient temperature was calculated and it was designated as canopy temperature depression (CTD I, II and III). The infrared thermometer was used to measure the canopy temperature. SPAD value was observed at flowering stage by SPAD meter. The statistical analysis was performed by Indostat Hyderabad.

(A) Analysis of variance and means: Characters under study were analyzed using analysis of variance to test whether treatments were differing significantly among themselves. The model is as follows:

$$Y_{ij} = \mu + b_i + t_j + e_{ij}$$

Where,

- i = 1, 2, ----- r (replication)
 j = 1, 2, ----- t (treatment)
 Y_{ij} = performance of jth variety in the ith block
 μ = population mean
 b_i = true effect of ith block

- t_j = true effect of jth treatment
 e_{ij} = random error
 r = number of replications
 t = number of treatments

$$\text{Restrictions are } \sum_{i=1}^r b_i = 0 \text{ and } \sum_{j=1}^t t_j = 0$$

(B) Estimation of variability

$$\text{CV (\%)} = \frac{\text{Standard deviation}}{\text{Mean}} \times 100$$

$$\text{Genotypic coefficient of variation (GCV \%)} = \frac{\sigma_g}{\bar{X}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV \%)} = \frac{\sigma_p}{\bar{X}} \times 100$$

$$\text{Environmental coefficients of variation (ECV \%)} = \frac{\sigma_e}{\bar{X}} \times 100$$

Where,

- σ_g = Genotypic standard deviation
 σ_p = Phenotypic standard deviation
 σ_e = Environmental standard deviation
 \bar{X} = Grand mean

(C) Estimation of Heritability: The heritability in broad sense h² (b) was estimated for each character as the ratio

of genotypic variance to phenotypic variance by the formula:

$$\text{Heritability (\%)} = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

(D) Genetic Advance: The expected genetic advance under selection for the different characters was estimated as suggested by Allard (1960)^[2].

$$GA = h_b^2 \times \sigma_p \times K$$

Where,

GA = expected genetic advance

h_b^2 = heritability in broad sense

σ_p = phenotypic standard deviation for ith character

K = intensity of selection, the value of which is 2.06 at 5 % (Lush, 1949)

Results and Discussion

Analysis of variance for yield and physiological traits: The analysis of variance was carried out for all the characters in Randomized Block Design and the result are presented in the Table 2. The mean sum of square of the differences among the treatments is highly significant for all the characters under timely sown condition. This type of result indicated existence of inherent genetic differences among genotypes for different characters. The analysis of variance revealed significant difference among the genotypes which validated further on the basis of genetic and statistical analysis of the data. It revealed that mean squares due to genotypes were found to be significant for all the characters.

Table 2: Analysis of variance for yield, yield attributes and physiological traits

SV	df	DH	DA	DM	PH	GFD	SL	NSS	NGS	GWS	NTP
Replication	2	26.313	4.312	12.75	35.906	10.507	0.316	2.445	38.500	0.045	0.126
Treatment.	31	98.88**	36.623**	53.52**	417.616**	22.317**	2.749**	6.676**	128.838**	0.477**	1.503**
Error	62	2.67	1.581	4.654	15.260	4.951	0.288	0.643	12.888	0.029	
GM		87.198	93.02	132.406	100.007	39.458	11.062	19.196	57.302	2.412	6.150
SEm±		0.943	0.727	1.245	2.255	1.284	0.309	0.463	2.072	0.098	0.160
CD at 1%		3.544	2.729	4.68	8.476	4.828	1.165	1.741	7.790	0.370	0.604
CD at 5%		2.67	2.052	3.52	6.376	3.631	0.876	1.309	5.859	0.278	0.454
CV		1.88	1.351	1.629	3.906	5.639	4.853	4.180	6.265	7.078	4.527

Continued...

