International Journal of Bio-resource and Stress Management 2018, 9(6):754-761

Research Article

Doi: HTTPS://DOI.ORG/10.23910/IJBSM/2018.9.6.1926a

Stress Management

Bread Wheat Germplasm Evaluation for Soil Moisture Stress Tolerance under Rainfed Condition

Arvind Kumar[1*], P. C. Sharma[1], R. Singh[1] and J. Kumari[2]

[1]ICAR-Central Soil Salinity Research Institute, Karnal, Haryana (132 001), India
[2]ICAR-National Bureau of Plant Genetic Resources, Pusa Campus, New Delhi (110 012), India

Corresponding Author

Arvind Kumar
e-mail: arvind.kumar2@icar.gov.in

Article History

Article ID: AR1926a
Received in 01st November, 2018
Received in revised form 19th December, 2018
Accepted in final form 31st December, 2018

Abstract

A preliminary yield trial was conducted with 1358 bread wheat germplasm including four national checks (C-306, KRL 210, HD 2967 and Kharchia, 65) for identifying moisture stress tolerant genotypes. The experiment was conducted at experimental farm, Central Soil Salinity Research Institute, Karnal under rainfed conditions during 2015-16 cropping season. The new germplasm were compared against four standard varieties using an augmented design with fifteen blocks. Evaluation of germplasm accessions revealed considerable variation among grain yield (g)$^{-m}$, effective tillers per meter and days to 50% heading traits studied. The adjusted grain yield of sixty two germplasm (38 accessions of NBPGR and 24 salt tolerant lines of CSSRI) were out yield the best check (C-306). However seventeen genotypes, namely, EC463441, EC534443, EC609338, IC543290, IC321905, IC535493, IC547643, KRS-611, KRL-112, KRL-105, KRL-136, KRL-119, KRS-621, KRL2-10, KRL-340, KRL-90 and KRL-35 were found most desirable for yield potential. These germplasm can be considered as an important source of genes for earliness, higher grain yield and for improving number of effective tillers in wheat improvement programme for drought tolerance. Non-significant differences for grain yield between the salt tolerant (KRL 210 and Kharchia 65) and drought tolerant (C-306) checks shows co-existence of salt and water stress tolerance in KRL 210 and Kharchia 65, although both the cultivars were developed for salt prone area, it is, as such, they are likely fit for cultivation under conditions with low soil moisture.

Keywords: Wheat, soil moisture stress and germplasm

1. Introduction

Wheat is the most widely grown cereal crop, as it is a staple food for about 40% of the world population (Malik et al., 2015). It is exposed to numerous edaphic stressors i. e. biotic and abiotic (Water scarcity, high temperature, problematic soils and freezing etc.) during the cropping season. Although, among all abiotic stresses, moisture stress is the single most important stress leading to maximum reduction in crop productivity (Kang et al., 2009). Irregular and unpredictable rainfall caused by climate change is likely to further aggravate water stress leading to a decline in productivity of all cereals including wheat in many areas around the world (Collins et al., 2008, Reynolds and Ortiz, 2010). In most of the irrigated regions of the India, receding water tables (Rodell et al., 2009), non-availability of irrigation water, irregular and unpredictable rainfall leads also soil moisture stress from mild to severity (drought) and ultimately affect the productivity of the wheat crop. The North-Western plains (wheat bowl of India) are too seriously challenged by the twin threat of heat and drought. On the other hand nearly 2.5 mha area of wheat in central India is grown under residual moisture regimes and suffers from stress of drought, heat and salinity (Anonymous, 2015). Approximately 20% of the area of wheat under cultivation is under rainfed environment (Reynolds et al., 1999). Even under irrigated conditions, 66% area of wheat receives only 1-2 irrigations (Joshi et al., 2007) subjecting to the crop to moisture stress and resulting in reduced grain yield. Further depletion of underground water and limited rainfall exacerbate the scarcity of water due to climate change in near future has been predicted. Severe soil moisture stress during anthesis could decrease the grain yield of wheat crop up to 50% by reducing the number of grains (Joshi et al., 2007). Soil moisture stress is managed by drought avoidance or dehydration tolerance (Kramer and Boyer, 1995). Drought avoidance includes root depth of the plant, maximum use of available water by plant, however dehydration tolerance include the capability of the plant to partially dehydrate and grow again when moisture received through rainfall. In the rain-fed environments of developing countries, national average yields of wheat differ from 0.8 to 1.5 t ha^{-1} (Morris et al., 1991). The reaction of plants to water stress is important from two stand-points, survival and productivity. While survival is important for native vegetation, productivity or grain yield is the major concern for most crop plants (Begg, 1980). Thus, tolerance to a moderate water stress is of significance to crop plants, whereas plants which can survive a severe water stress would be expected to have low productivity (Kramer, 1980). Consequently, breeding for enhanced moisture stress tolerance is essential for achieving greater food security for the hundreds of millions of rural poor (Ortiz et al., 2008). Intended for a successful breeding program, the presence of broader genetic variability plays a vital role. Development of higher-yielding wheat cultivars for water-limited environments is the most viable solution to stabilizing and increasing wheat production under current climatic conditions. The development of high yielding and stable varieties requires a continuous supply of new germplasm as a source of desirable genes and/or gene combinations (Ayana and Bekele 1998). The genetic potential for high productivity is already present in crops, but productivity is limited due to stressors, therefore selections should be made under conditions more likely to be encountered in the field rather than under ideal conditions (Boyer, 1982). More diverse parents create the greater chance of exploiting productive recombinants and broad variability in segregating generations during genetic improvement of crop plants (Mohammadi and Prasanna, 2003). Hence precise information on the nature and degree of genetic variability and divergence among the germplasm is a pre requisite for crop improvement programs as it would help in the development of superior recombinants adaptable for different abiotic stresses (Rauf et al., 2012). Although grain yield is a complex trait dependent on several contributing factors which are in turn highly susceptible to environment. Presently, in India the progress for breeding drought tolerant varieties has been rather slow. The wheat variety C 306 released in the year 1969 is still considered the most droughts tolerant under soil moisture deficit condition and is used as a standard check throughout the country (Joshi et al., 2007a). The first approach to assist breeders in their efforts is screening of the germplasm for the identification of good donor for yield potential. Germplasm either for potential varieties or for useful parents must be based on multiple breeding traits (Yan and Fregeau-Reid, 2008). Therefore genetic variability in the germplasm for yield potential under soil moisture stress was investigated in order to breed superior moisture stress tolerant genotypes. The main objectives of this study were to (i) examine the variation in yield potential within the bread wheat germplasm using the univariate technique and (ii) compare the germplasm with the currently grown bread wheat cultivar and national checks.

