Original Research Article

ASSESSMENT OF GENETIC VARIABILITY FOR PHYSIOLOGICAL TRAITS AND YIELD IN BREAD WHEAT (*TRITICUMAESTIVUM*L. EM.THELL.)

ABSTRACT

The present investigation was carried out with 32 diverse genotypes of bread wheat in completely randomized block design with 3 replications at Norman E. Borlaug Crop Research Centre, G.B. Pant University of agriculture & TechnologyPantnagar for the screening ofgenetic variabilityunder threeenvironments viz., timely sown (E1), late sown (E2) and very late sown (E3) seasons.The observations were recorded on 16 agronomic traits and 3 physiological traits. The statistical analysis for genetic variability was done using ANOVA, h^2, GCV, PCV, GAand genotypic correlation. The analysis of variance was carried out for all the characters in randomized block design indicated highly significant differences among treatments for all the characters under study. High heritability values were observed in all the characters studied except grain filling duration in which heritability was moderate. High ECV was observed for characters such as canopy temperature depression-I, canopy temperature depression-II, canopy temperature-III, and canopy temperature depression-IV.Characters plot yield, canopy temperature depression-I, and canopy temperature depression-IV were marked with high GCV.Characters days to 75% heading, days to 75% anthesis, days to 75% maturity, grain yield per plant, plot yield, canopy temperature depression-I, canopy temperature depression-II, canopy temperature depression-III, and canopy temperature depression-IV exhibited high PCV values. The genetic advance was observed high for plot yield. There were highly significant positive as well as highly significant negative correlations were observed among physiological and yield related traits.The CTD-I, III, IV, and relative water content had shown highly significant positive correlation with days to 75 % heading and days to 75 % anthesis. CTD-III, IV, SPAD and relative water content were also marked with highly significant positive correlations with different yield attributes.The genotypes bearing the desired values for different genetic variability parameters can be exploited in future breeding programme for the improving wheat genotypes. These genotypes can be used as donor parents in crop improvementprogramme.

Keywords:-Bread wheat, ANOVA, heritability, GCV, PCV, and genetic advance.

1. Introduction:

“Wheat is one of the most important and widely grown crops in the world having thearea about 223.04 million hectares holding the position of highest estate among all crops with annual production hovering around 784.91 million tons**.** In India, it's grown in an area of 31.40 million hectares with a production of 110.55 million metric tons and output of 3.52 metric tons/hectares correspondingly**.** In India uppermost area under wheat cultivation is 9.54 million hectares”**(Anonymous 2024).** India is second largest producer of wheat in the world. “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).**

“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 rogramme. 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” [48-51]. “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 variabilitycan 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 F_1 and greater amount of genetic variability in segregating populations”**(Shekhawat*et al*., 2001).**

“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)**. “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 transgressivesegregants, genetic variability between parents is necessary”**(Joshi *et al*., 2004)**. “The higher genetic variability between parents, the higher heterosis in progeny can be observed”**(Joshi and Dhawan, 1966).**In wheat hybridization programs, one suitable approach for parental selection is the estimation of genetic variability. In order to maximize genetic recombination and perhaps boost output, crossing nurseries must employ parents who have been carefully chosen. Given the foregoing, screening the variability of bread wheat genotypes using morphological and physiological criteria is necessary to determine their appropriateness for various breeding programs.Given the foregoing, it is necessary to screen the bread wheat genotypes according to physiological and morphological characteristics in order to determine the genetic variability parameters of each genotype across the sowing times and to identify genotypes exhibiting a broad range of genetic variability for physiological and yield features.

2. 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**(Table 1)** of bread wheat including 3 checks, namely, HD-2967, PBW-343 and C-306. The experiment was laid out in randomized complete block design (RBD) with three replications under three sowing seasonsviz., timely sown(E1), late sown(E2) and very late sown (E3)seasonson 15 November, 2014, 15 December, 2014, 15 January,2015 respectively. 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.

Table 1: List of Genotypes.

