The Pharma Innovation

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Assessment of genetic variability, heritability and genetic advance for yield and physiological traits under very late 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 most of the yield contributing and physiological traits except days to 75% anthesis, spike length, number of spikelets per spike and 1000 grain weight in which heritability was observed moderate. High GCV and PCV were observed for the characters characters plot yield, canopy temperature depression-I, -II, -III, and biological yield etc. Moderate GCV and PCV were found for the characters 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 moderate for number of grains per spike, harvest index and SPAD while low for rest of the charaters.

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

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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

Sl. 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 jth variety in the i^{th}block
μ=population mean
b_i=true effect of ith block

t_j=true effect of jth treatment
e_i=random error
r =number of replications
t =number of treatments

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

(B) Estimation of variability

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

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

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

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

Where,
σ_g= Genotypic standard deviation
σ_p= Phenotypic standard deviation
σ_e= Environmental standard deviation
$\overline{X}$ = 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:

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

Where,

$\sigma_g^2 =$ Genotypic variance

$\sigma_p^2 =$ 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

σpi = phenotypic standard deviation for ith character

K= intensity of selection, the value of which is 2.06 at 5%

(Lush, 1949)[17]

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.

The mean performance of 32 varieties for 20 characters has been listed in the Table 3. Under very late sown condition, plot yield exhibited highest range varying from 249.3 g (Raj 4037) to 1529 g (Chirya-3). Among the physiological traits the highest range was found in case of RWC that was 58.29% (Raj 3765) to 88.13% (BABAX).

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	22.171	32.265	69.531	1.656	4.031	0.184	3.293	75.57	0.074	0.278
Treatment.	31	25.817**	22.386**	76.124	306.651**	61.698**	1.52**	7.784**	144.11**	0.126**	2.44**
Error	62	4.585	5.378	6.359	5.033	3.31	0.141	2.065	10.282	0.013	0.307
GM		67.01	69.645	103.406	75.156	33.75	9.62	17.681	44.006	1.417	6.305
SEm±		1.236	1.338	1.455	1.295	1.05	0.217	0.829	1.851	0.067	0.32
CD at 1%		4.646	5.032	5.472	4.868	3.948	0.816	3.118	6.958	0.254	1.203
CD at 5%		3.495	3.785	4.115	3.661	2.969	0.613	2.345	5.233	0.191	0.905
CV		3.195	3.329	2.438	2.985	5.391	3.909	8.128	7.286	8.267	8.797
SV	d. f.	BY	GY	PY	TGW	HI	CTD I	CTD-II	CTD-III	SPAD	RWC
Replication	2	0.072	0.354	814	21.011	18.953	0.151	0.013	0.0003	54.101	75.875
Treatment.	31	26.342**	4.169**	380761.5**	44.413**	112.180**	5.635**	1.801**	1.696**	47.496**	153.085**
Error	62	0.200	0.177	587.241	5.656	9.181	0.070	0.026	0.036	4.840	4.472
GM		14.191	4.779	780.208	32.919	33.94	4.151	3.323	2.307	45.039	74.368
SEm±		0.258	0.243	13.99	1.373	1.749	0.153	0.093	0.11	1.270	1.22
CD at 1%		0.972	0.914	52.584	5.161	6.575	0.577	0.352	0.414	4.774	4.589
CD at 5%		0.731	0.688	39.552	3.882	4.945	0.434	0.264	0.312	3.591	3.451
CV		3.156	8.82	3.105	7.224	8.926	6.41	4.881	8.287	4.884	2.843

*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 %.