2. Materials and Methods

In this study a set of 1354 bread wheat germplasm including 1213 germplasm (780 indigenous collections and 433 exotic collections) received from National Bureau Plant Genetic Resources (NBPGR), New Delhi and 141 salt tolerant germplasm from Central Soil Salinity Research Institute (CSSRI), Karnal along with four national checks were evaluated under rainfed condition at experimental farm, CSSRI, Karnal during October to April in 2015-2016 cropping season. The farm is situated at 29°43' N latitude and 70°58' E longitude and 245 m altitude. The site is representative of the areas with semi-arid to dry sub humid climate with hot summer and a cold winter, the cropping season characterized by minimum and maximum temperature of 4.6 and 36.4 °C respectively. The seasonal precipitation of 46.2 mm in 5 rainy days of the site is recorded. The soil at the site was reclaimed sodic (pH: 7.80-8.21) clay loam. The planting was carried out after applying a pre-planting soaking irrigation of approximately 50 mm. The plant materials (100 seeds per entry) were sown in 1 row of 2 meter length with 30 cm apart in a non- replicated trial. The experiment was laid out in augmented randomized complete block design (Federer and Raghavarao, 1975) with fourteen blocks with 94 accessions and 15th block with 38 accessions and four standard varieties (checks) were repeated in every block randomly. These standard varieties, namely, C-306, KRL 210, HD 2967 and Kharchia 65, represented selective tolerance to particular osmotic stresses, highly drought tolerant (C-306) to highly salt tolerant (Kharchia 65). However HD 2967 and KRL 210 were chosen because they were the pioneer varieties extensively grown by the farmers and commonly used as standard varieties in irrigated high fertility and salinity/alkalinity tolerance evaluation trials respectively. These four varieties were sown in each block, but each entry to be evaluated was sown only once in the experiment. The positions of the 94 varieties and entries in each block were fully randomized. Weeds were controlled manually. Fertilizer rates were 90kg N, 60 kg P and 40 kg K ha^{-1} were applied at the time of sowing. The crop was maintained completely under rain-fed conditions. The main traits, which are important for preliminary evaluation of germplasm under rainfed condition, were recorded for each entry. These traits include, days to heading (DH), number of effective tillers (NET) and grain yield (YLD). Days to heading was designated as the day until 50% of the plant in the plot had at least one open flower. Numbers of effective tillers were counted at the time of physiological maturity. The yield after harvesting was measured for each genotype at each plot.

2.1. *Statistical analysis*

Several simple univariate statistics including minimum, maximum, range, mean, standard deviation and coefficient of variation were used to describe the variability among the genotypes, which were calculated for each trait based on the genotypes (Prosperi et al., 2006, Morris, 2009). Combinations of mean and SD for each attributes was also used to identify superior genotypes. In this case five categories of genotypes for each studied trait can be formed. In the case of YLD and NET, the genotypes with values >(mean+SD) and>(mean+2SD) can be identified as desirable genotypes and those with values<(mean-SD) and (mean-2SD) can be identified as undesirable ones (Shakhatreh et al., 2010). In the case of DH the genotypes with values less than mean, (mean –SD) and (mean-2SD) will be more desirable. The genotypes with values between mean±SD were average in the performance.