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

“Average datafrom five 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, days to 75% anthesis, days to 75% maturity, plant height, peduncle length, number of tillers per plant, grain filling duration, spike length, number of spikelets per spike, number of grains per spike, grain weight per spike, 1000 grain weight, biological yield per plant, grain yield per plot, harvest index and three physiological traits, canopy temperature depression (CTD), relative water content percent (RWC%) and chlorophyll content (SPAD value) of leaf.Canopy temperature was recorded 4 times at the interval of 10 days at different growth stages of the crop from the start of flowering (GS61) to early dough stage” (GS 83 as per **Zodoks*et al.*, 1974**) and it was mentioned as canopy temperature -I (CT–I), canopy temperature-II (CT-II), canopy temperature-III (CT-III) and canopy temperature-IV (CT-IV), and difference between canopy temperature and ambient temperature was calculated and it was designated as canopy temperature depression (CTD I, II, III and IV).The infrared thermometer was used to measure the canopy temperature. SPAD value was observed at flowering stage by SPAD meter. The data obtained from all the three sowing conditions were pooled. The statistical analysis for pooled genetic variability was done by analysis of variance **(Panse and Sukhatme, 1969)**, coefficients of variations **(Burton, 1952 and Johnson *et al*., 1955),** heritability (h^2) **(Allard, 1960),** genetic advance (GA) **(Allard, 1960)**, and genetic advance as percent of mean (GAM)**(Johnson *et al*., 1955)**and genotypic correlation among physiological and yield related traits **(Searle, 1961).**The statistical analysis was performed by **Indostat Hyderabad.**The software **Windostat Version 9.3** was to analyze the data.

(A) Analysis of variance and means: Characters under study were analyzed using analysis of variance to test whether treatments were differing significantly among themselves **(Panse and Sukhatme, 1969)**. The model is as follows:

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

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

bi = true effect of i^{th} block

tj = true effect of j^{th} treatment

eij = 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:

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

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

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

$$GA = h_b^2 \times \sigma pi \times K$$

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)**

(E) **Estimation of inter-character correlation coefficient:** The genotypic correlations among all the characters under were estimated according to the method given by **Searle (1961)** using the following formula:

Genotypic correlation between characters X and Y

$$r_{xy}(g) = \frac{Cov.XY(g)}{\sqrt{Var.X(g) \times Var.Y(g)}}$$

Where,

Var X (g) = Variance of character X at genotypic level.

Var Y (g) = Variance of character Y at genotypic level.

Cov XY (g) = Genotypic covariance between character X and Y.

Test statistics, $t_{cal} = \frac{r\sqrt{n-2}}{\sqrt{1-r^2}}$; (n-2) df.

Where, n = number of genotypes

3.Results and Discussion:

3.1 Analysis of variance for yield and physiological traits: The analysis of variance was carried out for all the characters in randomized block design and result are presented in **Table 2.**The mean sum of square of the differences among the treatments was observed highly significant for all the characters under study. The mean sum of square due to environments was also observed highly significant for all the characters under study indicated that different sowing conditions were differing significantly from each-other and environmental conditions affect performance of different genotypes. This type of result indicated existence of inherent genetic differences among genotypes for different characters. The analysis of variance revealed significant differences 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.

3.2 Mean performance: The mean performance of 32 genotypes for pooled data over all the three sowing conditions for 22 characters has been listed in the **Table 3**. Among yield contributing traits, plot yield exhibited highest range varying from from ARIANA-66 (2310.44) to RAJ 4037 (731.55) with a general mean of 1412.36 g. Among physiological traits, the highest range was observed in case of relative water content that was 58.39% (PBN-51) to 81.3% (GIZA-155) with a general mean of 69.82%.

Days to 75% heading had a range of variation from 68.11 days (SNORA-64) to 89.88 days (ARIANA-66) with a general mean of 76.87 days, days to 75% anthesis varied from 74.77 days (SONORA-64) to 87.77 days (ARIANA-66) with a general mean of 80.60 days, The mean value of days to 75% maturity ranged from 112.33 days (SONORA-64) to 128.77 days (ARIANA-66) with a general mean of 116.93 days.

Plant heightexhibited a wide range of variation from 71.73 cm (RAJ-4037) to 111.45 cm (C-306) with a general mean of 87.00 cm. The mean value of grain filling duration ranged from 32 days (K-9465) to 41.88 days (OTHERY EGYPT) with a general mean of 36.35 days. Spike length exhibited a wide range of variation from 8.74 cm (IC-532653) to 12.09 cm (BWL-1793) with a general mean of 10.11 cm. Number of spikelets per spike was marked with the range of variation from 15.54 (RJ-4037) to 21.80 (ARIANA-66) with a general mean of 18.20. Number of grain per spike exhibited a wide range of variation from 41.94 (C-306) to 61.51 (PBN-51) with a general mean of 50.27. Grain weight per spike exhibited a range of variation from 1.29 g (SNORA-64) to 2.21 g (OTHERY EGYPT) with a general mean of 1.81 g. Number of tillers per plant revealed a range of variation from 5.33 (WH-730) to 7.16 (CHIRYA-3) with a general mean of 6.32.Biological yield per plantexhibited a wide range of variation from 12.08 g (SONORA-64) to 21.91 g (CHIRYA-3) with a general mean of 17.61 g.
Grain yield per plantexhibited a wide range of variation from 4.42 g (SNORA-64) to 8.33 g (CHIRYA-3) with a general mean of 6.50 g. 1000-grain weightexhibited a wide range of variation from 26.66 g (SONORA-64) to 42.95 g (CUS/79/PRULLA) with a general mean of 35.83g. Harvest indexexhibited a wide range of variation from 29.96 % (ARIANA-66) to 46.34% (WH-730) with a general mean of 36.85%.

