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

Santosh and JP Jaiswal

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 late 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 most of the yield contributing and physiological traits except grain filling duration and number of tillers per plant. High GCV and PCV were observed for the characters plot yield, canopy temperature depression-I, -II, -III, and biological yield etc. Moderate GCV and PCV were found for the characters relative water content, plant height, harvest index and 1000 grain weight etc. whereas low GCV and PCV were observed for the characters days to 75% heading, days to 75% anthesis, days to 75% maturity and SPAD. The genetic advance was observed high for the character such as plant height and relative water content while moderate for number of grains per spike and low for days to 75% heading, days to 75% anthesis, days to 75% maturity and SPAD.

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). 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

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(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 late sown condition on 15 December,

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	Sl. No.	Genotype	Sl. No.	Genotype	Sl. 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 j^{th} variety in the i^{th} block
- μ = population mean
- b_i = true effect of i^{th} block
- t_j = true effect of j^{th} treatment
- e_{ij} = random error
- r = number of replications

t = number of treatments

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

Restrictions are

(B) Estimation of variability

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

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

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

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

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 h^2 (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].

$$GA = h_b^2 \times \sigma_{pi} \times K$$

Where,

GA = expected genetic advance
 h_b^2 = heritability in broad sense
 σ_{pi} = 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 late 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	20.187	15.187	2.375	1.062	19.542	0.065	0.551	143.179	0.578	0.416
Treatment.	31	67.074**	50.276**	30.731**	322.631**	14.083**	2.272**	6.341**	92.897**	0.253**	1.245**
Error	62	2.413	3.230	2.041	1.832	4.573	0.093	0.427	5.282	0.020	0.269
GM		76.416	79.135	115	85.862	35.864	9.668	17.738	49.525	1.615	6.522
SEm±		0.896	1.037	0.824	0.781	1.234	0.176	0.377	1.326	0.083	0.299
CD at 1%		3.370	3.90	3.100	2.937	4.640	0.664	1.418	4.987	0.313	1.126
CD at 5%		2.535	2.933	2.332	2.209	3.490	0.500	1.066	3.751	0.235	0.847
CV		2.032	2.271	1.242	1.576	5.963	3.169	3.683	4.640	8.930	7.959

Continued...

SV	d.f.	BY	GY	PY	TGW	HI	CTD I	CTD-II	CTD-III	SPAD	RWC
Replication	2	0.224	0.135	1400	0.714	9.507	0.201	0.018	0.197	0.218	0.046
Treatment.	31	48.745**	6.717**	677499.1**	59.503**	119.75**	5.656**	3.677**	4.087**	23.049**	387.482**
Error	62	0.235	0.179	537.967	2.365	5.992	0.076	0.027	0.046	0.377	1.229
GM		18.631	6.831	1246.542	36.099	37.122	3.201	2.619	2.593	42.557	68.767
SEm±		0.279	0.244	13.391	0.888	1.413	0.16	0.095	0.124	0.354	0.640
CD at 1%		1.051	0.918	50.33	3.337	5.311	0.601	0.357	0.467	1.332	2.406
CD at 5%		0.790	0.691	37.857	2.51	3.995	0.452	0.268	0.351	1.002	1.809
CV		2.600	6.198	1.860	4.26	6.594	8.659	6.289	8.298	1.443	1.612

*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. Under late sown condition plot yield exhibited highest range varying from 270 g (Raj 4037) to 2723 g (Salembo). Among the physiological traits the highest range was found in case of RWC that was 47.27% (Seri 82) to 92.95% (Giza 155).