SV	d.f.	BY	GY	PY	TGW	HI	CTD I	CTD-II	CTD-III	SPAD	RWC
Replication	2	0.144	0.367	912	13.281	6.179	0.034	0.464	0.070	26.820	26.83
Treatment.	31	26.024**	8.466**	692888.8**	50.728**	99.268**	14.537**	3.119**	3.088**	227.094**	168.93**
Error	62	0.318	0.176	829.419	3.511	5.562	0.053	0.054	0.050	1.740	1.706
GM		20.008	7.910	2210.354	38.481	39.501	3.994	4.313	2.681	40.544	66.341
SEm±		0.325	0.242	16.627	1.081	1.362	0.133	0.134	0.130	0.761	0.754
CD at 1%		1.224	0.911	62.494	4.066	5.117	0.501	0.504	0.489	2.862	2.834
CD at 5%		0.921	0.685	47.006	3.058	3.849	0.377	0.379	0.368	2.153	2.132
CV		2.820	5.311	1.302	4.869	5.970	5.788	5.388	8.413	3.253	1.969

*Significant at 5% level, ** Significant at 1% level

DH-Days to 75% heading, DA-Days to 75% anthesis, DM-Days to 75% maturity, GFD-Grain filling duration, PH-Plant height, PL-Peduncle length, SL-Spike length, NSS- Number of spikelets per spike, NGS-Number of grains per spike, GWS-Grain weight per spike, NTP-Number of tillers per plant, BY-Biological yield per plant, GY- Grain yield/plot, TGW-1000 grain weight, CTD-Canopy temperature depression, RWC-Relative water content %, SPAD- Soil-plant analysis development (chlorophyll content), HI-Harvest index %.

The mean performance of 32 varieties for 20 characters has been listed in the Table 3. Plot yield exhibited the highest range varying from 915.333 g (IC 532653) to 3141.33 g

(BWL 1771) among yield contributing traits. Among physiological traits RWC exhibited the highest range varying from 48% (BWL 0924) to 83.83% (C- 306).

Table 3: Mean Performance of Grain Yield, Yield Components and Physiological Traits.

S. No.	Genotype	DH	DA	DM	PH	GFD	SL	NSS	NGS	GWS	NTP
1.	PBN-51	90.33	93.7	134	90.07	40.33	10.36	18.6	72.87	2.79	6.13
2.	BWL-0814	89.33	94.7	135.3	98.6	40.67	10.91	18.87	61	2.59	5.47
3.	BWL-1771	90.67	94.3	132	94.8	37.67	11.07	21.3	58.33	2.54	5.8
4.	BWL-9022	83.67	91	131.3	96.33	40.33	11.42	19.13	61.93	2.95	6.4
5.	BWL-0924	89.33	94	132	92.13	38	10.45	17.87	57.13	2.33	6.13
6.	BWL-1793	83.33	89.3	131.3	92.73	42	10.94	18.33	54.8	2.52	6.8
7.	CUS/79/PRULLA	90.33	93	132.7	114.9	39.67	12.55	17.07	54.8	3.09	7.03
8.	IEPACA RABE	83.33	90.7	131.7	96.8	41	12.36	21.23	54.8	2.43	5.4
9.	CHIRYA-3	89.67	92.7	133.3	91.67	40.67	10.5	20	66.2	3.04	6.47
10.	DHARWAD DRY	94.67	98	139.7	117.7	41.67	11.43	19.93	59	2.28	7.2
11.	RAJ3765	81.33	89.7	132	95.73	42.33	11.85	20	59.33	2.47	5.67
12.	HI1563	79	88.7	131.3	94.6	42.67	12.49	20.13	53.87	2.19	6.53

13.	HD2864	81	93.3	126.3	88.27	33	11.39	17.6	59.73	2.33	6.37
14.	RAJ4083	82.67	91	131	85.33	40	10.85	18.4	52.2	2.18	6.67
15.	DBW-14	78	88	127.7	86.67	39.67	10.84	18.87	48.53	2.08	7.8
16.	WH730	88	92	131.7	113.3	39.67	12.72	18.67	55.27	3.05	5.43
17.	K9465	87.67	92.7	126.7	96.07	34	11.19	18.87	52.8	2.51	5.27
18.	RAJ4037	87.67	93.3	131	90.4	37.67	10.75	15.73	45.73	2.16	6.2
19.	TEPOKO	86	93	132	103.3	39	11.44	17.4	67.8	2.92	6.6
20.	BABAX	90.67	93.7	134.7	103.2	41	12.88	20	62	2.65	6
21.	OTHERI RGYPT	89.67	92.7	137.3	101	44.67	10.86	18.47	62.6	2.84	5.73
22.	IC532653	95.33	102	142	113.7	40.33	9.74	20.67	56.07	2.11	5.7
23.	SERI82	77.67	90	128	95.33	38	10.23	20.73	58.13	1.92	6.53
24.	SONORA64	74	84.7	126.7	90.07	42	9.23	17.67	42.13	1.41	5.67
25.	SALEMBO	91	94.7	135.7	96.4	41	11.09	20.47	58.73	2.41	5.2
26.	ARIANA66	102.7	103	143.3	131.9	41	11.32	22.2	57.53	1.83	5.53
27.	GIZA155	88.67	94	136	118.1	42	9.113	19.8	56	2.43	7
28.	BACANORA88	89.33	93.7	132	87.93	38.33	10.5	19.77	58.53	2.4	6.2
29.	IC118737	88.33	93	126.3	96.53	33.33	12.23	21.73	68.2	1.7	4.47
30.	C-306	86.67	93.3	126.7	125.5	35	9.827	16.93	51.33	2.33	5.73
31.	HD2967	90.33	94.3	132.7	106.9	38.33	11.35	19.27	59.53	2.64	7.2
32.	PBW343	90	95	132.7	94.2	37.67	10.14	18.6	46.73	2.07	6.47
Range		74.7-102.7	84.7-103	126.3-143.3	85.33-131.9	33-44.67	9.113-12.128	15.73-22.2	42.13-72.87	1.41-3.09	4.47-7.8
GM		87.19	93.042	132.406	100.007	39.458	11.078	19.197	57.281	2.409	6.15