In case of Canopy Temperature Depression, the observation was recorded in four different days during wheat growing period. The first observation which was recorded at the time of heading ranged from 1.80^{0}C (SONRA-64) to 5.77^{0}C (PBN-51) with an average of 3.78^{0}C. During second observation *i.e.*10 days after heading it varied from 2.50^{0}C (BWL-0814) to 4.47^{0}C (SERI-82) with an average of 3.41^{0}C. The third observation, 20 days after heading ranged from 1.12^{0}C (PBN-51) to 3.71^{0}C (RAJ-3765) with a general mean of 2.52^{0}C. The fourth observation, 30 days after heading ranged from 1.07^{0}C (IC-118737) to 3.45^{0}C (RAJ-3765) with a general mean of 1.92^{0}C. SPAD valuerepresented a range of variation from 35.38 (DHARWAR DRY) to 52.72 (K-9465) with a general mean of 42.71 while Relative water content (%)was marked with a wide range of variation from 58.39% (PBN-51) to 81.36% (GIZA-155) with a general mean of 69.82%.

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) and Balyaeva (1991)**.

3.3 Genetic Variability Parameters: The coefficient of variation at genotypic, phenotypic and environmental level, heritability (broad sense), genetic advance, and genetic advance as percent of meanare presented in **Table 4.**One of the most important trait plot yield exhibited high values of heritability, GCV, PCV, genetic advance, and genetic advance as percent of mean.

3.3.1 Heritability: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 traits such as days to75% heading, days to75% maturity, plant height, peduncle length, spike length, plot yield, and 1000 grains weight. 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. Traits such as days to 75% anthesis, number of spikelets per spike, number of grains per spike, grain weight per spike, biological yield per plant, grain yield per plant, and canopy temperature depression-I were marked with moderate values of heritability while low values of heritability were observed in traits like grain filling duration, number of tillers per plant, canopy temperature depression- IV, relative water content, SPAD, and harvest index.These finding are similar with the findings of **Rahim *et al.* (2010),Salem *et al.* (2008)**, **Ali *et al.* (2008)** and **Khan *et al.* (2010), Teerbatar (1988), Wrigley *et al*., (1994), Sharma and Tandon (1997), Ibrahim and Quick (2001).**

3.3.2 Coefficient of variation: Deshmukh*et al.* (1986) classified PCV and GCV values as low (0-10%), moderate (10-20%) and high (20% and above) values. According to this classification, high ECV was observed for characters such as canopy temperature depression-I, canopy temperature depression-II, canopy temperature-III, canopy temperature depression-IV, moderate for characters such as number of grains per spike, grain weight per spike, number of tillers per plant, biological yield per plant, grain yield per plant, plot yield, relative water content , SPAD, harvest index, low for characters such as days to 75% heading, days to 75% anthesis, days to 75% maturity, grain filling duration, plant height, peduncle length, spike length, number of spikelets per plant, and 1000 grains weight.Characters such as plot yield, canopy temperature depression-I, and canopy temperature depression-IV were marked with high GCV; characters such as plant height, peduncle length, grain weight per spike, biological yield per plant, grain yield per plant, canopy temperature depression-II, and canopy temperature depression-III were marked with moderate GCV; and characters such as days to 75 % heading, days to 75% anthesis, days to 75% maturity, grain filling duration, spike length, number of spikelets per spike, number of grains per spike, number of tillers per plant, 1000 grains weight, relative water content, SPAD, and harvest index were marked with low GCV.Characters like days to 75% heading, days to 75% anthesis, days to 75% maturity, grain yield per plant, plot yield, canopy temperature depression-I, canopy temperature depression-II, canopy temperature depression-III, and canopy temperature depression-IV exhibited high PCV; characters such as grain filling duration, plant height, peduncle length, number of grains per spike, grain weight per spike, number of tillers per plant, biological yield per plant, 1000 grains weight, relative water content, SPAD, harvest index exhibited moderate PCV; and characters spike length and number of spikelets per spike exhibited low PCV.These findings are in agreement with the findings of **Wani*et al.(*2011) and Monpara (2011).**