Table 3: Mean performance of grain yield, yield components and physiological traits

Sl. No.	Genotype	DH	DA	DM	PH	GFD	SL	NSS	NGS	GWS	NTP
1.	PBN-51	77.67	80	113.3	87.27	33.33	9.113	18.8	61.73	1.819	8
2.	BWL-0814	77.33	79.33	116	87.8	36.67	9.987	17.23	47.73	1.516	6.833
3.	BWL-1771	77.67	80	118.3	80.57	38.33	9.53	19.19	49.47	1.774	7.067
4.	BWL-9022	74.33	76	113.3	86.93	37.33	10.81	19.69	50.47	1.952	6.067
5.	BWL-0924	77	80.33	114.7	76.27	34.33	8.967	15.21	50.73	1.622	6.6
6.	BWL-1793	74.33	76	113.3	80.27	37.33	10.4	18.1	53.4	1.809	7.2
7.	CUS/79/PRULLA	77.33	79.33	115.3	103.1	36	11.94	16.74	50.1	2.053	6.9
8.	IEPACA RABE	74.33	76.33	113.7	86.17	37.33	10.48	19.1	49	2.213	5.767
9.	CHIRYA-3	77.33	78	114.3	86.87	36.33	8.397	17	52.73	1.923	7.6
10.	DHARWAD DRY	82	83.67	118.7	99.47	35	10.89	19.03	50.53	1.848	6.467
11.	RAJ3765	73.67	79.33	114.3	78.6	35	9.8	18.71	49.6	1.605	7.467
12.	HI1563	73.67	78	113.7	81.23	35.67	10.07	16.68	49.13	1.71	6.333
13.	HD2864	69.67	76.67	111.7	81.97	35	10.48	17.15	52.67	1.731	5.733
14.	RAJ4083	72.33	75	112	76.3	37	9.77	17.19	49	1.739	6.733
15.	DBW-14	70.33	75.33	111.7	71.8	36.33	9.807	17.47	43.4	1.547	5.8

16.	WH730	78	79	113.7	90.47	34.67	10.83	17.21	44.27	1.623	6.167
17.	K9465	77.33	79.33	112	90.1	32.67	10.19	18.62	46.67	1.79	6.2
18.	RAJ4037	77.67	80	118.3	67.33	38.33	9.017	14.71	41.67	1.164	6.8
19.	TEPOKO	74.67	78.33	113	89.67	34.67	9.35	16.5	54	1.671	5.5
20.	BABAX	78.67	83.67	117.7	86.97	34	10.74	19.15	57.53	1.703	7
21.	OTHERI RGYPT	78.33	79.67	118.3	88	38.67	9.423	17.51	57.87	2.121	7
22.	IC532653	84.67	86.33	122.3	103.7	36	7.853	17.15	37.67	1.06	6.467
23.	SERI82	69.67	74.67	112.7	74.87	38	8.633	17.5	52.93	1.165	5.333
24.	SONORA64	68	74	111.3	71.27	37.33	8.777	16.4	47.2	1.24	7.1
25.	SALEMBO	78	81.67	117.3	85	35.67	9.29	19.22	46.8	1.624	6.267
26.	ARIANA66	94.33	96	125	102.8	29	9.61	21.15	48.4	1.428	5.9
27.	GIZA155	75.67	77	115.7	104	38.67	9.54	19.47	44.93	1.126	6.733
28.	BACANORA88	77	78.33	113.7	74.07	35.33	8.983	19.01	56.47	1.51	6.567
29.	IC118737	75.67	77.33	111	83.4	33.67	9.867	17.27	58.13	1.376	7.2
30.	C-306	75	76.33	116.3	107.3	40	8.653	14.89	37.57	1.285	5.633
31.	HD2967	77	78.33	114.7	84.07	36.33	9.023	17.88	48.53	1.541	6
32.	PBW343	76.67	79	112.7	80	33.67	9.157	16.72	44.47	1.414	6.3
Range		68-94.33	74-96	111-125	67.33-107.3	29-40	7.853-11.94	14.71-21.15	37.57-61.73	1.06-2.213	5.333-8
GM		74.62	79.13	115	85.863	35.86	9.668	17.73	49.52	1.616	6.502

Continued...