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

SI. No.	Genotype	DH	DA	DM	PH	GFD	SL	NSS	NGS	GWS	NTP
1.	PBN-51	68.67	70.67	101.3	72	30.67	8.76	16.53	49.93	1.395	5.2
2.	BWL-0814	67.67	69.67	102	81.43	32.33	9.633	16.67	42.6	1.301	7.2
3.	BWL-1771	69.67	72	105.3	73.27	33.33	9.433	18.53	30.53	1.255	5.867
4.	BWL-9022	60.67	63	97.67	75.1	31.67	10	18.67	44.53	1.478	6.8
5.	BWL-0924	68	71	102.7	64.3	31.67	8.633	16	44.6	1.63	4.8
6.	BWL-1793	66	68	100.7	64.73	32.67	10.05	17	48.2	1.585	7
7.	CUS/79/PRULLA	66.33	69	101.7	87.93	32.67	11.79	16.13	40.33	1.498	7.567
8.	IEPACA RABE	65	67.67	100	75.5	32.33	9.607	18.93	45.67	1.613	6.233
9.	CHIRYA-3	66	68.67	100.3	76.2	31.67	7.933	17	47.67	1.659	7.433
10.	DHARWAD DRY	73	74.67	113	87.53	41	9.727	20	52.87	1.259	6.933
11.	RAJ3765	65	69.33	99.67	72.87	30.33	9.593	16.67	52.2	1.642	6.867
12.	HI1563	65.33	70	101.7	70.87	31.67	10.01	16.13	45.67	1.513	5.467
13.	HD2864	62.67	66.67	100.7	73	34	9.747	16.4	38.2	1.371	8.2
14.	RAJ4083	63.33	66.33	98.67	69.1	32.33	9.26	17.6	44.07	1.342	7.067

SI. No.	Genotype										
15.	DBW-14	64	69	108.7	68.9	43	10.17	19	46.13	1.619	6.533
16.	WH730	69.33	71	102	63.63	31	10.5	16.4	37.67	1.313	4.4
17.	K9465	69	71.33	100.7	72.87	29.33	9.593	18.2	32.73	1.483	5.8
18.	RAJ4037	69	72.67	107	57.47	34.33	9.413	16.2	41.87	1.343	6.267
19.	TEPOKO	68.67	73.33	101.3	80.53	28	10.37	19.4	59.2	2.028	5.8
20.	BABAX	68.33	71.67	113	74.7	44.33	10.81	20.07	40.93	1.174	6.6
21.	OTHERI RGYPT	67.33	70.33	111.3	72.27	42.33	9.68	16.4	42.87	1.694	5.867
22.	IC532653	71.67	74.33	111	93.23	33.67	8.653	18.2	34.2	1.039	7.4
23.	SERI82	64.33	67.67	99.33	69.8	34	8.873	17.07	47.2	1.259	5.8
24.	SONORA64	62.33	65.67	99	62.97	35.33	9.187	17.2	56.4	1.238	4.8
25.	SALEMBO	69.67	71.67	105	71.7	33.33	9.36	17.47	38	1.327	6.267
26.	ARIANA66	72.67	64.33	118	84.6	44.67	10.31	22.07	34.73	1.143	5
27.	GIZA155	67.33	69.67	105	96.83	35.33	9.887	21.07	42.93	1.17	6.667
28.	BACANORA88	66.67	69.33	100.7	65.4	31.33	9.14	18.8	52.13	1.505	6.533
29.	IC118737	66.33	69.33	98.67	81.27	29.33	9.52	17	52	1.211	6
30.	C-306	64	68.33	102.7	101.6	34.33	9.38	15.8	36.93	1.448	6.933
31.	HD2967	66.67	68.67	100	76.73	31.33	9.453	17.8	47.87	1.531	6.933
32.	PBW343	69.67	73.67	100.3	66.7	26.67	9.373	15.4	37.33	1.289	5.533
Range		60.67-73	63-74.67	97.67-118	57.47-101.6	26.67-44.67	7.933-11.79	15.4-22.07	30.53-59.2	1.039-2.028	4.4-8.2
GM		67.01	69.646	103.406	75.156	33.75	9.589	17.681	44.006	1.421	6.305

