



PERFORMANCE AND YIELD EVALUATION OF RELEASED BREAD WHEAT (*TRITICUM AESTIVUM* L.) VARIETIES IN JAJURA DISTRICTS OF HADIYA ZONE OF SNNP, ETHIOPIA

Kedir Wolchafo Hussien

Ethiopian Institute of Agricultural Research (EIAR), Wondogenet Agricultural Research Center, Wondogenet (WGARC), Ethiopia. P.O.Box 198, Shashamene, Ethiopia

*Corresponding author E-mail: Kedir Wolchafo, Email address: Kedir.wulchafo@ymail.com or umi.kedir2004@gmail.com

ABSTRACT

In Ethiopia, a number of improved bread wheat (*Triticum aestivum* L.) varieties have been released by different research centers. However, all of these varieties were not evaluated in Jajura district for growth characters, yield and yield components which are necessary for identification of adaptable varieties for this major wheat growing district. Therefore, a field experiment was conducted in 2022 cropping season using 12 released varieties in Randomized Complete Block Design with three replications. Data were recorded for 5 characters. The objectives of this experiment were to estimate the performance released bread varieties in the district and also to see the variability, heritability in bread wheat varieties. Results of the analysis of variance revealed that varieties were differed significantly for all characters studied. Highly significant variability observed among varieties for grain yield kg/ ha, which was ranged from 5644.6-7088.5kg/ha with the mean value of 6235.77 kg/ha. The highest grain yield (7088.5kg/ha) was recorded for Boru while low yield of 5644.6kg/ha was obtained from Lemu.

Keywords: bread wheat, grain yield, genetic variability, phenotypes, genotypes

INTRODUCTION

Globally, attainment of food security in relation to population growth and protection of the environment are two of the greatest challenges facing human kind today. Particularly, the population growth phenomenon in developing countries, diversity of foods, and their high consumption in the advanced countries have led to an increase in the global demand for food to an unprecedented level in the history (Khabiriet.al., 2012).

The role of more productive, profitable agricultural production in fostering food security, generating local employment, raising local incomes, and thus alleviating poverty particularly in developing world, where it serves as an economic source is incomparable (Reeves *et al.*,1999). In this regard, increasing cereal crops productivity plays a great role as they are an important source of human nutrition since pre-historic times, dating back to 8000 B.C (Curtis, 2002).

Wheat is considered as the earliest domesticated cereal crop and the most important agricultural product of the world. Today, wheat is grouped among the big three cereal crops of the world

with its high tons of grain yield being harvested annually (Shewry, 2009). Wheat is produced under a wide range of climatic conditions and geographical areas and due to its high adaptability with various climatic conditions of environment, its distribution range is more than any other plant species and it is the staple food for most of the world's increasing population (Kamali, 2008). It is grown from temperate, irrigated to dry and high-rain-fall areas and from warm, humid to dry, cold environments. Wheat is a C3 plant and as such it thrives in cool environments, but it has a wide adaptation. Undoubtedly, this wide adaptation has been possible due to the complex nature of the plant's genome, which provides great plasticity to the crop (Acevedo *et al.*, 2002).

In Ethiopia, bread wheat improvement has started in 1949 and up to now many varieties have been released by the national and regional research institutes in collaboration with several international organizations focusing on increasing yield through the development of varieties which are resistant to several diseases, lodging and are adaptable to a wide range of environments for commercial production (MoA, 2011). However, those varieties are not widely distributed to all parts of the country. This is because of several constraints including the remoteness and inaccessibilities of the growing areas that limited to test the adaptability and yields of the varieties in such areas. It is necessary to evaluate varieties for the intended growing regions since varieties were recommended as high yielding after evaluating a few representative wheat growing areas, in other words the varieties were not evaluated in all wheat growing regions.

Jajura district in Hadya Zone of SNNP region is one of the areas where improved varieties are not widely distributed so far, most probably due to the above indicated problems. Particularly, the potential of the area to wheat crop is not exploited due to lack of improved varieties, poor management practices, biotic factors (weeds, diseases and insect pests etc.) and abiotic factors (frost), rain fall variability (intensity as well as duration). With this in mind, there is no detail information indicating the adaptability and production status of the improved bread wheat varieties in the area. Therefore, it is important to evaluate those varieties released by different research centres in Jajura district of Hadya Zone to identify high yielding and more adaptable varieties to improve productivity and production of wheat. In the process of testing varieties for yield and adaptability it is also equally important to study the genetic variability and heritability since it provides information that can be utilized to improve wheat yield through breeding.