Analysis of variance (ANOVA) was carried out based on augmented complete block design using Windostat (Indostat service Hyderabad, India) accounting for both inter- and intra- block differences. The following linear model was used: $y_{ij}=\mu+g_i+c_j+\beta_j+\varepsilon_{ij}$ Where: yij is the observation of treatment i in jth block, μ is the general mean g_i is the effect of test treatment, c_j is the effect of control treatments in jth block, β_j is the block effects and ε_{ij} is the residual error. The plot numbers were considered in the residual to account for any measurement errors. Means were adjusted for inter and intra block variations and were compared based on the standard errors of the differences between two means with controls and with new entries. Due to the imbalance created owing to the occurrence of new entries in a block, four different standard errors (Federer, 1956; Federer and Raghavarao, 1975) were computed as follows:

1. Between means of *two check varieties* (Ci – Cj): Sc=√2MSE/r
2. Between adjusted yields of two new selections in the same block (BiTi–BiTj): Sd=√2MSE
3. Between adjusted yields of two new selections in different blocks (BiTi–BjTj): S*v*=√2(C+1)MSE/c
4. Between adjusted yield of a new selection and a check mean (Ci – Ti:): S*vc*=√2(r+1) (c+1)MSE/rc

The phenotypic, genotypic and environmental variances were calculated according Weber and Stamp (1988).

From the genotypic, phenotypic, and environmental variances, different genetic parameters like (a) phenotypic coefficient of variation (PCV), (b) genotypic coefficient of variation (GCV), which has paramount importance in the selection process of breeding experiments were calculated according to (Singh and Chaudhury, 1985):

(a) Phenotypic coefficient of variation (PCV): $PCV=\sigma^2_P/\bar{x}$
(b) Genotypic coefficient of variation (GCV): $GCV=\sigma^2_g/\bar{x}$

GCV and PCV values were categorized as low (0-10%), moderate (10-20%) and high (20% and above) values as indicated by Burton and de vane (1953). Broad sense heritability (h^2 b) for all characters was estimated as the ratio of genotypic variance to the phenotypic variance and expressed in percentage according to the methods suggested by Falconer and Mackay (1996) h^2 b=σ2 g/σ^2p, where σ^2 g and σ^2p are the components of variance for the genotypic and genotypic effects respectively. Robinson et al. (1949) classified heritability values as high (>60%), moderate (30-60%) and low (0-30%). The difference between the mean of the selected individuals ($\bar{x}_s$) and the mean of the population from which the selection has been made ($\bar{x}_P$) i.e. genetic gain or advance is worked out as $GA=k.h^2_{b.}\sigma_P$ (Allard, (1960) where k is the standardized selection differential having constant values at 5% selection intensity (K=2.063) and $h^2_{b.}$ and σ_P are the heritability in broad sense and phenotypic standard deviation respectively. Genetic advance as % of mean was calculated to compare the extent of predicted advance of different traits under selection, using the $GAM=GA/\bar{\chi}\times100$ Where, GA, represent genetic advance under selection and $\bar{x}$, represent grand mean of the population. Genetic advance as % mean was categorized as low (0-10%), moderate (10-20%) and high (>20%) according to Falconer and Mackay (1996). To pick the winners national checks are included along with the new genotypes to provide a base against which yield superiority could be measured. Ultimate goal is to find new entries that are out yielder the checks. The breeder is normally not interested in entries those having the yield less than the checks, whether difference is significant or not. In the study we rejected $H_0=\mu_G=\mu_C$ in favor of $H_1:\mu_G>\mu_C$, where μ_G is the true mean of the new genotype/germplasm and μ_C is the true mean of the check. Statistic, least significant increase (LSI or one-sided least significant difference) was used against which we could compare yield increases for those entries that out yield the checks (Petersen, 1994). $LSI=SEd\times t_\alpha(\text{at error df})$ Where t, is the one-tailed t test at α probability level at error df. In practice, if a new germplasm mean, $\overline{Y_G}$, is greater than $\overline{Y_C}+LSI$ the increase yield of the germplasm over the check yield is said to be significant at the 100% level.

