International Journal of Agriculture Innovations and Research
Volume 3, Issue 3, ISSN (Online) 2319-1473
Manuscript Processing Details (dd/mm/yyyy) :
Received : 05/12/2014 | Accepted on : 20/12/2014 | Published : 24/12/2014

Assessment of Genetic Variability of Bread Wheat (*Triticum aestivum* L.) Genotypes for Salinity using Salt Tolerance Indices

Sanjay Singh*, R. S. Sengar, S. K. Bhatnagar, Pooran Chand, M. K. Yadav and R. R. Singh
Sardar Vallabhbhai Patel University of Agriculture and Technology,
Meerut-250110, India
*Corresponding Author's Email: sanjaydbtster@gmail.com;
Mob. No.: +91-9456838576

Abstract **– In India about 6.73 million hectare land area is salt affected. Wheat is the second most important crop after rice in India and occupies approximately 28.5 million hectare area. In this investigation, we calculate several tolerance indices for salinity and its ability to understand which one or more predictor among studied indices based on correlation, principal component analysis and cluster analysis. Ten wheat genotypes were evaluated two successive growing seasons (2012-2014), with complete randomized design with three replications under both salinity stress and non-salinity to identify salt tolerant genotypes to the target environment. Multiple indices for salt tolerance were calculated based on the potential yield (Yp) under non-stress and yield (Ys) under stress conditions. The Ys and Yp showed highest significant and positive correlations with GMP, MP and STI among indices studied. Therefore, these indices were considered as a better predictor of Ys and Yp than TOL, SSI and YSI. Principal component (PCs) analysis classified the genotypes into two groups. The first two PCs with eigen values >1 contributed 99.73% of the variability amongst genotypes. PC1 accounted for about 4.85% of the variation in salt tolerance indices and PC2 for 4.12%. The first PC was related to Ys, Yp, MP, GMP, STI and YI whereas the second PC related to Yp, TOL and SSI. The cluster analysis sequestrated ten genotypes into three clusters based on Ward's method. According to results, salinity significantly reduced the yield of some genotypes while some were found to tolerant to stress indicating that sufficient genetic variability for salinity tolerance among the studied genotypes were present and the genotypes K72 and HUW570 can be recommended for cultivation in salt affected areas.**

Keywords **– Bread Wheat, Grain Yield, Salinity, Salt Tolerance Indices.**

I. Introduction

Among abiotic stress, salinity is one of the major factors reducing plant growth and productivity worldwide, and affects about 7% of world's total land area [1]. Percentage of cultivated land affected by salt is even greater, with 23% of the cultivated land being saline and 20% of the irrigated land suffering from secondary salinization. Furthermore, there is also a dangerous trend of a 10% per year increase in the saline area throughout the world [2]. In India about 6.73 million hectare ha land area is salt affected out of which 3.77 and 2.96 million hectare are afflicted by sodicity and salinity, respectively [3]. Wheat is the second most important crop after rice in India and occupies approximately 28.5 million hectare area. According to some estimates FAO ([4], [5] and [6] the global wheat production must increase by at least 1.6 per cent annually during 2010-2020 to meet a projected wheat demand of 760 million tons by 2020. In order to achieve this goal therefore, improving wheat productivity will be essential to meet the growing demand for food under shrinking cultivable land area. It is imperative in this context to look for tools not only to increase the crop productivity but also ensure protection against loss of potential productivity due to environmental vagaries [7]. Several selection criteria have been proposed for selecting genotypes based on their performance in stress and non-stress environments [8], [9] and [10]. Some researchers recommend selection under favourable environments, with a point of view that high yield potential is expected to sustain high yields under stress environments [11], [12] and [13]. Many scientists have chosen a compromise solution and believe in selection under both stress and non-stress conditions [8], [14], [10], [15], [16] and [17]. Stress susceptibility index (SSI) and showed that it is not independent of yield potential [8]. Tolerance index (TOL) based on the differences in yields measured under non-stress (Yp) and stress (Ys) conditions [9]. Mean productivity index (MP) as the average of Yp andYs but MP has an upward bias when there are larger differences between Yp and Ys [9]. The geometric mean productivity (GMP), which is less sensitive to extreme values, is a better indicator than MP for separating superior genotypes in both stress and non-stress environments [9]. Stress tolerance index (STI), which can be used to identify genotypes which produce high yields under both stress and non-stress conditions [10]. For selection based on a combination of indices, some researchers [18], [19] and [20] have used principal component analysis (PCA). PCA is one of the most successful techniques for reducing the multiple dimensions of the observed variables to a smaller intrinsic dimensionality of independent variables [21]. These tolerance indices have been widely used in different regions for the evaluation of wheat genotypes [16], [22], [23] and [24] for drought but very limited work has been reported to date for salinity tolerance. To improve wheat yield and its stability in stress environments, there is a need to identify selection indices able to distinguish high yielding wheat cultivars in these conditions. Thus, the aim of this study was to evaluate the effectiveness of several salinity tolerance indices for screening and identification of salt tolerance wheat genotypes.