3.3.3 Genetic advance: Falconer and Mackay (1996)“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).**“The estimates of genetic advance help in understanding the type of gene action involved in the expression of various quantitative characters”.[52]“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).** The genetic advance was observed high for plot yield; moderate for plant height and low for rest of the characters.The genetic advance as percent of mean was observed high for traits like plot yield and canopy temperature depression-I; moderate for traits like plant height and peduncle length, low for spike length, number of spikelets per spike, number of grains per spike, grain weight per spike, number of tillers per plant, biological yield per plant, grain yield per plant, 1000 grains weight, canopy temperature depression-II, canopy temperature depression-III, canopy temperature depression-IV, relative water content, SPAD, and harvest index.These findings are similar with the findings of **Degewione*et al.* (2013), Singh and Narayanan (1999) and Munir*et al.* *(*2007).**

3.4 Genotypic correlations among physiological and yield related traits.

Days to 75 % heading showed highly significant positive correlation with days to 75 % anthesis, days to 75 % maturity, number of spikelets per spike, relative water content, significant positive correlation with grain filling duration and highly significant negative correlation with number of grains per spike, grain weight per spike, number of tillers per plant, canopy temperature depression-III, significant negative correlation with harvest index. Days to anthesis showed highly significant positive correlation with days to 75 % maturity, canopy temperature depression-I, canopy temperature depression -II, canopy temperature depression –IV, relative water content and highly significant negative correlation with canopy temperature depression -III.

Days to maturity showed highly significant positive correlation with grain filling duration, plant height, spike length, number of spikelets per spike, relative water content whereas highly significant negative correlation with number of grains per spike, grain weight per spike, grain yield per plant, plot yield, harvest index, canopy temperature depression -III. Grain filling duration showed highly significant positive correlation with spike length, number of spikelets per spike, significant positive correlation with relative water content and canopy temperature depression –IV whereas highly significant negative correlation with grain weight per spike, grain yield per plant, plot yield, harvest index, canopy temperature depression -III.

Plant height showed highly significant positive correlation with number of spikelets per spike, number of tillers per plant, significant positive correlation with spike length, biological yield per plant and highly significant negative correlation with harvest index, significant negative correlation with canopy temperature depression -II. Spike length showed highly significant positive correlation with number of spikelets per spike, 1000- grains weight, SPAD and highly significant negative correlation with canopy temperature depression -II. Number of spikelets per spike showed highly significant positive correlation with relative water content and highly significant negative correlation with SPAD, canopy temperature depression -II, significant negative correlation with harvest index and 1000- grains weight. Number of grains per spikes showed highly significant positive correlation with grain weight per spike, significant positive correlation with canopy temperature depression -II and highly significant negative correlation with 1000- grains weight and SPAD.

Grain weight per spike showed highly significant positive correlation with grain yield per plant, 1000- grains weight, harvest index, canopy temperature depression -III and significant positive correlation with biological yield per plant. Number of tillers per plant showed highly significant positive correlation with biological yield per plant, grain yield per plant, plot yield, 1000- grains weight, significant positive correlation with canopy temperature depression -III and significant negative correlation with harvest index. Biological yield per plant showed highly significant positive correlation with grain yield per plant, plot yield, canopy temperature depression -III and significant positive correlation with 1000- grains weight and significant negative correlation with harvest index. Grain yield per plant showed highly significant positive correlation with plot yield, 1000- grains weight, harvest index and canopy temperature depression -III.

Plot yield showed highly significant positive correlation with 1000- grains weight, canopy temperature depression -I, canopy temperature depression -II and significant positive correlation with canopy temperature depression -III. 1000-grain weight showed highly significant positive correlation with canopy temperature depression -I and SPAD. Harvest index showed highly significant negative correlation with relative water content. Canopy temperature depression -I showed highly significant positive correlation with canopy temperature depression –II and relative water content.

Canopy temperature depression -II showed significant positive correlation with relative water content and canopy temperature depression-IV whereas significant negative correlation with canopy temperature depression -III. Canopy temperature depression -III showed significant negative correlation with relative water content.
Canopy temperature depression –IV exhibited highly significant positive correlation with days to 75 % flowering, days to 75 % anthesis and spike length whereas significant positive with grain filling duration, grain yield per plant and canopy temperature depression-II. The present findings are in agreement with the findings of **Warrington *et al.* (1977), Blum *et al.* (1990), Cupina*et al.* (1979), Reynolds *et al.* (1998), Fisher et al. (1991), Rane *et al.* (2002), Fellahi *et al.* (2013),** and **Khan *et al.* (2014).**

4. Conclusion: These findings suggested thatthe experimental material had sufficient genetic variability for yield contributing as well as physiological traits in bread wheat. The traits which had desired value of variability parameters can be utilized in crop improvement programme. This study generally indicated that there was significanct genetic variability among the genotypes studied. This correlation study has clearly demonstrated that physiological traits are significantly correlated with yield related traits and selection of physiological traits exhibiting significant positive association with yield related traits will help in indirect selection for yield and its attributes.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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Table2:Analysis of Variance for Physiological Traits and Yield Attributes.