SI. No.	Genotype	BY	GY	PY	TGW	HI	CTD I	CTD-II	CTD-III	SPAD	RWC
1.	PBN-51	8.667	3.2	664.7	32.28	37.16	6.467	3.5	1.333	42.55	72.41
2.	BWL-0814	20.8	5.733	1441	32.68	27.52	6.433	3.533	2.1	52.24	73.47
3.	BWL-1771	14.67	4.533	942	37	30.91	6.167	3.7	3.333	48.54	83.22
4.	BWL-9022	13.6	4.533	1039	38.65	33.27	2.433	1.767	2.9	47.69	65.25
5.	BWL-0924	12.8	4.933	534	33.62	38.5	4.8	3.433	2.733	46.87	63.96
6.	BWL-1793	17.07	6.133	882.3	33.87	35.93	3.367	3.133	2.7	50.1	74.09
7.	CUS/79/PRULLA	14	6.267	1161	37.7	44.76	5.667	3.4	2.633	51.58	74.5
8.	IEPACA RABE	15.27	5.867	862	32.93	38.4	2.533	3.633	3.167	43.29	63.54
9.	CHIRYA-3	17.53	6.4	1529	34.13	36.53	7.1	4.333	2.567	41.8	84.62
10.	Dharwad DRY	16.73	3.467	982.7	31.97	20.72	4.3	3.6	2.167	37.25	82.24
11.	RAJ3765	16.07	5.6	458	32.62	34.83	2.6	2.4	4.5	43.62	58.29
12.	HI1563	16.27	4.333	460.7	33.6	26.66	3.467	2.533	3.567	42.62	82.62
13.	HD2864	14.53	5.067	1157	33.7	34.9	2.867	2.633	2.767	42.63	71.99
14.	RAJ4083	13.93	4.2	629.3	32.4	30.19	2.2	2.667	2.633	44.31	75.07
15.	DBW-14	16.8	6.333	344	35.37	37.7	3.533	2.367	2.333	47.03	80.56
16.	WH730	10.53	3.933	257.3	33.13	37.41	3.8	2.767	1.467	50.13	70.13
17.	K9465	13	5.667	842.7	37.7	43.63	5.333	3	1.533	41.07	78.26
18.	RAJ4037	16.67	5.6	249.3	35	33.59	3.367	3.9	1.367	43.65	72.84
19.	TEPOKO	14.47	5.333	988.7	32.02	36.9	4.233	3.533	2.067	44.11	83.09
20.	BABAX	11.2	2.133	339.3	32.53	19.02	5.233	3.633	1.033	41.73	88.13
21.	OtheriRGYPT	10.93	3.2	746	39.23	29.3	5.1	4.4	1.5	52.39	75.09
22.	IC532653	14.53	4	452	27.92	27.51	4.1	2.767	2.1	43.43	73.13
23.	SERI82	11.07	3.067	572.7	24.93	27.69	3.367	4.767	2.8	51.11	82.4
24.	SONORA64	7.733	3.067	360	21.93	39.65	2.6	4.467	1.567	38.24	65.01
25.	SALEMBO	15.07	4.667	1167	36.67	30.95	5.6	4.1	2.567	50.32	71.77
26.	ARIANA66	14	4.667	546.7	28.37	33.38	1.733	1.6	2.333	44.83	73.39
27.	GIZA155	13.87	5.067	670.7	34.58	36.5	5.233	2.733	1.467	42.54	77.99
28.	Bacanora88	14.53	6.2	847.3	26.7	42.73	4.4	3.533	1.6	42.73	70.17
29.	IC118737	14	4.533	841.3	28.72	32.43	3.6	3.133	2.067	43.31	80.26
30.	C-306	14.87	4.4	441	34.3	29.63	3.667	3	2	44.09	63.32
31.	HD2967	19.93	6.933	1427	32.98	34.81	3.667	4.333	2.867	42.95	75.37
32.	PBW343	9	3.867	1131	34.18	43.19	3.867	4.067	2.067	42.5	73.59
Range		7.733-20.8	2.133-6.933	249.3-1529	21.93-39.23	19.02-44.76	1.733-7.1	1.6-4.767	1.033-4.5	37.25-5239	58.29-88.13
GM		14.192	4.779	780.208	32.919	33.946	4.151	3.324	2.307	45.04	74.369

Under very late sown condition, Days to 75% Heading had a range of variation from 60 days (BWL 9022) to 73 days (Dharwar Dry) with a general mean of 67 days. Days to 75% Anthesis varied from 63 days (BWL 9022) to 74 days (Dharwar Dry) with a general mean of 69 days. Days to 75% Maturity ranged from 97 days (BWL 9022) to 118 days (Ariana 66) with a general mean of 103 days. Plant Height exhibited a wide range of variation from 57.47 cm (Raj 4037) to 101.6 cm (C 306) with a general mean of 75.156 cm. Grain filling duration ranged from 26 days (PBW 343) to 44 days (Ariana 66) with a general mean of 33 days. Spike length exhibited a wide range of variation from 7.933 cm (Chiry-3) to 11.79 cm (CUS/79/PRULLA) with a general mean of 9.589 cm. Number of spikelets per spike exhibited a wide range of variation from 15.4 (PBW 343) to 22.07 (Ariana 66) with a general mean of 17.681. Number of grain per spike exhibited