International Journal of Agriculture Innovations and Research
Volume 3, Issue 3, ISSN (Online) 2319-1473

II. Materials and Methods

Pot experiment was laid out by planting ten bread wheat genotypes (Table I). The experiment was laid out at the experimental farm, Department of Agriculture Biotechnology, SVPUA&T: Meerut, during November, 2012-13 and 2013-14 and the experimental soil was sandy loam with initial pH 7.2 and ECe 1.13 dS m^{-1}.

Table I: The details of Indian wheat cultivars used in the present investigation.

S. No.	Genotypes	Parentages	Developed by	Year
1	HUW 510	HD 2278/HUW 234//DL230-16	VARANASI	2001
2	K 9533	HI 1077 / HUW 234	KANPUR	2002
3	VL 404	KT/BAGE//FN/GU/3/ST 464/P174106	ALMORA	1978
4	K 710	PBW343/K 9162	KANPUR	1985
5	VL 719	VEE # 5"S"	ALMORA	1994
6	UP 2425	HD 2320/UP 2263	PANTNAGAR	1999
7	NW 1076	OPATA/KILL	FIAZABAD	2004
8	HUW 318	HUW 206/HUW 202	VARANASI	1991
9	HUW 213	NORTENO/MOTI//HD2160	VARANASI	1983
10	K 72	PV 18/K68	KANPUR	1983

To create the irrigation water of desired salinity level (EC_{iw}=10.0 dS m^{-1}), required quantity of NaCl, Na_2SO_4 and $CaCl_2$ (7:1:2) were thoroughly mixed with irrigating water to the pots. The pot experiment was performed in complete randomized design (CRD) with three replications. Two level of soil salinity i.e, control (normal irrigation water) and saline (saline irrigation after sowing) condition. Salt tolerance indices for each genotype were calculated using the following formulas:

Yield stability index (YSI) = Ys/Yp [25].

Yield index (YI) =Ys/$\bar{Y}$s [26].

Stress tolerance index (STI) = Yp x Ys/$\bar{Y}p^2$ [10].

Geometric mean productivity (GMP) = $\sqrt{Yp\ x\ Ys}$ [10].

Stress susceptibility index (SSI) = (1-Ys/Yp)/SI; SI=1-$\bar{Y}$s/$\bar{Y}$p [8].

Mean productivity (MP) = $\frac{Yp+Ys}{2}$ [9].

Tolerance index (TOL) = Yp –Ys [9].

Where Ys and Yp are the yields of genotypes evaluated under saline (stress) and non-saline (non-stress) conditions and $\bar{Y}$s and $\bar{Y}$p are the mean yields over all genotypes evaluated under stress and non-stress conditions.The combined data of grain yield under both stress and non-stress condition were subjected to analysis to estimate the simple statistic i.e., mean, standard error and simple correlation. Salt tolerance indices were analyzed by cluster and principal component analysis with the help of Software program 'SPSS' v 16.0 for windows. Cluster analysis identifies variable which are further clustered into main group and subgroups using Ward's method. The genotypes in each cluster were also analyzed for basic statistics. This was done to interpret relationships among selection criteria, to compare genotypes on the basis of salt tolerance indices and to identify genotypes or groups of genotypes with a certain level of salt tolerance. All the statistical analysis was performed using SPSS v 16.0 software programme [27].

III. Result and Discussion

The genotypes K72, HUW570, NW1076, HUW318 and VL404 had the best performance for grain yield in salt stressed conditions, while the genotypes HUW213, VL404, HUW318, HUW570 and K72 had the best performance under non-stressed conditions (Table II). The genotypes also exhibited highly significant differences for all the salt tolerance indices (Table III).