MATERIALS AND METHODS

Description of the study area

The experiment was conducted at Wondogenet Agricultural Research Center's (WGARC) sub-testing site in Jajura woredain SNNP Regional State in the southern part of Ethiopia during the main cropping season of 2022. Jajura woredais some of the main wheat cultivating areas in SNNP Region. Jajura woreda has a unimodal rainfall pattern, which starts at the end of June and extends to mid-October. the maximum rainfall is received during June to September. The major soil type is Nitosol with a dark reddish-brown color.

Experimental Materials

In this experimental study, a total of 12 released bread wheat varieties were used (Table 1). These varieties were obtained from Kulumsa Agricultural Research Center (KARC) which conducted

research on wheat for more than six decades and considered the center of excellence for wheat research.

Experimental Design

Twelve bread wheat varieties were organized in a randomized complete block design with three replications. Six rows of 2 m length were used for each plot. Inter-row spacing of 20 cm were used thus making a plot size of 2.4 m² (6 rows x 2 m x 0.2 m). The spacing between plots and blocks was 0.5 m and 1.5 m, respectively.

Table 1. List of 12 bread wheat varieties used in the study area

Item number	Name of Genotypes
1	ETBW9089
2	Jajabo
3	Liben
4	Lemu
5	Wane
6	Huluka
7	Alidoro
8	Hidasse
9	Ogolcho
10	Daka
11	Danda'a
12	Boru

Management Practices

All recommended agronomic practices which included land preparation to harvesting were followed as per the recommendations from research. Plantings were carried out in July. Recommended NPS and urea fertilizers (each at 100 kg per hectare) were applied at sowing and later after plant establishment. All NPS was applied at sowing time while urea was applied in split, 2/3 at sowing and 1/3 at initial flowering stage. To control grass and broad leaf weeds, two hand weeding were performed at critical stages of crop development. The first-hand weeding was carried out 35 days after seedling emergence and the second weeding 65 days after emergence or 30 days after the first weeding.

Data Collection

Yield and yield related parameters and morphological and agronomic data were collected and recorded on a plot basis from the central three rows and on a plant basis from randomly selected plants from the central three rows in each plot.

Measurement of phenological and growth parameters

Data of different traits were collected and recorded either from randomly selected plants or on a plot basis. Days to seedling emergence (DSE) was recorded as the number of days from plating to the time when 50% of the seedlings have emerged in each plot. Days to initial flowering (DIF) was recorded as the number of days from seedling emergence to the appearance of first flowers in each plot. Days to 50% flowering was recorded as number of days from seedling emergence to a growth stage when about 50% of plants have flowered in each plot. Days to maturity was

recorded as days from seedling emergence to the appearance of openflower on about 95% of the plants in each plot. Plant height (PHt) was recorded by measuring the height of 5 randomly selected plants at maturity from ground level to the tip of the stem and taking mean of the total.

Data Analysis

Analysis of variance

The data collected were subjected to statistical analysis. First, the analysis was done using the SAS computer program, version 9.0 (SAS, 2002). Mean separation was conducted using Least Significance Difference (LSD) at 0.05 probability level. The simple correlation coefficients were computed to determine the degree of association between pair of characters using PROC CORR procedure of SAS (SAS, 2002) program based on across location mean data.

Table 2. Analysis of variance in randomized complete block design and expected mean square.

Source of Variation	Df	Mean Square	Expected Mean Square
Replication	r-1	MSr	$\sigma^2 e + g\sigma^2 r$
Genotypes	g-1	MSg	$\sigma^2 e + r\sigma^2 g$
Error	(r-1)(g-1)	MSe	$\sigma^2 e$

Where,

r = number of replications;

g = number of genotypes;

MSr = mean square due to replications;

MSg = mean square due to genotypes;

MSe = mean square of error; and

$\sigma^2 r$, $\sigma^2 g$, and $\sigma^2 e$ are variances due to replication, genotype, and error, respectively.

Analysis of variance in a randomized complete block design was computed using the following model:

$$Y_{ij} = \mu + r_j + g_i + \epsilon_{ij}$$

Where,

Y_{ij} = the response of trait Y in the i th genotype and the j th replication

μ = the grand mean of trait Y;

r_j = the effect of the j th replication;

g_i = the effect of the i th genotype; and

ϵ_{ij} = experimental error effect.