3. Results and Discussion

Univariate statistics of recorded data on 1358 genotypes (1354 germplasm, four checks) for three traits are summarized in Table 1. For each trait, the overall means, maximum, minimum, range, and SD are given. All the trait values were checked for the normality through Shapiro-Wilks test (Shapiro and Wilk, 1965). Test showed that all the recorded traits followed normal distribution. For days to heading (DH), the values ranged from 72-128 days with a mean value of 93. The DH values for the national checks ranged from 87 to 102 days. This data showed the existence of 190 genotypes heading, 7 days earlier than the national check (C 306) for rainfed condition. High variation was found among the genotypes for number of effective tillers (NET). The values recorded for the NET varied from 7 to 190 with a mean of 63 (Table 1) and highest value (190) recorded for the indigenous germplasm IC 534198. The grain yield (YLD) varied from 13 to 459 g m^{-1}

Table 1 : Univariate statistics and test of normality for days to heading, number of effective tillers^{-m} and grain yield (g)$^{-m}$ from germplasm and national checks evaluated under rainfed condition in 2015–16

Statistics	DH	NET	YLD
Mean	93	63	117
Min	72	7	13
Max	128	190	459
Range	56	183	446
SD	8.34	28.86	47.20
Test of Normality			
Shapiro-Wilk (w)	0.884	0.962	0.972
p Value	0.000	0.000	0.000

DH: days to heading, NET: Number of effective tillers, YLD: Grain yield with average mean of 117 g m^{-1}. Among the national checks, the YLD varied from 111 to 147 g m^{-1}, while 643 experimental entries had yield performance greater than the mean, showing the potential to select higher yielding genotypes from the germplasm. Number of effective tillers and yield showed symmetrical histogram about the mean, and about 95% of the population observations lie within 2 standard deviations of the mean in the large population. Therefore the superior genotypes can be identified for each trait based on integrating of mean values with SD. The groups which include genotypes with a trait value of (mean+SD) and (mean+2SD) will provide an indication of the superior genotypes and also indicate high probability of success in selection in the case of sufficient high heritability (Shakhatreh et al. 2010). The number and percentage of bread wheat genotypes which had a better performance than mean, (mean+SD) and (mean+2SD) based on each trait are presented in Table 2. The percentage of genotypes with values higher than the mean across all traits varied from 31% (for DH) to 47% (for YLD) (Table 2). Based on these three agronomic traits, in general, about 40% of the genotypes had a better performance than the overall mean.

Table 2: Grouping of bread wheat genotypes based on integrating mean values and SD for studied trait

Statistic Group	NET	DH	YLD
>Mean	570	421	643
>Mean+SD	191	207	174
>Mean+2SD	56	72	40
<Mean	765	839	696
<Mean-SD	190	96	219
<Mean-2SD	0	4	4
Percentage (%) of the genotypes in each group			
>Mean	42	31	47
>Mean+SD	14	15	13
>Mean+2SD	4	5	3
<Mean	56	62	51
<Mean-SD	14	7	16
<Mean-2SD	0	0.30	0.30

NET: Number of effective tillers; DH: days to heading; YLD: Grain Yield

In the case of days to heading, 62% of the genotypes had DH values less than the mean. In screening about 96 genotypes tend to headed and mature before other genotypes and this set of genotypes will be suitable for improving the ruling varieties based on earliness. However 13% of genotypes had YLD better than the (mean+SD), while 14% of the genotypes showed NET higher than the (mean+SD). In contrast, just 7 % of the genotypes had DH values less than the (mean-SD) (Table 3). The percentage of genotypes with values better than the (mean+2SD) for YLD, and NET were 3 and 4% respectively. However no genotype was found for the DH with values less than the (mean-2SD). Mean squares of the 3 characters from analysis of variance (ANOVA) are presented in Table 3. Significant differences were observed among germplasm for all three characters studied. This indicating the presence of variability, which can be exploited through selection for further breeding programs. Similarly, works of Kalimullah et al. (2012) reported that number of tillers per plant, grain yield per plant showed significant differences between forty one bread wheat genotypes were studied. Shashikala (2006) reported significant differences for days to heading, number of effective tillers^{-m} and grain yield (g)$^{-m}$. The PCV ranged from 40.64 for YLD to 45.94 for NET whereas 37% GCV estimated for YLD and NET. Phenotypic coefficients of variation were generally higher than genotypic coefficients of variation for all traits studied indicating the influence of environment. Burton and devane (1953) classified PCV and GCV values as high (>20%), medium (10-20%) and low (<10%). Accordingly, high PCV and GCV were observed in all the three (DH, NET and YLD) traits. The high PCV and GCV indicate that selection may be effective based on these traits. In support of this study Tarekegne et al. (1994) reported high PCV and GCV for grain yield in wheat. The bread wheat genotypes showed array of variations in grain yield. Broad sense heritability estimates ranged from 66.8% for NET to 99.9% for DH. The high heritability for all the three traits is encouraging from the breeding standpoint for high value of studied traits. Robinson et al. (1949) classified heritability values as high (>60%), moderate (30-60%) and values less than 10% low. Accordingly, high heritability was observed for all three characters of 1354 bread wheat germplasm. 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. This may be attributed due to uniform environmental conditions during the conduct of the experiment. The obtained results were in agreement with results of Rasal et al. (2008) which also noticed higher heritability values for DH, number of productive tillers and grain yield per plot. Genetic advance expressed as a percentage of the mean ranged from 63.23% for NET to 86.42% for DH. Falconer and Mackay (1996) classified genetic advance as % of mean as low (0-10%), medium (10-20%) and high (20% and above). Accordingly, genetic advance as percentage of mean was higher for all characters studied. The estimates of genetic advance help in understanding the type of gene action involved in the expression of various polygenic characters. High values of genetic advance are indicator of additive gene action whereas low values are indicator of non-additive gene action (Singh and Narayanan, 1993). Therefore, heritability and genetic advance are important selection parameters. The estimate of genetic advance is more useful as a selection tool when considered jointly with heritability estimates (Johnson et al., 1955). High heritability associated with high genetic advance was observed for all the three traits. The positive correlation ($r=0.55^{***}$) between YLD and NET