Table II: The mean of pooled data (2012-14) of yield and their corresponding tolerance indices.

Genotypes	Ys	Yp	TOL	MP	GMP	SSI	STI	YSI	YI
HUW 570	4.95(2)	11.65(4)	6.70(4)	14.13(3)	7.59(2)	1.01(5)	0.60(2)	0.42(7)	1.18(2)
K 9533	3.00(10)	6.74(10)	3.75(9)	8.25(10)	4.50(10)	0.97(6)	0.21(10)	0.44(5)	0.71(10)
VL 404	4.12(5)	12.20(2)	8.10(2)	14.25(2)	7.07(4)	1.16(2)	0.52(4)	0.34(9)	0.97(4)
K 710	3.65(8)	6.75(9)	3.10(10)	8.58(9)	4.96(9)	0.80(8)	0.26(9)	0.54(3)	0.87(8)
VL 719	3.85(7)	9.05(6)	5.20(5)	10.98(7)	5.90(7)	1.02(4)	0.36(7)	0.43(6)	0.91(7)
UP 2425	3.60(9)	7.85(8)	4.25(7)	9.65(8)	5.32(8)	0.95(7)	0.29(8)	0.46(4)	0.86(9)
NW 1076	4.90(3)	8.95(7)	4.05(8)	11.40(6)	6.62(6)	0.79(9)	0.46(6)	0.55(2)	1.16(3)
HUW 318	4.13(4)	11.90(3)	7.80(3)	13.95(4)	6.98(5)	1.15(3)	0.51(5)	0.35(8)	0.96(5)
HUW 213	4.10(6)	12.60(1)	8.50(1)	14.65(1)	7.19(3)	1.18(1)	0.54(3)	0.33(10)	0.95(6)
K 72	5.85(1)	10.40(5)	4.55(6)	13.33(5)	7.80(1)	0.77(10)	0.63(1)	0.56(1)	1.39(1)

The numbers in the parentheses are the ranks of the genotype for each index.

Ys – grain yield under stressed environment, Yp – Grain yield under non-stressed environment, SI – stress intensity, MP – mean productivity, GMP – geometric mean productivity, STI – stress tolerance index, SSI – stress susceptibility index, TOL – tolerance index, YSI – yield stability index, YI –yield index.

The two-year mean values of screening methods for characterizing salt tolerance and adaptation of genotypes to different environments are presented in Table II. The highest TOL value was calculated for HUW213 followed by VL404 and HUW318, indicating that these genotypes had a greater grain yield (GY) reduction under salt stress condition and higher salt sensitivity, whereas the lowest TOL value was found in K710, followed by K9533 and NW1076 indicating these genotypes had a lower GY reduction in stress condition. According to SSI, the genotype HUW213 followed by VL404 and HUW318 had the highest values while genotype K72 followed by NW1076 and K710 had the lowest values and were considered as genotypes with high salt susceptibility and poor yield stability in both stress and non-stress conditions. Based on ranking of MP, STI and GMP indices, genotypes HUW213, K72, VL404 and HUW570 had the highest values, whereas the genotypes remained had the lower values. Similar ranks of the genotypes for MP and GMP parameters as well as STI suggest that these three indices are comparable for selecting genotypes. The highest YSI was obtained by genotype K72 followed by NW1076 and K710 whereas the lowest YSI was obtained for genotype HUW213 followed by VL404 and HUW318. The genotype K72 followed by HUW510 and NW1076 had the highest YI and the genotype K9533 followed by UP2425 and K710 had the lowest YI value. The yield under salt-stressed conditions (Ys) had a very weak association with the yield under non-stressed conditions (Yp) indicating that high potential yield under optimal conditions does not necessarily result in improved yield in a salinity-prone environment. For example, the genotypes HUW213 VL404 and HUW318 produced the highest yield under non-stressed conditions but failed to produce high yields in the stressed environment. Therefore, indirect selection for such conditions based on the results of optimum conditions will not be efficient. These results are supported by [28], [29] and [24] who found a positive but non-significant association between yield in stress and non-stress environments. The results showed that the greater the TOL and SSI values, the higher the yield production under non-stressed conditions and conversely, there was a trend for smaller TOL and SSI values to be associated with larger yield production under stressed conditions (Table II). These relationships are obvious in Table III, in that Yp significantly and positively correlated with TOL and SSI, but Ys correlated negatively and non-significantly with SSI while positively and non-significantly with TOL. These results suggest that selection based only on low values of TOL and SSI will result in reduced yield under non-stressed conditions. Similar results were reported by [14], [30], [31] and [29].