Phenotypic and genotypic variances

The phenotypic and genotypic variances of each trait were estimated from the RCBD analysis of variance and the expected mean squares under the assumption of random effects model computed from linear combinations of the mean squares and the phenotypic and genotypic coefficient of variations, which were also computed as per the methods suggested by Burton *et al.* (1953).

$$\text{Genotypic variance } (\sigma^2 g) = \frac{\text{Msg} - \text{Mse}}{r}$$

$$\text{Environmental variance } (\sigma^2 e) = \text{MSe}$$

Where,

MSg and MSe are the mean sum of squares for the genotypes and error in the analysis of variance, respectively.

r is the number of replications.

Then, the phenotypic variance was estimated as the sum of the genotypic and environmental variances:

$$\text{Phenotypic variance } (\sigma^2_{ph}) = \sigma^2_g + \sigma^2_e$$

Genotypic and phenotypic coefficient of variations

The genotypic and phenotypic coefficients of variability were estimated according to the formulae of Singh and Chaudhary, (1977) as follows

$$\text{Genotypic Coefficient of Variation (GCV)} = (\sigma_g/\text{grand mean}) * 100$$

$$\text{Phenotypic Coefficient of Variation (PCV)} = (\sigma_{ph}/\text{grand mean}) * 100$$

Where,

σ_g and σ_{ph} are genotypic and phenotypic standard deviations, respectively.

Heritability analysis

Broad sense heritability values were estimated based on the formula of Falconer *et al.*, 1996 as follows:

$$\text{Heritability in broad sense } (H^2) = (\sigma^2_g/\sigma^2_{ph}) * 100$$

Then, the genetic advance for selection intensity (k) at 5% was estimated by the following formula (Allard, 1960):

$$\text{EGA} = k * \sigma_{ph} * H^2$$

Where,

EGA represents the expected genetic advance under selection;

σ_{ph} is the phenotypic standard deviation;

H^2 is heritability in broad sense and k is selection intensity.

The genetic advance as percent of population mean was also estimated following the procedure of Johnson *et al.* (1955b):

$$\text{Genetic advance as percent of population mean} = (\text{EGA}/\text{grand mean}) * 100$$

Correlation analysis

Estimations of genotypic and phenotypic correlation coefficients were done based on the procedure of Dabholkar (1992) as follows:

$$\text{Genotypic correlation coefficient } (r_g) = \frac{\text{COV}_g(xy)}{\sigma_g(x) * \sigma_g(y)}$$

$$\text{Phenotypic correlation coefficient } (r_{ph}) = \frac{\text{COV}_{ph}(xy)}{\sigma_{ph}(x) * \sigma_{ph}(y)}$$

Where,

COV_g(xy) and COV_{ph}(xy) are the genotypic and phenotypic covariance of two variables (X and Y), respectively; $\sigma_g(x)$ and $\sigma_g(y)$ are the genotypic standard deviations for variables X and Y, respectively, while $\sigma_{ph}(x)$ and $\sigma_{ph}(y)$ are the phenotypic standard deviations of variables X and Y, respectively.

The calculated phenotypic correlation values were tested for its significance using t-test:

$$t = r_{ph}/SE(r_{ph})$$

Where,

r_{ph} = Phenotypic correlation; SE_{rph} = Standard error of phenotypic correlation obtained using the following formula (Sharma, 1998).

$$SE(r_{ph}) = \sqrt{(1-r_{ph}^2)/(n-2)}$$

Where,

n is the number of genotypes tested,

r²_{ph} is phenotypic correlation coefficient.

The coefficients of correlations at genotypic levels were also tested for their significance by the formula described by Robertson (1959) as indicated below:

$$t = r_{gxy}/SE_{r_{gxy}}$$

The calculated "t" values were compared with the tabulated "t" value at (n-2) degree of freedom at 5% level of significance. Where, n is number of genotypes.

$$SE_{r_{gxy}} = \sqrt{(1-r_{gxy}^2)/2H^2_x.H^2_y}$$

Where,

H²_x = Heritability of trait x; and H²_y = Heritability of trait y.

RESULT

Analysis of variance

The analysis of variance results for the five traits studied are given in Tables 3. Highly significant (P<0.01) differences among varieties were observed in the testing site for days to 95% maturity, Septoria leaf blotch and thousand kernel weight. However, traits namely days to heading, yellow rust, leaf rust, stem rust, and grain yield showed significant difference at the <0.05 probability level. Whereas plant height showed none significant difference among the listed varieties.