Table 3: Analysis of variance (Mean Squares), heritability, coefficient of variation, genetic advance and variances estimates for studied traits of bread wheat

Source of variation	DF	MS		
		DH	NET	YLD
Block (eliminating Check+tests.)	14	4.59^{*}	790.32^{**}	2439.94^{***}
Entries (ignoring Blocks)	1357	1577.46^{***}	850.78^{***}	2283.02^{***}
Checks	3	75.31^{***}	5540.11^{***}	4127.75^{***}
Germplasm	1353	1581.37^{***}	837.99^{***}	2264.74^{***}
Checks vs. Germplasm	1	791.09^{***}	4070.82^{***}	21478.06^{***}
Error	42	2.11	276.19	364.22
Residual CV (%)		1.543	26.476	16.373
Block CV (%)		0.587	11.564	10.942
Genotypic variance ($\sigma^2 g$)		1561.961	555.648	1879.693
Phenotypic variance ($\sigma^2 P$)		1564.070	831.843	2243.918
Environmental variance ($\sigma^2 e$)		2.109	276.195	364.225
Heritability ($h^2 b$)		99.90	66.80	83.80
Genetic advance		81.360	39.687	81.743
Genetic advance as % of mean		86.424	63.226	70.130
ECV %		1.543	26.476	16.373
GCV %		41.982	37.553	37.196
PCV %		42.010	45.948	40.640
µ (Varietal)		90.430	71.180	135.900
µ (Germplasm)		94.140	62.770	116.560
CD values		3.44	39.39	45.23

: Represents significance at (*p*=0.01) level; *: represents significance at the (*p*=0.001) level

would be useful if we are selecting for high levels of both traits. However, the strong negative correlation ($r=-0.23^{***}$) between yield and days to heading (DH) under rainfed conditions would be helpful when selecting for high yield and earliness.

LSD values were computed for testing intra and inter block variations. For this purpose we used two-sided t_α test (Table 4). For this trial, however, the most useful comparison would be between the adjusted yield of a new selection and a check mean. Therefore to find those new selections that out yield the checks, we compute the LSI for this purpose: LSI $=t_\alpha \times Svc$, For the 0.5% LSI we have the 0.5% one tailed t at 42 df t (α=0.005)=2.704 and LSI=(2.704) (22.04)=59.58 Then any adjusted selection yield greater than

1. 139.52+59.58=199.40 significantly out yields 'KRL 210'
2. 145.67+59.58=205.55 significantly out yields 'C 306'
3. 111.49+59.58=171.37 significantly out yields 'HD 2967'
4. 146.91+59.58=206.79 significantly out yields 'Kharchia 65'

Table 4: Standard errors and least significant differences

Comparisons	NET		DH		YLD	
	SEd	CD	SEd	CD	SEd	CD
Ci - Cj	6.07	12.25	0.53	1.07	6.97	14.06
BiTi-BiTj	23.50	47.43	2.05	4.14	26.99	54.47
BiTi-zBjTj	26.28	53.03	2.29	4.63	30.18	60.89
Ci-Ti	19.52	39.39	1.71	3.44	22.41	45.23

CD: CD at (*p*=0.05)

The adjusted and observed grain yield of 62 germplasm (38 germplasm from NBPGR and 24 salt tolerant germplasm from CSSRI) which was greater than observed grain yield of C-306 (drought tolerant check) is given in Table 5. Non-significant difference between the salt tolerant (KRL 210 and Kharchia 65) and drought tolerent (C-306) checks (Table 6) shows co-existence of salt and water stress tolerance in KRL 210 and Kharchia 65 although both the cultivars were developed for salt affected areas, it is, as such, they are likely fit for cultivation under conditions with low water potential, which in turn creates high osmotic pressure in the outer environment. The most desirable genotypes were identified for each trait based on integrating of mean-value with SD. The groups including genotypes with a trait value of (mean+2.576 SD) will give an indication of the superior donors (Table 7). In normally