Continued...

S. No.	Genotype	BY	GY	PY	TGW	HI	CTD I	CTD-II	CTD-III	SPAD	RWC
1.	PBN-51	20	6.8	2335.33	40.78	34.04	5.3	2.43	1.53	42.43	49.78
2.	BWL-0814	20.2	8.07	2562.67	39.37	39.94	5.6	2.23	2.3	32.67	61.72
3.	BWL-1771	18	7.47	3141.33	37.28	41.48	5.17	4.07	3.2	32.83	74.09
4.	BWL-9022	25.27	10.9	2430	46.97	43.29	1.17	5.08	1.33	39.6	65.51
5.	BWL-0924	18	6.93	2730.67	44.23	38.53	5.3	3.2	1.9	46.87	48
6.	BWL-1793	19.2	8.53	2534	41.73	44.44	1.63	3.63	1.57	33.9	70.77
7.	CUS/79/PRULLA	24.53	8.67	1934	45.48	35.32	5.03	3.27	1.7	33.23	68.09
8.	IEPACA RABE	20.47	8.73	2640	39.88	42.68	1.17	4.51	1.37	33.37	64.88
9.	CHIRYA-3	24.6	9.13	2533.33	34.73	37.12	4.23	3.4	3.3	40.97	74.01
10.	DHARWAD DRY	21	7.87	2347.33	35.73	37.47	5.1	4.37	3.4	33.07	69.85
11.	RAJ3765	19.13	6.93	2351.33	36.32	36.24	0.83	4.41	2.47	67.43	62.91
12.	HI1563	20	8.2	2560.67	36.07	40.99	1.27	5.4	4.33	34.23	61.19
13.	HD2864	17.6	6.33	2457.33	34	36.02	1.57	4.35	4	50.2	62.05
14.	RAJ4083	20.93	8.53	2160.67	36.48	40.78	0.97	4.69	2.9	47	62.15
15.	DBW-14	22.27	9.33	2144.67	36.43	41.91	0.4	5.6	3.87	41.47	67.52
16.	WH730	21.07	10.6	1950	37.63	50.34	4.5	6.37	1.23	45.1	64.07
17.	K9465	22.53	7.87	1756.67	42.73	34.9	4.07	4.07	2.2	69.9	67.41
18.	RAJ4037	16.6	8.33	1675.33	38.3	50.25	5.33	4.33	2.73	32.63	65.62
19.	TEPOKO	16.47	7.53	2032.67	34.27	45.78	6.23	4.67	2.53	36.5	65.29
20.	BABAX	21.47	10.1	2257.33	37.2	47.46	6.57	4.63	2.57	38.16	59.83
21.	OTHERI RGYPT	20.47	9.47	2071.33	42.13	46.25	5.7	3.9	2.33	41.4	61.98
22.	IC532653	16.67	6.13	915.333	35.3	36.87	3.67	2.57	2.47	42.8	68.2
23.	SERI82	22.93	8	2140.67	35.72	34.9	0.8	6.03	4.43	36.63	51.02
24.	SONORA64	13.07	5	1670.67	30.48	38.24	1.4	4.93	4.65	37	66.65
25.	SALEMBO	20.93	6.33	3042	39.77	30.28	6	3.47	1.67	36.4	72.83
26.	ARIANA66	19.27	5.07	1758	37.28	26.27	1.6	4	3.47	41.23	74.2
27.	GIZA155	18.53	6.27	1574.67	42.67	33.76	6.47	5.2	4.07	40.17	73.16
28.	BACANORA88	20.47	8.67	2433.33	32.92	42.35	6.13	3.93	1.53	34.73	73.54
29.	IC118737	14.13	5.4	1676	31.95	38.2	6.37	5.77	3.17	36.97	72.02
30.	C-306	17.67	5.2	1538.67	45.45	29.46	6.73	5.53	1.4	37.38	83.83
31.	HD2967	21.33	9.6	2630	40.68	45.02	5.9	3.53	2.67	41.47	70.93
32.	PBW343	25.47	11.1	2745.33	41.43	43.48	5.63	4.47	3.53	39.67	69.84
Range		13.07-25.47	5-11.1	915.333-3141.33	30.48-47.97	26.27-50.35	0.4-6.73	2.23-6.37	1.23-4.65	32.63-69.9	48-83.83
GM		20.008	7.91	2210.35	38.49	39.50	3.995	4.313	2.85	40.544	66.321