Sl. No.	Genotype	BY	GY	PY	TGW	HI	CTD I	CTD-II	CTD-III	SPAD	RWC
1.	PBN-51	25.07	7.6	1257	32.32	28.13	5.567	1.767	0.5	43.67	53
2.	BWL-0814	20.4	7.2	1904	32.32	37.25	1.5	1.733	0.733	42.41	54
3.	BWL-1771	24.67	8.8	1448	35.88	38.33	5.533	2.7	1.4	44.15	64.33
4.	BWL-9022	23.07	9.2	1316	42.92	40.68	1.933	1.6	2.8	44.25	73.11
5.	BWL-0924	25.07	6.6	1267	40.25	28.69	4.6	2.3	1.5	40.75	82.78
6.	BWL-1793	25.07	8.67	842.7	38.22	37.1	1.7	3.6	2.667	42.7	71.24
7.	CUS/79/PRULLA	21	8.67	1833	45.67	40.38	2.6	3.433	2.967	44.95	71.91
8.	IEPACA RABE	21.2	8.67	1368	38.22	39.62	2.367	4.633	4.8	45.55	71.47
9.	CHIRYA-3	23.6	9.47	1741	38.02	39.66	4.3	2.433	1.433	38.79	64.67
10.	DHARWAD DRY	16.27	5.6	1125	29.92	33.33	5.367	4.5	4.167	35.83	50.33
11.	RAJ3765	17.73	6.67	1026	40.27	36.96	2.367	3.133	4.167	42.23	64.21
12.	HI1563	18.53	6.4	1072	36.18	34.04	1.6	3.167	2.2	37.83	62.3
13.	HD2864	12.6	7.2	1249	40.55	53.33	2.433	1.633	1.3	40.83	85.57
14.	RAJ4083	19.47	8.13	1136	36.33	40.82	2.833	1.433	1.7	46.67	47.89
15.	DBW-14	16.93	6.67	1370	41.57	36.36	2.467	1.133	1.1	44.83	70.19
16.	WH730	13	6.67	752.7	37.07	51.52	3.133	1.6	2.5	48.33	62.84
17.	K9465	19.4	8.73	1341	41.18	45.83	2.333	0.7	4.567	47.2	71.81
18.	RAJ4037	13.47	4.8	270	34.18	34.38	3.033	1.8	3.267	42.2	65.89
19.	TEPOKO	14.53	5.8	1567	33.9	40.54	4.133	3.767	2.9	39.97	65.23
20.	BABAX	19.27	7.07	868	34.23	38.3	2.233	3.633	2.467	40	63.9
21.	OTHERI RGYPT	24.8	8.2	1472	38.75	34.13	2.367	2.633	2.667	45.3	76.97
22.	IC532653	16	4.47	1052	31.7	25	4.5	4.567	3.333	43.17	76.06
23.	SERI82	12.53	4.53	1038	28.7	36.67	2.3	2.633	3	42.6	47.27
24.	SONORA64	15.47	5.2	776.7	27.57	33.33	1.4	3.133	1.9	39.25	69.06
25.	SALEMBO	21.13	7.53	2723	38.88	35.19	4.533	1.767	3.3	44.77	71.28
26.	ARIANA66	16.73	5.07	548	30.98	29.27	5.733	3.4	0.533	44.08	72.02
27.	GIZA155	20.33	5.53	1039	33.62	29.41	3.4	2.2	3.7	41.75	92.95
28.	BACANORA88	17.2	6.73	1884	31.02	37.21	4	1.467	2.933	40.12	88.96
29.	IC118737	17.13	6.73	858.7	33.03	40.91	2.333	1.567	2.433	42.34	63.96
30.	C-306	12.8	4.8	971.7	42.07	35.48	2.6	3.933	4.2	40.37	89.16
31.	HD2967	16.93	6.53	1861	36.6	36.59	5.6	4.2	3.633	43.13	65
32.	PBW343	14.8	4.67	914	33.08	30.56	1.633	1.633	2.233	41.82	71.19
Range		12.53-25.07	4.47-9.47	270-2723	27.57-45.67	25-53.33	1.4-5.733	0.7-4.633	0.5-4.8	35.83-48.33	47.27-92.95
GM		18.631	6.83	1246.50	36.09	37.12	3.201	2.62	2.594	42.56	68.767