Table III: Relationships among traits studied in this investigation.

Tolerance Indices	Ys	Yp	TOL	MP	GMP	SSI	STI	YSI
Yp	0.472^{ns}							
TOL	0.122^{ns}	0.932^{**}						
MP	0.597^{ns}	0.989^{**}	0.869^{**}					
GMP	0.831^{**}	0.883^{**}	0.653^{*}	0.942^{**}				
SSI	-0.344^{ns}	0.655^{*}	0.878^{**}	0.539^{ns}	0.232^{ns}			
STI	0.839^{**}	0.872^{**}	0.638^{*}	0.934^{**}	0.998^{**}	0.214^{ns}		
YSI	0.351^{ns}	-0.649^{*}	-0.874^{**}	-0.532^{ns}	-0.224^{ns}	-0.999^{**}	-0.208^{ns}	
YI	1.000^{**}	0.465^{ns}	0.114^{ns}	0.590^{ns}	0.827^{**}	-0.351^{ns}	0.835^{**}	0.358^{ns}

ns, * and ** non-significant and significant at the 5% and 1% levels of probability, respectively.
Ys – grain yield under stressed environment, Yp – Grain yield under non-stressed environment, SI – stress intensity, MP – mean productivity, GMP – geometric mean productivity, STI – stress tolerance index, SSI – stress susceptibility index, TOL – tolerance index, YSI – yield stability index, YI –yield index.

Grain yield under stressed conditions (Ys) and non-stressed conditions (Yp) were significantly and positively correlated with MP, GMP and STI which indicated that they were better predictors of Ys and Yp than TOL and SSI. The indices, MP, GMP and STI were able to identify high yielding wheat genotypes in both stressed and non-stressed conditions and these findings are consistent with the findings of [10], [18], [16] and [17]. These three indices were correlated with yield under both environments (Table III).The YI and YSI were significantly and positively correlated with Ys, and negatively correlated with SSI (Table III), indicating that these two indices are useful to discriminate salt tolerant and yield stable genotypes. YSI to be a more useful index to discriminate tolerant from susceptible genotypes due to its negative correlation with TOL and SSI [16]. SSI as stability parameter to identify drought-resistant genotypes of wheat [32]. In this study, genotype K72 followed by NW1076, K710 and UP2425 had the lowest SSI values and therefore, these genotypes have low salt susceptibility and high yield stability in both conditions, whereas the genotype HUW213, followed by VL404, HUW318 and VL719 had the highest SSI value can be considered as genotypes with high salt susceptibility and poor yield stability in both stress and non-stress conditions. Similar results were reported in durum wheat by [18], [31] and [17] for drought tolerance evaluation.

International Journal of Agriculture Innovations and Research
Volume 3, Issue 3, ISSN (Online) 2319-1473

Table IV: Principal component analysis for Ys, Yp and their corresponding tolerance indices

Traits	Component1	Component2
Ys	0.971	-0.237
Yp	0.670	0.741
TOL	0.356	0.932
MP	0.771	0.636
GMP	0.939	0.342
SSI	-0.115	0.991
STI	0.944	0.325
YSI	0.123	-0.990
YI	0.969	-0.245
Eigenvalue	4.852	4.124
Percent of variation	53.915	45.817
Cumulative percentage	53.915	99.732

Germplasm improvement and genetic diversity is a key to reliable and sustainable production of the food crops. For effective evaluation and utilization of germplasm, measure of extent of available genetic diversity is of utmost importance [33]. The use of multivariate statistical algorithms is an important strategy for classification of germplasm and analysis of genetic relationships among breeding material [34]. In order to maintain, evaluate and utilize germplasm effectively, it is important to investigate the extent of genetic diversity available.