Under normal sown condition, Days to 75% heading had a range of variation from 74 days (Sonora 64) to 102 days (Ariana 66) with a general mean of 87 days, days to 75% anthesis varied from 84 days (Sonora 64) to 103 days (Ariana 66) with a general mean of 93 days, The mean value of days to 75% maturity ranged from 126 days (HD 2864) to 143 days (Ariana 66) with a general mean of 132 days.

Plant height exhibited a wide range of variation from 85.33 cm (Raj 4083) to 131.9 cm (Ariana 66) with a general mean of 100.007 cm. The mean value of grain filling duration ranged from 33 days (HD 2864) to 44 days (Othery Egypt) with a general mean of 39 days. Spike length exhibited a wide range of variation from 9.113 cm (Giza 155) to 12.88 cm (Babax) with a general mean of 11.078 cm. Number of

spikelets per spike was marked with the range of variation from 15.73 (Raj 4037) to 22.2 (Ariana 66) with a general mean of 19.197. Number of grain per spike exhibited a wide range of variation from 42.13 (Sonora 64) to 72.87 (PBN 51) with a general mean of 37.281. Grain weight per spike exhibited a range of variation from 1.41 g (Sonora 64) to 3.09 g (CUS/79/PRULLA) with a general mean of 2.400 g. Number of tillers per plant revealed a range of variation from 4.47 (IC 118737) to 7.8 (DBW 14) with a general mean of 6.15. Biological yield per plant exhibited a wide range of variation from 13.07 g (Sonora 64) to 25.47 g (PBW 343) with a general mean of 20.008 g. Grain yield per plant exhibited a wide range of variation from 5 g (Sonora 64) to 11.1 g (PBW 343) with a general mean of 7.91 g. Plot yield was marked with the range of variation from 915.333 g (IC 532653) to 3141.33 g (BWL 1771) with a general mean of 2210.35 g. 1000-grain weight exhibited a wide range of variation from 30.48 g (Sonora 64) to 46.97 g (BWL 9022) with a general mean of 38.495 g. Harvest index exhibited a wide range of variation from 26.27% (Ariana 66) to 50.35% (DBW 14) with a general mean of 39.501%.

In case of Canopy Temperature Depression, the observation was recorded in three different days during wheat growing period. The first observation which was recorded at the time of heading ranged from 0.4°C (DBW14) to 6.73°C (C-306)

with an average of 3.995°C. During second observation *i.e.* 10 days after heading it varied from 2.23°C (BWL 0814) to 6.37°C (WH 730) with an average of 4.313°C. The third observation, 20 days after heading ranged from 1.23°C (WH 730) to 4.65°C (Salemba) with a general mean of 2.85°C. SPAD value represented a range of variation from 32.63 (Raj 4037) to 69.9 (K 9465) with a general mean of 40.544 while Relative water content (%) was marked with a wide range of variation from 48% (BWL 0924) to 83.83% (C-306) with a general mean of 66.321%.