Table 5: Observed and Adjusted yield $(g)^{-m}$ of significant out yielder germplasm of bread wheat in rain fed trial

Sl. No.	Accessions/ germplasm name	Observed	Adjusted	Sl. No.	Accessions/ germplasm name	Observed	Adjusted
1.	EC463441	258.60	319.00	33.	EC609570	176.20	209.35
2.	EC534443	296.40	295.30	34.	EC374949	148.40	208.80
3.	EC609338	212.60	273.00	35.	IC28658	148.20	208.60
4.	IC543290	269.80	267.15	36.	IC539184	192.80	208.50
5.	IC321905	206.60	267.00	37.	IC145237	175.00	208.15
6.	IC535493	188.80	249.20	38.	IC547655	146.60	207.00
7.	IC547643	183.40	243.80	1.	KRS-611	458.60	418.63
8.	IC333151	201.40	234.55	2.	KRL-112	325.60	307.87
9.	IC585637	218.00	233.70	3.	KRL-105	288.80	271.07
10.	IC416119	199.60	232.75	4.	KRL-136	282.20	264.47
11.	EC463433	171.40	231.80	5.	KRL-119	282.00	264.27
12.	EC575881	197.60	230.75	6.	KRS-621	299.60	259.63
13.	IC564126	169.60	230.00	7.	KRL2-10	245.80	254.00
14.	EC609557	169.00	229.40	8.	KRL-340	271.60	253.87
15.	IC252463	168.80	229.20	9.	KRL-90	268.60	250.87
16.	EC552088	166.20	226.60	10.	KRL-35	258.60	240.87
17.	IC539313	165.60	226.00	11.	KRL-302	252.80	235.07
18.	IC396619	189.60	222.75	12.	KRL-113	251.20	233.47
19.	EC574724	211.00	222.00	13.	KRL-339	249.20	231.47
20.	IC534046	160.00	220.40	14.	CSSRI-9001	271.40	231.43
21.	IC138600	187.00	220.15	15.	KR-2-22	217.40	225.60
22.	IC531505	157.60	218.00	16.	KRL-261	240.60	222.87
23.	IC542494	220.60	217.95	17.	CSSRI-9033	262.40	222.43
24.	IC531531	157.40	217.80	18.	KRL-99	238.00	220.27
25.	IC416168	200.00	215.70	19.	KNS-99	259.20	219.23
26.	IC547650	153.60	214.00	20.	KRL-301	236.20	218.47
27.	IC582727	153.40	213.80	21.	KRL-115	233.20	215.47
28.	IC539315	152.60	213.00	22.	KRL1-4	204.40	212.60
29.	IC296767	179.80	212.95	23.	KRL-123	227.00	209.27
30.	EC463415	151.40	211.80	24.	KRL-337	226.40	208.67
31.	IC252349	150.20	210.60				
32.	EC568041	176.40	209.55				

Table 6: Mean comparison of check cultivars

Standard checks	DH	NET	YLD
C-306	90	66	139.52
KRL 210	91	78	145.67
HD 2967	93	47	111.49
Kharchia 65	88	93	146.91
CD (*p*=0.05)	1	12	14.06

distributed population 99% of the individuals lies within 2.576 standard deviations of the population mean. With respect to early heading (mean-1.96SD) IC282300, IC539399, IC111959, IC111914, IC128388, IC398067, IC402048, IC543367, IC415861, IC524288, IC408334 and EC578119 accessions were most desirable. These germplasm can be considered as an important source of genes for earliness under rainfed conditions. Accessions IC534198, IC279060, IC564126, IC78926, IC279328, IC543290, IC542983,IC310071, IC430369,

Table 7: Promising wheat germplasm for various traits identified in the germplasm pool

Traits	Criteria*	Germplasm accessions
YLD	>Mean+2.576SD (>238 g)	EC463441, EC534443, EC609338, IC543290 IC321905, IC535493, IC547643 KRS-611, KRL-112, KRL-105, KRL-136, KRL-119, KRS-621, KRL2-10, KRL-340, KRL-90, KRL-35
NET	>Mean+2.576SD (>137)	IC534198, IC279060, IC564126, IC78926, IC279328, IC543290, IC542983,IC310071, ,IC430369, IC536339, IC533809, IC585637, IC138543, IC469480, IC393128 IC535350, IC542968, IC279030, IC543262 EC217847, EC575756, EC218116, EC575648, EC374915, EC534433, EC534528, EC557001, EC575737, EC575712, EC217899 KRL-136, KRL-112, KRL-2-22
DH	<Mean -1.96SD (<76 Days)	IC282300, IC539399, IC111959, IC111914, IC128388, IC398067, IC402048, IC543367, IC415861, IC524288, IC408334, EC578119

*In normal Distribution 95% of the population is within 1.96 standard deviations of the mean; * In normal Distribution 99% of the population is within 2.576 standard deviations of the mean