The cluster analysis sequestrates genotypes into clusters which exhibit high homogeneity within a cluster and high heterogeneity between clusters [35]. Cluster analysis (Ward's method) based on salt tolerance indices and grain yield under stressed and non-stressed conditions classified the genotypes into three groups (Fig. I). Within group genotypes show minimum variance and genetic distance, while between-group genotypes are dissimilar with maximum genetic distance (Table V). Members of each cluster are presented in Table V. Similar results were obtained by various researchers worldwide previously i.e., [36] used seven statistical procedures to study the relationship between wheat grain yield and its components. Seventy wheat genotypes were evaluated for variability parameter including cluster analysis for eight traits by [37]. Cluster analysis using Wards algorithm and squared Euclidean distances and assigned 94 bread wheat inbred lines into three groups [38].

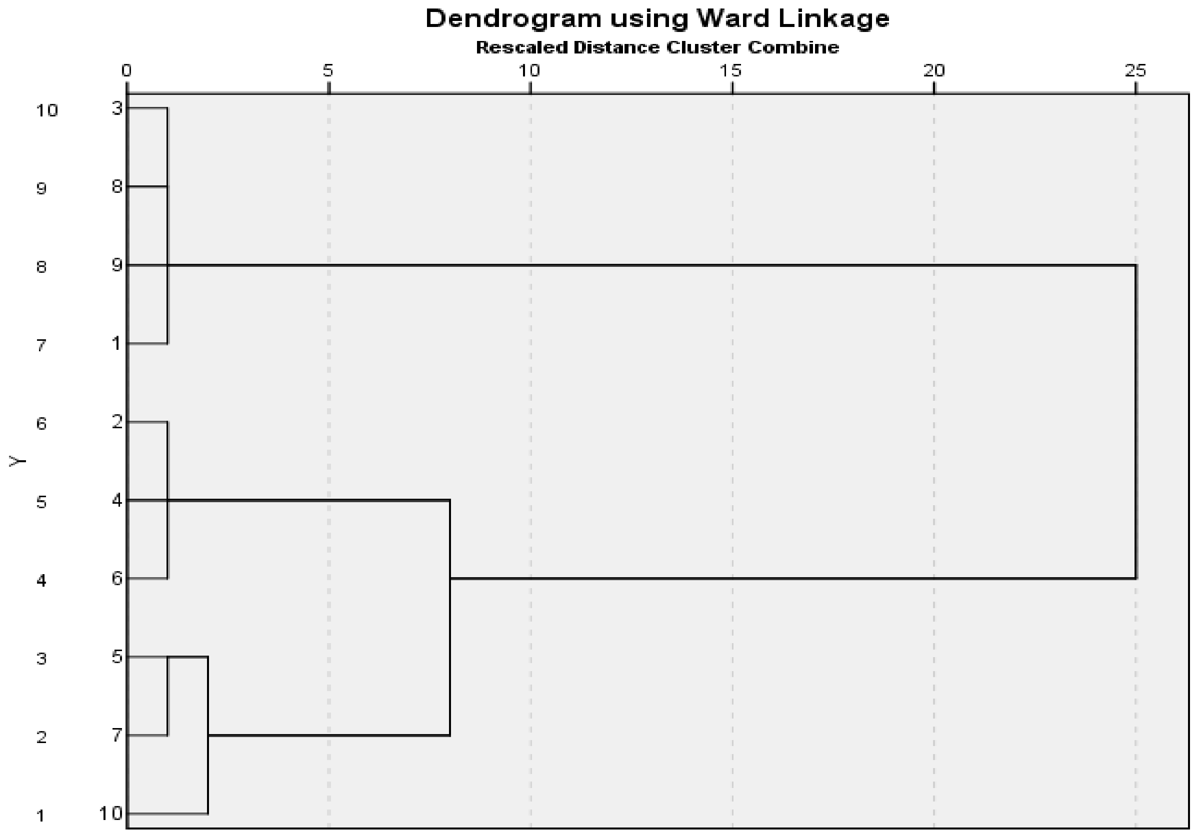

Fig.I. Dendrogram resulting from cluster analysis of bread wheat genotypes based on studied trait.

Table V: Grouping of genotypes based on nine studied characters.