a wide range of variation from 30.53 (BWL 1771) to 59.2 (Tepoko) with a general mean of 44.006. Grain weight per spike exhibited a wide range of variation from 1.039 g (IC 532653) to 2.028 g (Tepoko) with a general mean of 1.421 g. Number of tillers per plant exhibited a wide range of variation from 4.4 (WH 730) to 8.2 (HD 2864) with a general mean of 6.305. Biological yield per plant exhibited a wide range of variation from 7.733 g (Sonora 64) to 20.8 g (BWL 814) with a general mean of 14.192 g. Grain yield per plant exhibited a wide range of variation from 2.133 g (BABAX) to 6.933 g (HD 2967) with a general mean of 4.779 g. Plot yield exhibited a wide range of variation from 249.3 g (Raj 4037) to 1529 g (Chiry-3) with a general mean of 780.208 g. 1000-grain weight exhibited a wide range of variation from 21.91 g (Sonora 64) to 39.23 g (Othery Egypt) with a general mean of 32.919 g. Harvest index per plant exhibited a wide range of

variation from 19.02% (BABAX) to 44.76% (CUS/79/PRULLA) with a general mean of 33.946%.

Canopy Temperature Depression (CTD) was recorded in three different days during wheat growing period. The first observation which was recorded at the time of heading ranged from 1.733^0C (Ariana 66) to 7.1^0C (Chirya-3) with an average of 4.151^0C.During second observation *i.e.* 10 days after heading it varied from 1.6^0C (Ariana 66) to 4.768^0C (Seri 82) with an average of 3.324^0C.The third observation, 20 days after heading ranged from 1.033^0C (BABAX) to 4.5^0C (Raj 3765) with a general mean of 2.307^0C.SPAD exhibited a wide range of variation from 37.25 (Dharwar Dry) to 52.39 (Othery Egypt) with a general mean of 45.04. Relative water content (%) exhibited a wide range of variation from 58.29% (Raj 3765) to 88.13% (BABAX) with a general mean of 74.369%.

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

SI No.	Character	h^2 (%)	GA	GCV	PCV
1	DH	h^2(%)	GA	GCV	PCV
2	DA	60.68	4.26	3.97	5.096
3	DM	51.31	3.51	3.419	4.772
4	GFD	78.52	8.8	4.663	5.263
5	PH	85.46	8.4	13.07	14.14
6	SL	95.23	20.2	13.34	13.67
7	NSS	59.01	1.06	6.994	9.104
8	NGS	47.99	1.97	7.808	11.27
9	GWS	81.27	12.4	15.18	16.84
10	NTP	70.85	0.33	13.33	15.84
11	BY	69.79	1.45	13.37	16.01
12	GY	97.75	6.01	20.8	21.04
13	PY	88.21	2.23	24.14	25.7
14	TGW	99.54	7.32	45.63	45.73
15	HI	59.55	6.18	10.92	13.09
16	CTD-I	78.89	10.7	17.26	19.44
17	CTD-II	96.32	2.75	32.81	33.44
18	CTD-III	95.74	1.55	23.14	23.65
19	RWC	93.8	1.48	32.24	33.29
20	SPAD	91.71	13.9	9.464	9.882

Robinson *et al.* (1949) [21] 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 heritability was observed high for most of the characters except days to 75% anthesis, spike length, number of spikelets per spike and 1000 grain weight in which h^2 was found moderate.There is no lower heritability was observed in any character.

The value of h^2 was 60.679% for days to 75% heading, 51.314% for days to 75% anthesis, 78.523% for days to 75%

maturity, 85.462% for grain filling duration, 95.231% for plant height, 59.014% for spike length, 47.986% for number of spikelets per spike, 81.271% for number of grains per spike, 70.845% for grain weight per spike, 69.793% for number of tillers per plant, 97.747% for biological yield per plant, 88.214% for grain yield per plant, 99.539% for plot yield, 59.545% for 1000 grain weight, 78.891% for harvest index, 96.323% for canopy temperature depression-I, 95.739% for canopy temperature depression -II, 93.802% for canopy temperature depression -III, 91.714% for relative water content, 74.6% for SPAD . These finding are similar with the findings of Salem *et al.* (2008), Ali *et al.* (2008) and Khan *et al.* (2010)[22, 1, 16].