Success of any breeding programme depends upon the extent of variability present in the breeding population. The estimation of variability is of utmost importance in a crop for the identification of lines which can generate further variability so that artificial selection of desirable diverse genotypes may be made. Some of the very useful variations would go unutilized if not be identified by the breeder during selection process. In the present investigation material under study observed having high magnitude of variation for plot yield, grain yield/plant, and harvest index and plant height. These results are in agreement with those of Singh *et al.* (1970), Hirachand *et al.* (1978)^[10] and Balyaeva (1981)^[6].

Heritability, GCV, PCV and GA: The coefficient of variation at genotypic (GCV), phenotypic (PCV) level and genetic advance are presented in Table 4.

Table 4: Coefficient of Variation, Heritability and Genetic Advance

S. No.	Character	h^2 (%)	GA	GCV	PCV
1	DH	92.32	11.21	6.5	6.76
2	DA	88.98	6.773	3.75	3.97
3	DM	77.79	7.333	3.05	3.46
4	GFD	53.9	3.639	6.1	8.31
5	PH	89.78	22.6	11.6	12.2
6	SL	72.01	1.584	8.18	9.64
7	NSS	71.4	2.326	9.96	8.24
8	NGS	75.02	11.14	10.9	12.6
9	GWS	83.89	0.734	16.2	17.6
10	NTP	85.97	1.317	11.2	12.1
11	BY	96.42	5.921	14.6	14.9
12	GY	94	3.32	21	21.7
13	PY	99.64	9.87	21.7	21.8
14	TGW	82.65	7.421	10.3	11.3
15	HI	84.88	10.61	14.1	15.4
16	CTD-I	98.91	4.501	55	55.3
17	CTD-II	95.02	2.027	23.4	24
18	CTD-III	21.71	0.836	30.5	65.5
19	RWC	96.71	15.28	11.4	11.6
20	SPAD	97.74	17.65	21.4	21.6

Robinson *et al.* (1949) classified heritability values as high (>60%), moderate (30-60%) and values less than 30% low. Accordingly, the results of the present study indicated that high heritability values were observed in all the characters studied except grain filling duration in which heritability was moderate. High heritability values for these traits indicated that the variation observed was mainly under genetic control and was less influenced by the environment and the possibility of progress from selection. The value of broad sense heritability (h^2) was 92.322% for Days to 75% Heading, 88.984% for Days to 75% Anthesis, 77.785% for Days to 75% Maturity, 53.898% for Grain Filling Duration, 89.78% for Plant Height, 72.005% for Spike Length, 71.396% for Number of spikelets per spike, 75.019% for Number of Grains per Spike, 83.893% for Grains Weight per Spike, 85.971% for Number of Tillers per Plant, 96.422% for Biological Yield per plant, 93.996% for Grain Yield per plant,

99.639% for Plot Yield, 82.648% for 1000 Grain Weight, 84.876% for Harvest Index, 98.905% for Canopy Temperature Depression-I, 95.015% for Canopy Temperature Depression -II, 21.713% for Canopy Temperature Depression -III, 96.709% for Relative Water Content, 97.737% for SPAD. These findings are similar with the findings of Rahim *et al.* (2010), Salem *et al.* (2008)^[22], Ali *et al.* (2008)^[1] and Khan *et al.* (2010)^[16].

Deshmukh *et al.* (1986)^[8] classified PCV and GCV values as low (0-10%), moderate (10-20%) and high (20% and above) values. According to this classification, high GCV and PCV were observed for the characters plot yield, canopy temperature depression-I, canopy temperature depression-II, canopy temperature depression-III and SPAD value. Moderate GCV and PCV were found for the characters 1000 grain weight, harvest index, relative water content, grain weight per spike, plant height, number of tillers per plant and

biological yield per plant whereas low GCV and PCV were observed for the characters days to 75% heading, days to 75% anthesis, days to 75% maturity, grain filling duration, spike length and number of spikelets per spike.

The value of Genotypic Coefficient of Variation for Days to 75% Heading was 6.495, 3.746 for Days to 75% Anthesis, 3.048 for Days to 75% Maturity, 6.097 for Grain Filling Duration, 11.58 for Plant Height, 8.177 for Spike Length, 6.96 for Number of spikelets per spike, 10.903 for Number of Grains per Spike, 16.158 for Grains Weight per Spike, 11.209 for Number of Tillers per Plant, 14.63 for Biological Yield per plant, 21.015 for Grain Yield per plant, 21.729 for Plot Yield, 10.294 for 1000 Grain Weight, 14.148 for Harvest Index, 55.004 for Canopy Temperature Depression -I, 23.405 for Canopy Temperature Depression -II, 30.538 for Canopy Temperature Depression -III, 11.37 for Relative Water Content, 21.377 for SPAD.