Source of Variation	df	MS										
		DH	DA	DM	GFD	PH	PL	SL	NSS	NGS	GWS	NTP
Replication	2	3.89	4.82	7.29	16.72	14.9192	0.19	0.45	1.35	24.22	0.04	0.55
Environments	2	9795.97**	13267.96**	20454.28**	799.55**	14916.3721**	815.60**	64.43**	70.82**	4283.50**	26.65**	3.37**
Interactions	4	2.76	1.81	8.26	0.98	11.7893	2.94	0.06	1.62	10.47	0.01	0.14
Overall Sum	8	2451.34**	3319.10**	5119.52**	204.56**	3738.7175**	205.42**	16.25**	18.85**	1082.17**	6.68**	1.05**
Treatments	31	164.13**	71.63**	132.48**	42.97**	928.1021**	168.48**	5.23**	15.70**	232.96**	0.57**	2.03**
Error	248	6.35	7.60	7.24	10.22	20.3812	4.76	0.30	1.44	25.44	0.06	0.56
C.V.		3.28	3.42	2.30	8.79	5.19	6.38	5.37	6.58	10.03	13.13	11.81
CD 1%		2.3395	2.5602	2.4985	2.9689	4.1916	2.0254	0.5046	1.1123	4.6826	0.2212	0.6936
CD 5%		3.0834	3.3742	3.2929	3.9129	5.5244	2.6694	0.6651	1.4660	6.1714	0.2916	0.9141

Continued….

Source of Variation	df	MS										
		BY	GY	PY	TGW	CTD-I	CTD-II	CTD-III	CTD-IV	RWC	SPAD	HI
Replication	2	0.18	0.19	1625.86	1.32	0.03	0.00	0.005	0.078	0.054	1.16	13.45
Environments	2	887.04**	242.89**	51067496.00**	747.66**	24.91**	69.52**	3.679**	9.450**	1627.226**	486.85**	745.65**
Interactions	4	0.14	0.34	740.22	1.86	0.18	0.02	0.060	0.022	0.551	1.03	10.57
Overall Sum	8	221.87**	60.94**	12767650.00**	188.18**	6.32**	17.39**	0.951**	2.393**	407.095**	122.52**	195.06**
Treatments	31	41.08**	9.74**	1216545.50**	121.85**	15.50**	2.51**	2.588**	1.985**	247.814**	112.67**	138.98**
Error	248	7.69	1.34	67316.13	7.23	1.34	0.79	0.820	0.468	60.382	25.49	29.21
C.V.		15.75	17.76	18.37	7.50	30.62	26.02	35.83	35.90	11.13	11.82	14.66
CD 1%		2.5750	1.0729	240.8943	2.4957	1.0752	0.8260	0.8408	0.6351	7.2148	4.6876	5.0182
CD 5%		3.3938	1.4141	317.4880	3.2893	1.4171	1.0886	1.1082	0.8370	9.5087	6.1780	6.6138

***5% level of significance, ** 1% level of significance**

Table3: MeanPerformance of Physiological Traits and Yield Attributes.