Deshmukh *et al.* (1986)[8] classified PCV and GCV values as low (0-10%), moderate (10-20%) and high (20% and above) values. The high GCV and PCV values were observed for the characters such as biological yield per plant, grain yield per plant, plot yield, canopy temperature depression-I, II and III, moderate GCV and PCV were observed for the characters such as grain filling duration, plant height, number of spikelets per spike, number of grains per pike, grain weight per spike, number of tillers per plant, 1000 grain weight and harvest index while low GCV and PCV were observed for the characters such as day to 75% heading, days to 75% anthesis, days to 75% maturity, spike length, SPAD and relative water content.

The value of GCV for days to 75% heading was 3.97, 3.419 for days to 75% anthesis, 4.663 for days to 75% maturity, 13.072 for grain filling duration, 13.341 for plant height, 6.994 for spike length, 7.808 for number of spikelets per spike, 15.178 for number of grains per spike, 13.333 for grain weight per spike, 13.372 for number of tillers per plant, 20.8 for biological yield per plant, 24.137 for grain yield per plant, 45.627 for plot yield, 10.918 for 1000 grain weight, 17.262 for harvest index, 32.81 for canopy temperature depression -I, 23.14 for canopy temperature depression -II, 32.239 for canopy temperature depression -III, 9.464 for relative water content, 8.372 for SPAD.

The value of PCV for days to 75% heading was 5.096, 4.772 for days to 75% anthesis, 5.263 for days to 75% maturity, 14.14 for grain filling duration, 13.671 for plant height, 9.104 for spike length, 11.272 for number of spikelets per spike, 16.836 for number of grains per spike, 15.841 for grain weight per spike, 16.007 for number of tillers per plant, 21.039 for biological yield per plant , 25.699 for grain yield per plant, 45.732 for plot yield, 13.093 for 1000 grain weight, 19.435 for harvest index, 33.431 for canopy temperature depression-I, 23.649 for canopy temperature depression -II, 33.287 for canopy temperature depression -III, 9.882 for relative water content, 9.693 for SPAD. These findings are in agreement with the findings of Kalimullah *et al.* (2012) [15],Wani*et al.* (2011) and Monpara (2011)[27, 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 high genetic advance was observed for plant height, moderate for number of grains per spike, harvest index and relative water content while low for days to 75% heading, days to 75%

anthesis, days to 75% maturity, grain filling duration, spike length, number of spikelets per spike, grain weight per spike,number of tillers per plant, biological yield per plant, grain yield per plant, plot yield, 1000 grain weight, canopy temperature depression-I,II and III and SPAD.

The value of GA for days to 75% heading was 4.269, 3.513 for days to 75% anthesis, 8.803 for days to 75% maturity, 8.401 for grain filling duration, 20.157 for plant height, 1.061 for spike length, 1.97 for number of spikelets per spike, 12.404 for number of grains per spike, 0.328 for grain weight per spike, 1.451 for number of tillers per plant, 6.012 for biological yield per plant, 2.232 for grain yield per plant, 731.635 for plot yield, 6.175 for 1000 grain weight, 10.722 for harvest index, 2.754 for canopy temperature depression -I, 1.55 for canopy temperature depression -II, 1.484 for canopy temperature depression-III, 13.885 for RWC, 6.709 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 249.3 g (Raj 4037) to 1529 g (Chirya-3). Among the physiological traits the highest range was found in case of RWC that was 58.29% (Raj 3765) to 88.13% (BABAX). The results of the present study indicated that high heritability values were observed in most of the yield contributing and physiological traits except days to 75% anthesis, spike length, number of spikelets per spike and 1000 grain weight in which heritability was observed moderate. High GCV and PCV were observed for the characters characters plot yield, canopy temperature depression-I, -II, -III, and biological yield etc. Moderate GCV and PCV were found for the characters 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 moderate for number of grains per spike, harvest index and SPAD while low for rest of the charaters. 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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