IC536339, IC533809, IC585637, IC138543, IC469480, IC393128 IC535350, IC542968, IC279030, IC543262 EC217847, EC575756, EC218116, EC575648, EC374915, EC534433, EC534528, EC557001, EC575737, EC575712, EC217899 KRL-136, KRL-112 and KRL-2-22 would be most desirable for number of the effective tillers which are positively correlated with grain yield under rainfed condition. With respect to high grain yield per plot EC463441, EC534443, EC609338, IC543290, IC321905, IC535493, IC547643 KRS-611, KRL-112, KRL-105, KRL-136, KRL-119, KRS-621, KRL2-10, KRL-340, KRL-90 and KRL-35 accessions were identified as most potential donors. Results showed high and significant variation among genotypes compared with local check for the traits examined. It is well documented that in a breeding program, the first priority trait is economic yield (García del Moral et al., 2003). Any cultivar with good agronomic traits will not be successful if it has low yield potential. The screening of germplasm helped in identifying promising genetic donors for different characters. This result is supported by Mittal and Brar 2008, Ali et al., 2010.

4. Conclusion

Screened out germplasm can be considered as an important source of genes for earliness, number of effective tillers and higher grain yield under rain fed situation, where terminal drought stress is common phenomenon. Identified out yielder accessions may be used for introgression of desirable genes in the background of elite varieties to enhance yield under moisture stress environments.

5. Acknowledgement

The authors are highly thankful to Director, Central Soil Salinity Research Institute and Head, Division of Crop Improvement for providing necessary facilities to carry out this work and Director, NBPGR for providing bread wheat germplasm. The financially support by the Indian Council of Agricultural Research, Government of India, New Delhi is gratefully acknowledged.

6. References

Ali, M.B., Ibrahim, A.M.H., Hays, D.B., Ristic, Z., Fu, J.M., 2010. Response to heat tolerance stress wild tetraploid wheat (T. *turgidum* L.). J. Crop Improv 24(3), 228–243.

Allard, R.W., 1960. Principles of Plant Breeding. John Wiley and Sons, New York.

Anonymous, 2015. Vision 2050 Indian Institute of Wheat and Barley Research, Karnal, India, 45.

Ayana, A., Bekele, E., 1998. Geographical patterns of morphological variation in sorghum (*Sorghum bicolor* L. *Moench*) germplasm from Ethiopia and Eritrea: qualitative characters. Hereditas 129, 195–205.

Begg, J.E., 1980. Morphological adaptation of leaves to water stress. In: Turner, N.C., Kramer, P.J., (eds) Adaptation of Plants to Water and High Temperature Stress. John Wiley and Sons, New York, 33–42.

Boyer, J.S., 1982. Plant productivity and environment. Science 18, 443–448.

Burton, G.W., DeVane, E.H., 1953. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal 45, 478–481.

Collins, N.C., Tardieu, F., Tuberosa , R., 2008. Quantitative trait loci and crop performance under abiotic stress: Where do we stand? Plant Physiol 147, 469–486.

Falconer, D.S., Mackay, T.F.C., 1996. Introduction to Quantitative Genetics. 4th Ed. Longman, Essex.

Federer, W.T., 1956. Augmented (or hoonuiaku) designs. Hawaii. Plant. Rec. 2, 191–208.

Federer, W.T., Raghavarao, D., 1975. Augmented designs. Biometrics 31, 29–35.

Garcia del Moral, L.F., Rharrabti, Y., Villegas, D., Royo, C., 2003. Evaluation of grain yield and its components in durum wheat under Mediterranean conditions: An ontogenic approach. Agronomy Journal 95, 266-274.

Johnson, H.W., Robinson, H.F., Comstock, R.E., 1955.

Estimation of genetic and environmental variability in soybeans. Agronomy Journal 47, 314–318.

Joshi, A.K., Mishra, B., Chatrath, R., Ortiz, F.G., Singh, R.P., 2007. Wheat improvement in India: present status: emerging challenges and future prospects. Euphytica 157, 431–446.

Joshi, A.K., Chand, R., Arun, B., Singh, R.P., Ortiz, R., 2007a. Breeding crops for reduced-tillage management in the intensive, rice-wheat systems of South Asia. Euphytica 153, 135–151.

Kalimullah, S.J., Irfaq, K. M., Rahman, H. U., 2012. Genetic variability, correlation, and diversity studies in bread wheat (*Triticum aestivum* L.) germplasm. The Journal of Animal and Plant Sciences 22(2), 330-333.

Kang, Y., Khan, S., Ma, X., 2009. Climate change impacts on crop yield, crop water productivity and food security—A review. Prog. Nat. Sci., 19, 1665–1674.

Kramer, P.J., 1980. Drought, stress and the origin of adaptations. In: Turner, N.C., Kramer P.J., (eds) Adaptation of Plants to Water and High Temperature Stress. John Wiley and Sons, New York, 7–20.