Table 3. Analysis of variance (mean square) for nine traits of 12 bread wheat varieties grown at testing site.

Traits	Rep(2)	Gen(11)	Error(22)	CV(%)
DH	6.86ns	18.63*	7.86	4.36
DM	13.56ns	23.30**	12.25	3.05
PHt	11.44ns	48.56ns	29.44	5.13
TKW	1.45ns	490.24**	27.01	8.74
GYLD	1654160.19ns	657820.74*	558823.21	11.98

*, ** Indicate significance at the 0.05 and 0.01 levels, respectively; ns=non-significant.

DH=days heading, DM=Days to 95% maturity; PHt=Plant height;

TKW=thousand kernel weight in grams; GYLD=grain yield in kg per ha.

Yield and yield components of genotypes

Grain yield (GYLD) for varieties tested at the tested area ranged from 5644.6 to 7088.5kg/ha, and the mean value was 6235.77kg/ha (Table 4). The top yielders included Boru, Liben, Jajabo,

Ogolcho and Alidoro with 7088.5, 6805.5, 6722.6, 6494.7 and 6308.3 kg/ha, respectively. All of the above varieties, except Lemu, showed satisfactory grain yield potential. Intermediate yielders were Wane, Hidasse, Dnda'a, Huluka and Daka, all with grain yield of slightly lower than the mean value of 6235.77 kg/ha.

Table 4. Summarized mean values with their agronomic parameters along with their coefficient of variation, least significant differences of Late maturing Bread wheat varieties adaptation tested at Jajura.

Var. Name	DH	DM	PHt	TKW	GYLD
ETBW9089	61.67bdc	111bc	98.06c	63.94c	5742.3b
Jajabo	67.33a	119ba	110.93a	66.84b	6722.6ba
Liben	65.67ba	117.33a	101.2ba	46.40df	6806.5ba
Lemu	65.33bac	117a	105.67bac	43.15g	5644.6b
Wane	60.67dc	113.33bac	103.8bac	63.86c	6120.1ba
Huluka	65.67ba	118a	105.4bac	58.56dce	5896.3ba
Alidoro	66.33ba	113.67bac	111.6a	54.73dfe	6308.3ba
Hidasse	59d	109.33c	104bac	58.75dc	6187.8ba
Ogolcho	65bac	114.67bac	110ba	68.40a	6494.7ba
Daka	65.33bac	118a	108.67ba	57.20dce	5672.1b
Danda'a	64.67bac	116.33ba	106.73bac	49.88dfe	6145.4ba
Boru	63.67bdac	123.33bac	104.06bac	51.60dgfe	7088.5a
Mean	64.19	114.83	105.86	59.45	6235.77
CV	4.37	3.05	5.13	8.74	11.98
LSD	0.56	0.51	0.46	0.9	0.46

DH=days heading, DM=Days to 95% maturity; PHt=Plant height; TKW=thousand kernel weight in grams; GYLD=grain yield in kg per ha.

Variance components and coefficients of variation

Estimates of phenotypic (s^2_p), genotypic (s^2_g) and environmental (s^2_e) variances and phenotypic (PCV) and genotypic coefficients of variation (GCV) are given in Tables 5 below for testing site. Generally, the GCV values were lower than that of PCV in the testing site. The relatively larger differences between PCV and GCV for the rest of the traits suggests the high contribution of the environmental variance to the phenotypic variance.

The phenotypic and genotypic variances (> 20 %), were obtained from all traits i.e for Days to heading, Days to 95% maturity, Plant height, yellow rust, Leaf rust, Stem rust, Septorial leaf blotch, Thousand Kernel Weight and Grain yield. indicating high influence of the environment on these traits at the testing sites.

Estimation of broad-sense heritability

Estimate of broad sense heritability for 5 traits of *bread wheat varieties* ranged from 2% for Leaf rust and Stem rust to 99% for Thousand kernel weight (Table 5).

Under a range of high and moderately high heritability, but low genetic advance as percent of mean were observed for the trait days to heading and days to 95% maturity.

The high heritability may have been exhibited due to the influence of favorable environmental conditions rather than genotypic influences and selection for such traits may not be rewarding. The GCV values of most of the heritable traits were also relatively high in magnitude. Moreover, as the value of broad sense heritability becomes high it is used as an indicator of the ease of phenotype-based selection particularly when it is accompanied by a relatively high variability and genetic advance as percent of mean value.