SI. No.	Genotype	DH	DA	DM	GFD	PH	PL	SL	NSS	NGS	GWS	NTP
1.	**PBN-51**	78.89	81.44	116.22	34.78	83.11	32.13	9.41	17.98	61.51	2.00	6.44
2.	**BWL-0814**	78.11	81.22	117.78	36.56	89.28	30.79	10.18	17.59	50.44	1.80	6.50
3.	**BWL-1771**	79.33	82.11	118.56	36.44	82.88	29.41	10.01	19.67	46.11	1.86	6.24
4.	**BWL-9022**	72.89	76.67	114.11	36.44	86.12	34.87	10.74	19.16	52.31	2.13	6.42
5.	**BWL-0924**	78.11	81.78	116.44	34.67	77.57	30.06	9.35	16.36	50.82	1.86	5.84
6.	**BWL-1793**	74.56	77.78	115.11	37.33	79.24	34.76	10.46	17.81	52.13	1.97	7.00
7.	**CUS/79/PRULLA**	78.00	80.44	116.56	36.11	101.98	37.18	12.09	16.65	48.41	2.22	7.17
8.	**IEPACA RABE**	74.22	78.22	115.11	36.89	86.16	37.61	10.82	19.76	49.82	2.09	5.80
9.	**CHIRYA-3**	77.67	79.78	116.00	36.22	84.91	33.73	8.94	18.00	55.53	2.21	7.17
10.	**DHARWAD DRY**	83.22	85.44	123.78	39.22	101.57	38.64	10.68	19.66	54.13	1.79	6.87
11.	**RAJ3765**	73.33	79.44	115.33	35.89	82.40	33.42	10.41	18.46	53.71	1.91	6.67
12.	**HI1563**	72.67	78.89	115.56	36.67	82.23	35.56	10.85	17.65	49.56	1.80	6.11
13.	**HD2864**	71.11	78.89	112.89	34.00	81.08	35.51	10.54	17.05	50.20	1.81	6.77
14.	**RAJ4083**	72.78	77.44	113.89	36.44	76.91	32.03	9.96	17.73	48.42	1.75	6.82
15.	**DBW-14**	70.78	77.44	116.00	39.67	75.79	31.29	10.27	18.44	46.02	1.75	6.71
16.	**WH730**	78.44	80.67	115.78	35.11	89.12	33.00	11.35	17.43	45.73	1.99	5.33
17.	**K9465**	78.00	81.11	113.11	32.00	86.34	34.57	10.32	18.56	44.07	1.93	5.76
18.	**RAJ4037**	78.11	82.00	118.78	36.78	71.73	30.44	9.73	15.55	43.09	1.56	6.42
19.	**TEPOKO**	76.44	81.56	115.44	33.89	91.16	36.59	10.39	17.77	60.33	2.20	5.97
20.	**BABAX**	79.22	83.00	121.78	39.78	88.29	35.35	11.48	19.74	53.49	1.84	6.53
21.	**OTHERI RGYPT**	78.44	80.89	122.33	41.89	87.09	33.52	9.99	17.46	54.44	2.22	6.20
22.	**IC532653**	83.89	87.44	125.11	36.67	103.54	42.66	8.75	18.67	42.64	1.40	6.52
23.	**SERI82**	70.56	77.44	113.33	36.67	80.00	29.58	9.24	18.43	52.76	1.45	5.89
24.	**SONORA64**	68.11	74.78	112.33	38.22	74.77	30.23	9.06	17.09	48.58	1.29	5.86
25.	**SALEMBO**	79.56	82.67	119.33	36.67	84.37	30.73	9.91	19.05	47.84	1.79	5.91
26.	**ARIANA66**	89.89	87.78	128.78	38.22	106.44	36.83	10.41	21.81	46.89	1.47	5.48
27.	**GIZA155**	77.22	80.22	118.89	38.67	106.33	44.49	9.51	20.11	47.96	1.58	6.80
28.	**BACANORA88**	77.67	80.44	115.44	35.00	75.80	28.26	9.54	19.19	55.71	1.81	6.43
29.	**IC118737**	76.78	79.89	112.00	32.11	87.07	33.38	10.54	18.67	59.44	1.43	5.89
30.	**C-306**	75.22	79.33	115.22	36.44	111.46	45.94	9.29	15.87	41.94	1.69	6.10
31.	**HD2967**	78.00	80.44	115.78	35.33	89.24	34.06	9.94	18.31	51.98	1.90	6.71
32.	**PBW343**	78.78	82.56	115.22	32.67	80.30	28.27	9.56	16.91	42.84	1.59	6.10
	Mean	**76.88**	**80.60**	**116.94**	**36.36**	**87.01**	**34.22**	**10.12**	**18.21**	**50.28**	**1.82**	**6.33**
	Range Lowest	68.11	74.78	112.00	32.00	71.73	28.26	8.75	15.55	41.94	1.29	5.33
	Range Highest	89.89	87.78	128.78	41.89	111.46	45.94	12.09	21.81	61.51	2.22	7.17