Days to 75% Heading had a range of variation from 68 days (Sonora 64) to 94 days (Ariana 66) with a general mean of 76 days. Days to 75% Anthesis varied from 74 days (Sonora 64) to 96 days (Ariana 66) with a general mean of 79 days. Days to 75% maturity ranged from 111 days (IC 118737) to 125 days (Ariana 66) with a mean of 115 days. Plant Height exhibited a wide range of variation from 67.33 cm (Raj 4037) to 107.3 cm (C 306) with a general mean of 85.863 cm. Grain filling duration ranged from 29 days (Ariana 66) to 40 days (C 306) with a general mean of 35 days. Spike length exhibited a wide range of variation from 7.853 cm (IC

532653) to 11.94 cm (CUS/79/PRULLA) with a general mean of 9.668 cm. Number of spikelets per spike exhibited a wide range of variation from 14.71 (Raj 4037) to 21.15 (Ariana 66) with a general mean of 17.739. Number of grain per spike exhibited a wide range of variation from 37.57 (C-306) to 61.73 (PBN 51) with a general mean of 49.525. Grain weight per spike exhibited a wide range of variation from 1.06 g (IC 532653) to 2.213 g (IEPACA RABE) with a general mean of 1.616 g. Number of tillers per plant exhibited a wide range of variation from 5.333 (Seri 82) to 8 (PBN 51) with a general mean of 6.502. Biological yield per plant exhibited a wide

range of variation from 12.53 g (Seri 82) to 25.07 g (PBN 51) with a general mean of 18.631 g. Grain yield per plant exhibited a wide range of variation from 4.47 g (IC 532653) to 9.47 g (Chirya-3) with a general mean of 6.831 g. Plot yield exhibited a wide range of variation from 270 g (Raj 4037) to 2723 g (Salemba) with a general mean of 1246.50 g. 1000-grain weight exhibited a wide range of variation from 27.57 g (Sonora 64) to 45.67 g (CUS/79/PRULLA) with a general mean of 36.092 g. Harvest index per plant exhibited a wide range of variation from 25% (IC 532653) to 53.33% (HD 2864) with a mean of 37.122%.

In case of CTD, 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 1.4°C (Sonora 64) to 5.733°C (Ariana 66) with an average of 3.201°C. During second observation *i.e.* 10 days after heading it varied from 0.7°C (K 9465) to 4.633°C (IEPACA RABE) with an average of 2.62°C. The third observation, 20 days after heading ranged from 0.5°C (PNB 51) to 4.8°C (IEPACA RABE) with a mean of 2.594°C. SPAD exhibited a wide range of variation from 35.83 (Dharwar Dry) to 48.33 (WH 730) with a general mean of 42.56. Relative water content (%) exhibited a wide range of variation from 47.27% (Seri 82) to 92.95% (Giza 155) with a general mean of 68.767%.

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 (1991).

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	89.93	9.07	6.08	6.41
2	DA	82.92	7.49	5	5.5
3	DM	82.41	5.78	2.69	2.96
4	GFD	40.93	2.35	4.96	7.76
5	PH	98.32	21.1	12	12.1
6	SL	88.55	1.65	8.81	9.37
7	NSS	82.2	2.62	7.92	8.73
8	NGS	84.68	10.2	10.9	11.9
9	GWS	78.83	0.51	17.2	19.4
10	NTP	50.68	0.82	8.54	12
11	BY	98.57	8.22	21.6	21.7
12	GY	92.4	2.92	21.6	22.5
13	PY	99.76	9.77	38.1	38.2
14	TGW	88.75	8.45	12.1	12.8
15	HI	86.36	11.8	16.6	17.9
16	CTD-I	96.03	2.75	42.6	43.5
17	CTD-II	97.82	2.25	42.1	42.6
18	CTD-III	96.68	2.35	44.7	45.5
19	RWC	99.05	23.3	16.5	16.6
20	SPAD	95.15	5.51	6.44	6.6