Kramer, P.J., Boyer. J. S., 1995. Water Relations of Plants and Soils. Academic Press, San Diego, California.

Malik, S., Rahman, M., Malik, T.A., 2015. Genetic mapping of potential QTLs associated with drought tolerance in wheat. The Journal of Animal & Plant Sciences 25(4), 1032–1040.

Mittal, V.P., Brar, K.S., 2008. Divergence analysis for some yield contributing characters in wheat (*Triticum aestivum* L.). Crop Improvement 35(1), 1–3.

Mohammadi, S. A. and Prasanna, B.M. 2003. Analysis of genetic diversity in crop plants: salient tools and considerations. *Crop Science* 43, 1235–1248.

Morris, J.B., 2009. Characterization of sesame (*Sesamum indicum* L.) germplasm regenerated in Georgia, USA. Genetic Resources and Crop Evolution 56, 925-936.

Morris, M. L., Belaid, A., Byerlee, D., 1991. Wheat and barley production in rainfed marginal environment of the developing world. In 1990–1991 CIMMYT World Wheat Factors and Trends (Mexico: CIMMYT), 1–28.

Ortiz, R., Braun, H.J., Crossa, J., Crouch, J., 2008. Wheat genetic resources enhancement by the International Maize and Wheat Improvement Center (CIMMYT). Genetic Resources and Crop Evolution 55, 1140–1195.

Petersen, R.G., 1994. Agricultural Field Experiments: Design and Analysis, Marcel Dekker, New York.

Peterson, D.M., Wesenberg,D.M., Burrup, D.E., Erickson, C.A., 2005. Relationships among agronomic traits and grain composition in oat genotypes grown in different environments. Crop Science 45, 1249–1255.

Prosperi, J.M., Jenczewski, E., Angevain, M., Ronfort, J., 2006. Morphologic and agronomic diversity of wild genetic resources of *Medicago sativa* L. collected in Spain. Genetic Resource Crop Evolution 53, 843–856.

Rasal, P.N., Bhoite, K.D., Godekar, D.A., 2008. Genetic variability heritability and genetic advance in durum wheat. Journal of Maharastra Agricultural University 33(1), 102–103.

Rauf, S., Tariq, S.A., Hassan, S.W., 2012. Estimation of pedigree based diversity in Pakistani wheat (*Triticum aestvium* L.) germplasm. Communications in Biometry and Crop Science 7 (1), 14–22.

Reynolds, M., Skovmand, B., Trethowan, R., Pfieffer, W., 1999. Evaluating a conceptual model for drought tolerance. In Molecular Approaches for Genetic Improvement of Cereals for Stable Production in Water-Limited Environments; Ribaut, J.M., Poland, D., (eds.).; CIMMYT: El Batan, Mexico, 49–53

Reynolds, M.P., Ortiz, R., 2010. Adapting crops to climate change: A summary. In Climate Change and Crop Production; Reynolds, M.P., (eds.); CABI Series in Climate Change: Cambrigde, MA, USA, Volume 1, 1–8.

Robinson, H.F., Comstock, R.E., Harvey, P.H., 1949. Estimates of heritability and the degree of dominance in corn. Agronomy Journal 41, 353–359.

Rodell, M., Velicogna, I., Famiglietti, J.S. 2009. Satellite-based estimates of groundwater depletion in India. Nature 460, 999–1002.

Shakhatreh, Y., Haddad, N., Alrababah, M., Grando, S., Ceccarelli, S., 2010. Phenotypic diversity in wild barley (*Hordeum vulgare* L. ssp. *spontaneum* (C. Koch) Thell.) accessions collected in Jordan. Genetic Resources and Crop Evolution 57, 131–146.

Shapiro, S.S., Wilk, M.B., 1965. An analysis of variance test for normality (complete samples). Biometrika 52(3–4), 591–611.

Shashikala, S.K., 2006. Analysis of genetic diversity in wheat. M.Sc. (Agri.) Thesis, University of Agricultural Sciences, Dharwad, India.

Singh, P., Narayanan S.S., 1993. Biometrical techniques in plant breeding. Kalayani Publisher, New Delhi, India

Singh, R.K., Chaudhary, B.D., 1985. Biometrical methods in quantitative genetic analysis. Kalyani Publisher, New Delhi, India.

Tarekegne, A., Tanner, D.G., Gebeyehua, G., 1994. Effect of genetic improvement of morpho-physiological character related to grain yield of bread wheat in Ethiopia. African Crop Science Journal 2(3), 247–255.

Weber, W.E., Stam, P., 1988. On the optimum grid size in field experiments without replication. Euphytica 39, 273–247.

Yan, W., Fregeau-Reid, J., 2008. Breeding line selection based on multiple traits. Crop Science 48, 417–423.