Continued…

SI. No.	Genotype	BY	GY	PY	TGW	CTD-I	CTD-II	CTD-III	CTD-IV	RWC	SPAD	HI
1.	**PBN-51**	17.91	5.87	1418.89	35.13	5.78	2.57	1.12	1.54	58.40	42.88	33.86
2.	**BWL-0814**	20.47	7.00	1969.33	34.79	4.51	2.50	1.71	1.84	63.06	42.44	34.25
3.	**BWL-1771**	19.11	6.93	1843.78	36.72	5.62	3.49	2.64	2.20	73.88	41.84	36.03
4.	**BWL-9022**	20.64	8.22	1595.11	42.84	1.84	2.82	2.34	1.91	67.96	43.84	38.81
5.	**BWL-0924**	18.62	6.16	1510.44	39.37	4.90	2.98	2.04	1.54	64.91	44.83	34.47
6.	**BWL-1793**	20.44	7.78	1419.67	37.94	2.23	3.45	2.31	1.72	72.03	42.23	38.32
7.	**CUS/79/PRULLA**	19.84	7.87	1642.67	42.95	4.43	3.37	2.43	1.72	71.50	43.26	40.45
8.	**IEPACA RABE**	18.98	7.76	1623.33	37.01	2.02	4.26	3.11	1.74	66.63	40.74	40.66
9.	**CHIRYA-3**	21.91	8.33	1934.22	35.63	5.21	3.39	2.43	1.94	74.43	40.52	37.92
10.	**DHARWAD DRY**	18.00	5.64	1485.11	32.54	4.92	4.16	3.24	2.67	67.47	35.38	30.89
11.	**RAJ3765**	17.64	6.40	1278.44	36.40	1.93	3.32	3.71	3.46	61.80	51.10	36.23
12.	**HI1563**	18.27	6.31	1364.44	35.28	2.11	3.70	3.37	2.43	68.70	38.23	34.07
13.	**HD2864**	14.91	6.20	1621.33	36.08	2.29	2.87	2.69	1.88	73.20	44.56	42.66
14.	**RAJ4083**	18.11	6.96	1308.56	35.07	2.00	2.93	2.41	1.70	61.70	45.99	37.58
15.	**DBW-14**	18.67	7.44	1286.22	37.79	2.13	3.03	2.43	2.20	72.76	44.44	39.68
16.	**WH730**	14.87	7.07	986.67	35.94	3.81	3.58	1.73	1.77	65.68	47.86	46.35
17.	**K9465**	18.31	7.42	1313.33	40.54	3.91	2.59	2.77	1.46	72.49	52.72	41.18
18.	**RAJ4037**	15.58	6.24	731.56	35.83	3.91	3.34	2.46	2.04	68.12	39.49	39.82

19.	**TEPOKO**	15.16	6.22	1529.56	33.39	4.87	3.99	2.50	2.11	71.20	40.19	40.86
20.	**BABAX**	17.31	6.44	1154.89	34.66	4.68	3.97	2.02	1.36	70.62	39.96	34.39
21.	**OTHERI RGYPT**	18.73	6.96	1429.78	40.04	4.39	3.64	2.17	1.68	71.34	46.36	36.20
22.	**IC532653**	15.73	4.87	806.44	31.64	4.09	3.30	2.63	1.76	72.46	43.13	30.77
23.	**SERI82**	15.51	5.20	1250.44	29.78	2.16	4.48	3.41	2.14	60.23	43.45	32.92
24.	**SONORA64**	12.09	4.42	935.78	26.66	1.80	4.18	2.70	2.41	66.91	38.16	37.16
25.	**SALEMBO**	19.04	6.18	2310.44	38.44	5.38	3.11	2.51	2.29	71.96	43.83	32.29
26.	**ARIANA66**	16.67	4.93	950.89	32.21	3.02	3.00	2.11	1.92	73.21	43.38	29.96
27.	**GIZA155**	17.58	5.62	1094.67	36.96	5.03	3.38	3.08	1.80	81.37	41.49	32.49
28.	**BACANORA88**	17.40	7.20	1721.56	30.21	4.84	2.98	2.02	1.27	77.56	39.19	41.40
29.	**IC118737**	15.09	5.56	1125.33	31.23	4.10	3.49	2.56	1.08	72.08	40.87	36.64
30.	**C-306**	15.11	4.80	983.78	40.61	4.33	4.16	2.53	2.46	78.77	40.61	32.19
31.	**HD2967**	19.40	7.69	1972.44	36.76	5.06	4.02	3.06	1.26	70.43	42.52	39.47
32.	**PBW343**	16.42	6.53	1596.67	36.23	3.71	3.39	2.61	1.68	71.54	41.33	39.41
	Mean	**17.61**	**6.51**	**1412.37**	**35.83**	**3.78**	**3.42**	**2.53**	**1.91**	**69.83**	**42.71**	**36.86**
	Range Lowest	12.09	4.42	731.56	26.66	1.80	2.50	1.12	1.08	58.40	35.38	29.96
	Range Highest	21.91	8.33	2310.44	42.95	5.78	4.48	3.71	3.46	81.37	52.72	46.35

Table4: Genetic Variability Parameters for Physiological Traits and Yield Attributes.