Table 5. σ^2p , σ^2g , σ^2e , GCV, PCV, h^2 , GA and GAM% for the 9 characters of the 12 bread wheat varieties

Traits	σ^2p	σ^2g	σ^2e	PCV%	GCV %	h^2 %	GA	GAM (%)
DH	29.76	16.01	13.75	68.09	49.94	0.54	6.05	9.43
DM	23.67	19.22	4.45	45.40	40.91	0.81	8.15	7.10
PHt	41.22	38.75	2.47	62.40	60.50	0.94	12.45	11.76
TKW	486.69	481.24	5.45	298.97	297.29	0.99	45.00	82.65
GYL	471549.1	471546.3					1416.6	
D	5	4	2.81	869.60	869.60	0.99	4	22.72

σ^2p =phenotypic variance, σ^2g =genotypic variance, σ^2e =Environmental variance, GCV=genotypic coefficient of variation, PCV=phenotypic coefficient of variation, h^2 =Heritability in broad sense and GA= genetic advance. DH=days heading, DM=Days to 95% maturity; PHt=Plant height; TKW=thousand kernel weight in grams; GYL=grain yield in kg per ha.

DISCUSSION

The study results clearly showed that the presence of considerable variations among genotypes for many of the traits measured. This indicated the presence of appreciable variations among genotypes for most of the characters. Significant effects for plant height, thousand kernel weight, and grain yield were observed, and this indicates the existence of sufficient phenotypic expressions and variations in quantitative characters. Data related to the mean performance of the quantitative traits are presented in Tables 4. It is assumed that the shorter the number of days taken to produce initial heading, the earlier is the maturity and hence the earlier the variety. Ali and Khan (2003) have also reported similar findings as it is considered an important determinant of earliness.

Quantitative characters or agronomic traits are highly influenced by the environment. In this study, different traits showed different phenotypic and genotypic coefficients of variation. According to Deshmukh *et al.* (1986), PCV and GCV values greater than 20% are regarded as high, whereas values less than 10% are considered low and values between 10% and 20% to be medium. Based on this description, in the testing site, both high levels of GCV and PCV (PCV values >20%) were recorded for Days to heading, Days to 95% maturity, Plant height, Thousand Kernel Weight and Grain yield. Similar observations of high PCV and GCV of these traits were reported by Dheva and Potdukhe (2002) and Preetha and Raveendran (2007).

In this study, phenotypic coefficient of variation was generally higher than genotypic coefficient of variation values at both testing sites in all of the traits. The genotypic coefficient of variation provides a measure to compare the genetic variability present in various quantitative characters. The study on genotypic and phenotypic coefficient of variation indicated the presence of variance and role of the environment on the expression of these traits. The extent of the environmental influence on any trait has been determined by the magnitude of the differences between the genotypic and phenotypic coefficients of variation. Large differences reflect high environmental influence, while small differences reveal high genetic influence. GCV alone is not helpful for effective selection, but together with heritability estimates could determine the extent of selection response (Mahaingam *et al.*, 2013).

Heritability estimate for characters under study are indicated in (Table 5. Different characters have different levels of heritability that can contribute for yield improvement in breeding programs. Johnson et al. (1955), classified heritability estimates as low (<30%), moderate (30 - 60%) and high (>60%). Based on this classification, it was observed that high heritability in thousand kernel weight and grain yield per hectare (99%) followed by days to 95% maturity (81%) and plant height (94%). This result indicates that environment has low influence for the expression of the characters which suggests direct selection using these characters as major contributors of yield components to improve yield of the study area. Days to heading (54%), showed moderate level of heritability this may be occurred due to influence of the environment on the polygenic nature of these characters. Low heritability was not found among the studied characters this indicates the possibility of including all the characters in order to select desirable genotypes. Berhanu, (2004); Birhanu (2010) and Degewione *et al.* (2013) were also reported high level of heritability for days to maturity, plant height, and grain yield/ plot and moderate heritability estimates for days to heading.