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 and number of tillers per plant 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 h² was 89.932% for Days to 75 % heading, 82.916% for Days to 75% anthesis, 82.407% for Days to 75% maturity, 40.933% for Grain filling duration, 98.315% for plant height, 88.553% forspike length, 82.204% for number of spikelets per spike, 84.684% for number of grains per spike, 78.833% for grain weight per spike, 50.678% for number of tillers per plant, 98.568% for biological yield, 92.4% for grain yield, 99.761% for plot yield, 88.747% for 1000 grain weight, 86.361% for harvest index, 96.033% for canopy temperature - I, 97.817% for canopy temperature -II, 96.675% for canopy temperature -III, 99.054% for relative water content (%), 95.151% for SPAD. These findings are similar with the findings of Rahim *et al.* (2010), Salem *et al.* (2008) [22], Ali *et al.* (2008) [11] 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, grain yield per plant and plot yield. 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 GCV for days to 75% heading was 6.075, 5.004 for days to 75% anthesis, 2.689 for days to 75% maturity, 4.964 for grain filling duration, 12.043 for plant height, 8.814 for spike length, 7.916 for number of spikelets per spike, 10.912 for number of grains per spike, 17.235 for grain weight per spike, 8.543 for number of tillers per plant, 21.583 for biological yield, 21.611 for grain yield per plant, 38.112 for plot yield, 12.068 for 1000 grain weight, 16.59 for harvest index, 42.603 for canopy temperature depression -I, 42.107 for canopy temperature depression -II, 44.747 for canopy temperature depression -III, 16.5 for relative water content, 6.439 for SPAD.

The value of PCV for days to 75% heading was 6.406, 5.496 for days to 75% anthesis, 2.962 for days to 75% maturity, 7.759 for grain filling duration, 12.146 for plant height, 9.366 for spike length, 8.731 for number of spikelets per spike, 11.858 for number of grains per spike, 19.411 for grain weight per spike, 12.001 for number of tillers per plant, 21.739 for biological yield, 22.482 for grain yield per plant, 38.157 for plot yield, 12.811 for 1000 grain weight, 17.852 for harvest index, 43.474 for canopy temperature depression - I, 42.575 for canopy temperature depression -II, 45.51 for canopy temperature depression -III, 16.589 for relative water content, 6.601 for SPAD. These findings are in agreement with the findings of Kalim *et al.* (2011) [15], 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 high for plant height and relative water content while moderate for number of grains per spike and harvest index and low for rest of the characters. The value of Genetic advance for days to 75% heading was 9.07, 7.428 for days to 75% anthesis, 5.783 for days to 75% maturity, 2.346 for grain filling duration, 21.122 for plant height, 1.652 for spike length, 2.623 for number of spikelets per spike, 10.245 for number of grains per spike, 0.509 for grain weight per spike, 0.815 for number of tillers per plant, 8.224 for biological yield, 2.923 for grain yield per plant, 977.467 for plot yield, 8.453 for 1000 grain weight, 11.789 for harvest index, 2.753 for canopy temperature depression -I, 2.248 for canopy temperature depression -II, 2.351 for canopy temperature depression -III, 23.264 for relative water content, 5.507 for SPAD.

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 highest range varying from 270 g (Raj 4037) to 2723 g (Salemba). Among the physiological traits the highest range was found in case of RWC that was 47.27% (Seri 82) to 92.95% (Giza 155). The highest heritability was observed for plot yield and lowest for grain filling duration among yield contributing traits while among physiological traits, relative water content exhibited highest and lowest by SPAD. High GCV and PCV were observed for the characters plot yield, canopy temperature depression-I, -II, -III, and biological yield etc. Moderate GCV and PCV were found for the characters relative water content, plant height, harvest index and 1000 grain weight etc. whereas low GCV and PCV were observed for the characters days to 75% heading, days to 75% anthesis, days to 75% maturity and SPAD. The genetic advance was observed high for the character such as plant height and relative water content while moderate for number of grains per spike and low for days to 75% heading, days to 75% anthesis, days to 75% maturity and SPAD.

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