Parameters	DH	DA	DM	GFD	PH	PL	SL	NSS	NGS	GWS	NTP
E.C.V.	3.27	3.42	2.30	8.79	5.18	6.37	5.37	6.58	10.03	13.12	11.80
G.C.V.	5.44	3.30	3.19	5.24	11.54	12.46	7.31	6.91	9.55	13.17	6.40
P.C.V.	6.35	4.76	3.93	10.24	12.65	14.00	9.07	9.54	13.85	18.59	13.43
h² (Broad Sense)	73.4	48.3	65.8	26.2	83.2	79.3	65.00	52.50	47.50	50.20	0.22
G.A. (5%)	7.39	3.82	6.23	2.01	18.86	7.82	1.22	1.87	6.82	0.34	0.39
G.A. M. (5%)	9.61	4.74	5.33	5.53	21.68	22.86	12.14	10.32	13.56	19.21	6.28

Continued…

Parameters	BY	GY	PY	TGW	CTD-I	CTD-II	CTD-III	CTD-IV	RWC	SPAD	HI
E.C.V.	15.74	17.75	18.37	7.50	30.61	26.01	35.82	35.89	11.12	11.82	14.66
G.C.V.	10.93	14.84	25.30	9.95	33.16	12.78	17.53	21.54	6.53	7.28	9.47
P.C.V.	19.17	23.14	31.26	12.46	45.13	28.99	39.89	41.86	12.90	13.88	17.46
h² (Broad Sense)	0.32	0.41	0.65	0.63	0.54	0.19	0.19	0.26	0.25	0.27	0.295
G.A. (5%)	2.26	1.27	20.5	5.87	1.89	0.39	0.40	0.43	4.76	3.36	3.904
G.A. M. (5%)	12.85	19.62	42.17	16.38	50.19	11.61	15.88	22.84	6.81	7.87	10.59

DF-Days to 75%, **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-C**anopy temperature depression, **RWC-**Relative water content %, **SPAD-** Soil-plant analysis development (chlorophyll content)**,** **HI-**Harvest index %, **PY-** Plot Yield.

Table 5:Genotypic Correlations among Physiological and Yield Related Traits.

rs																					
Characters	**DH**	**DA**	**DM**	**GFD**	**PH**	**SL**	**NSS**	**NGS**	**GWS**	**NTP**	**BY**	**GY**	**PY**	**TGW**	**HI**	**CTD-I**	**CTD-II**	**CTD-III**	**CTD-IV**	**RWC**	**SPAD**
DH																					
DA	0.589**																				
DM	0.624**	0.204**																			
GFD	0.329*	-0.086	0.768**																		
PH	0.293	0.044	0.396**	0.178																	
SL	-0.029	-0.158	0.387**	0.463**	0.313*																
NSS	0.325**	-0.074	0.740**	0.691**	0.522**	0.420**															
NGS	-0.435**	-0.098	-0.450**	-0.262	-0.186	-0.103	0.027														
GWS	-0.362**	-0.010	-0.348**	-0.379**	-0.174	0.082	-0.169	0.561**													
NTP	-0.405**	-0.122	-0.045	0.058	0.538**	0.107	-0.039	-0.043	0.047												
BY	0.014	0.004	0.023	-0.009	0.338*	0.098	0.119	0.044	0.347*	0.526**											
GY	-0.267	-0.158	-0.210**	-0.435**	0.003	0.208	-0.009	0.078	0.634**	0.320**	0.628**										
PY	-0.001	-0.047	-0.412**	-0.546**	0.165	-0.146	-0.069	0.037	0.336*	0.591**	0.521**	0.353**									
TGW	0.020	0.305*	0.016	-0.040	0.073	0.401**	-0.302*	-0.576**	0.426**	0.382**	0.331*	0.379**	0.407**								
HI	-0.306*	-0.176	-0.410**	-0.635**	-0.388**	-0.006	-0.314*	0.064	0.403**	-0.427*	-0.312*	0.402**	0.162	0.087							
CTD-I	0.503**	0.469**	0.074	-0.100	0.158	-0.159	-0.133	-0.158	0.068	0.096	0.056	0.038	0.307**	0.464**	-0.008						
CTD-II	0.214	0.596**	-0.159	-0.126	-0.360*	-0.530**	-0.468**	0.336*	0.084	-0.104	-0.148	-0.136	0.387**	-0.154	-0.004	0.332**					
CTD-III	-0.442**	-0.494**	-0.425**	-0.362**	-0.029	-0.057	-0.268	0.057	0.276**	0.354*	0.320**	0.455**	0.227*	0.127	-0.023	-0.297**	-0.329*				
CTD-IV	0.121**	0.136**	-0.113	0.212*	-0.016	0.521**	0.092	-0.098	-0.267	0.301	-0.056	0.129*	0.067	0.098	0.114	0.067	0.231*	0.091			
RWC	0.441**	0.300**	0.412**	0.457*	0.084	0.149	0.467**	-0.025	-0.115	0.084	0.117	-0.136	0.163	0.068	-0.482**	0.515**	0.317*	-0.327*	0.029		
SPAD	-0.060	-0.219	-0.029	0.016	-0.112	0.419**	-0.230**	-0.412**	0.156	0.008	0.165	0.107	0.125	0.480**	-0.029	0.195	0.046	0.272	0.025	-0.068	

***5% level of significance, ** 1% level of significance**