Conclusion and Recommendation

Jajura district in Hadiya Zone of SNNP region is one of the areas where improved varieties are not widely distributed so far. Particularly, the potential of the area to wheat crop is not exploited due to lack of improved varieties, poor management practices, biotic factors (weeds, diseases and insect pests etc.) and abiotic factors (frost), rain fall variability (intensity as well as duration). The current study was conducted to estimate the performance yield evaluation of released bread wheat varieties and also to study phenotypic variability, heritability and genetic advance under selection among growth characters, yield and yield components in 12 bread wheat varieties. Data recorded for 9 characters were subjected to analysis of variance and the results showed the presence of significant differences ($P < 0.01/0.05$) among the tested varieties for all characters indicating the presence of appreciable level of variability among the tested 12 bread wheat varieties.

The present study showed the presence of considerable variability among the tested bread wheat varieties and also showed the potential of the district for bread wheat production in advance for farmers in order to keep food security and sustainable agriculture. The top five varieties that performed better than other tested varieties for grain yield were Boru, Liben, Jajabo, Ogolcho, and Alidor with grain yields per hectare of 7088.5, 6806.5, 6722.6, 6494.7 and 6308.3 Kg/ha respectively.

Conflict of interest

I like to confirm that this research paper was not done by another author before and there is no conflict interest on this paper in general

REFERENCE

- Acevedo, E., Silva, P. and Silva, H., 2002. In Curtis, B.C., 2002. Wheat in the world. Bread wheat production and improvement. FAO Plant Production and Protection Series No. 30.
- Allard, R.W. 1960. Principles of Plant Breeding. John Wiley and Sons. Inc. New York. p430.
- Burton, G. W. and Devane, E. H. 1953. Estimating heritability in tall Fescue (*Festuca arundinacea*) from replicated clonal materials. *Agronomy Journal*, 45: 487-488.
- Curtis, B.C., 2002. Wheat in the world. Bread wheat production and improvement. FAO Plant Production and Protection Series No. 30
- Dabholkar, A.R., 1992. Elements of biometrical genetics. Concept Publishing Company, New Delhi, India, p431.
- Deshmukh, S.N., M.S. Basu and P.S. Reddy, 1986. Genetic variability, character association and path coefficient analysis of quantitative traits in Virginia bunch varieties of groundnut. *Indian Journal of Agricultural Science*, 56:816-821.
- Dheva N.G. and Potdukhe N.R. 2002. Studies on variability and correlations in upland cotton for yield and its components. *J. Indian Soc. Cotton Improv.* p.148-152.
- Falconer, D.S., Trudy F.C. and Mackay. 1996. Introduction to Quantitative Genetics. 4th ed., Longman Group Limited, Malaysia, p464.
- Johnson, H. W., Robinson, H.F. and Cosmtock, R. G. 1955b. Genotypic and phenotypic correlation in soybean and their implication in selection. *Agronomy Journal*, 47: 477-483.
- Kamalhi, J.M. 2008. Review on wheat status in the past, present and future. Key papers for 10th conference on sciences of breeding in Iran. Pp 23-45.
- Khabiri E., Imani A.A., and Shahbazi H., 2012. Studying the grain yield and yield components in advanced rain fed wheat genotypes. *Scholars Research Library. Annals of Biological Research*, 3 (12):5647-5650.
- Mahalingam A., Saraswathi R., Ramalingam J. and Jayaraj T. 2013. Genetics of floral traits in cytoplasmic male sterile (CMS) and restorer lines of hybrid rice (*Oryza sativa* L.). *Pak. J. Bot.* 45 (6):1897-1904.
- MoA (Ministry of Agriculture), 2011. Animal and plant Health Regulatory Directorate. Crop variety Register Issue No.14. Addis Ababa, Ethiopia.
- Reeves, T.G., S. Rajaram, M. van Ginkel, R. Trethowan, H.J. Braun and K. Cassaday, 1999. *New Wheat's for a Secure, Sustainable Future*. Mexico, D.F. CIMMYT
- Robertson, G.E., 1959. The sampling variance of the genetic correlation coefficient. *Biometrics*. 15: 469-485.
- SAS (Statistical Analysis system) software, 2002. Version 9.0. Inc., Cary, North Carolina, USA.
- Sharma, J. R. 1998. Statistical and biometrical techniques in plant breeding. New Age International (P) limited, publishers. New Delhi. P432.
- Shewry, P.R., 2009. Review Paper on wheat. *Journal of Experimental Botany*, 60(6): 1537–1553 doi:10.1093/jxb/erp058
- Singh, R.K. and Chaudhary. 1977. Biometrical methods in quantitative genetic analysis. Kalyani publishers, New Delhi-Ludhiana, India.