The value of Phenotypic Coefficient of Variation for Days to 75% Heading was 6.759, 3.971 for Days to 75% Anthesis, 3.456 for Days to 75% Maturity, 8.305 for Grain Filling Duration, 12.221 for Plant Height, 9.637 for Spike Length, 8.237 for Number of spikelets per spike, 12.589 for Number of Grains per Spike, 17.641 for Grains Weight per Spike, 12.089 for Number of Tillers per Plant, 14.899 for Biological Yield per plant, 21.676 for Grain Yield per plant, 21.769 for Plot Yield, 11.323 for 1000 Grain Weight, 15.357 for Harvest Index, 55.308 for Canopy Temperature Depression -I, 24.011 for Canopy Temperature Depression -II, 65.536 for Canopy Temperature Depression -III, 11.562 for Relative Water Content, 21.623 for SPAD. These findings are in agreement with the findings of Kalim *et al.* (2011), Wani *et al.* (2011)^[27] and Monpara (2011)^[5].

Falconer and Mackay (1996)^[9] classified genetic advance as percent of mean as low (0-10%), moderate (10-20%) and high (20% and above). Heritability and genetic advance are important selection parameters. The estimate of genetic advance is more useful as a selection tool when coupled with heritability estimates (Johnson *et al.*, 1955)^[12]. The estimates of genetic advance help in understanding the type of gene action involved in the expression of various quantitative characters. High values of genetic advance are indicative of additive gene action whereas low values are indicative of non-additive gene action (Singh and Narayanan, 1999)^[24]. The genetic advance was observed moderate for the character like relative water content, SPAD, harvest index, number of grains per spike and days to 75% heading while low genetic advance was estimated for the rest of the characters. High genetic advance was observed for none. The value of Genetic Advance for Days to 75% Heading was 11.209, 6.773 for Days to 75% anthesis, 7.333 for Days to 75% Maturity, 3.639 for Grain Filling Duration, 22.604 for Plant Height, 1.584 for Spike Length, 2.326 for Number of spikelets per spike, 11.144 for Number of Grains per Spike, 0.734 for Grains Weight per Spike, 1.317 for Number of Tillers per Plant, 5.921 for Biological Yield per plant, 3.332 for Grain Yield per plant, 9.87 for Plot Yield, 7.421 for 1000 Grain Weight, 10.606 for Harvest Index, 4.501 for Canopy Temperature Depression -I, 2.027 for Canopy Temperature Depression -II, 0.836 for Canopy Temperature Depression -III, 15.276 for Relative Water Content and 17.651 for SPAD. These findings are similar with the findings of Degewione *et al.* (2013)^[7], Singh and Narayanan (1999)^[24] and Munir *et al.* (2007)^[18].

Summary and Conclusion

The analysis of variance revealed significant difference

among the genotypes which validated further on the basis of genetic and statistical analysis of the data. It revealed that mean squares due to genotypes were found to be significant for all the characters. Plot yield exhibited the highest range varying from 915.333 g (IC 532653) to 3141.33 g (BWL 1771) among yield contributing traits while among physiological traits, relative water content (RWC) exhibited the highest range varying from 48% (BWL 0924) to 83.83% (C- 306). Broad sense heritability was found highest for plot yield (99.64) and lowest for grain filling duration (53.9) among yield contributing traits while among physiological traits, canopy temperature depression-I had highest value (98.91) and lowest by canopy temperature depression-III (21.71). Highest genetic advance was exhibited by SPAD (9.87) and lowest by grain weight per spike (0.734) among yield contributing traits while SPAD was marked by highest (17.65) and canopy temperature depression-III had lowest (0.836) among physiological traits. Plot yield exhibited highest GCV (21.7) and PCV (21.8) while lowest GCV (3.05) and PCV (3.46) were exhibited by Days to 75% maturity among yield contributing traits. Among physiological traits highest GCV and PCV were exhibited canopy temperature depression-I by (55) and canopy temperature depression-III (65.5) while relative water content had lowest GCV (11.4) and PCV (11.6) respectively. The traits which had desired value of variability parameters can be utilized in crop improvement programme. This study generally indicated that there was significance genetic variability among the genotypes studied. Thus, there is an opportunity of direct selection of superior varieties for different yield contributing and physiological traits in crop improvement programme.

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