Cluster	Frequency	Dendrogram representing no.	Cluster membership
I	4	1, 3, 8, 9	HUW510, VL404, HUW318, HUW213
II	3	2, 4, 6	K 9533, K710, UP2425
III	3	5, 7, 10	VL719, NW1076, K72

In addition to correlation analysis, principal component analysis based on salt tolerance indices was constructed to identify superior genotypes for both stressed and non-stressed environments. Principal component analysis simplifies the complex data by transforming the number of correlated variables into a smaller number of variables called principal components. The first principal component accounts for maximum variability in the data with respect to succeeding components [37]. The analysis had grouped the estimated wheat variables into two main components. The first two components with eigen values >1 accounted for 99.73% of the total variation of grain yield. PC1 accounted for about 4.85% of the variation in salt tolerance indices and PC2 for 4.12% (Table IV). The first PC was related to Ys, Yp, MP, GMP, STI and YI whereas the second PC related to Yp, TOL, MP and SSI (Table IV). The first PC was negatively related to SSI while PCII was negatively related to Ys, YSI and YI. MP, GMP, STI, TOL and SSI were strongly correlated with yield under normal irrigation and have significantly negative correlations with YSI indicating that these indices are able to select salt susceptible genotypes which only perform well under non-stressed conditions and have poor yield stability. Ys has a significantly positive correlation with GMP and STI while positive and non significantly with YSI and MP, and a significantly negative correlation with SSI, indicating that these indices are also able to select salt tolerant genotypes which performed well under stressed conditions and have low to moderate yield stability. Our results agreement with [39] who evaluated 113 accessions of barley by using cluster and principal component analysis.

IV. Conclusion

According to our results, salinity significantly reduced the yield of some genotypes while some were tolerant to stress indicating that sufficient genetic variability for salinity tolerance among the studied genotypes was present. Based on correlation and principal component analysis concluded that GMP and STI were the best indicators of yield under both stressed and non-stressed environments because these indices had positive and significant correlations with Ys and Yp. In conclusion, we can select suitable genotype and the genotypes K72 and HUW570 can be recommended for cultivation in salt affected areas.

Acknowledgement

The authors are gratefully acknowledged to Prof. H. S. Gaur, Vice Chancellor, Sardar Vallabhbhai Patel University of Agriculture & Technology (SVPUA&T), Meerut, for providing facilities to conduct research work (Ph.D) in the Department of Agriculture Biotechnology.

References

[1] T. J. Flowers, A. Garcia, M. Koyama and A. R. Yeo. Breeding for salt tolerance in crop plants, the role of molecular biology. *Acta Physiol. Plant.* 1997, 19(4): 427-433.

[2] P. N. Ponnamieruma. Role of cultivars tolerance in increasing rice production on saline land. In: Staples RC, Toenniessen GH (Eds.), Salinity tolerance in plants strategies for crop improvement. Wiley, New York, 1984, 255-71.

[3] A. K. Mondal, R. C. Sharma, G. Singh and J. C. Dagar. Computerised database on salt affected soils in India. *Tech. Bull.* 2010/2. CSSRI, Karnal.

[4] FAO. World Agriculture towards 2030/2050 Interim report Global Perspective Studies Unit, FAO, Rome. 2006.

[5] FAO. http://faostat.fao.org/faostat/ : accessed September, 2007.

[6] M. Rosegrant, M. Paisner, S. Meijer and J. Witcover. 2001. Global Food Projections to 2020.

[7] S. Kumar, R. Singh, M. Grover and A. K. Singh. Terminal heat-An emerging problem for wheat production. *Biotech Today.* 2012, 2(2): 7-9.

[8] R. A. Fischer and R. Maurer. Drought resistance in spring wheat cultivars. I. Grain yield response. *Aust. J Agric Res.*1978, 29: 897-907.

[9] A. A. Rosielle and J. Hamblin. Theoretical aspects of selection for yield in stress and non-stress environments. *Crop Sci.* 1981, 21: 943-946.

[10] G. C. J. Fernandez. Effective selection criteria for assessing stress tolerance. In: Kuo CG (ed) Proceedings of the International Symposium on Adaptation of Vegetables and Other Food Crops in Temperature and Water Stress, Publication, Tainan, Taiwan. 1992.

[11] R. A. Richards. Defining selection criteria to improve yield under drought. *Plant Growth Regul.* 1996, 20: 157-166.

[12] M. Van-Ginkel, D. S. Calhoun, G. Gebeyehu, A. Miranda, C. Tian-you, R. Pargas Lara, R. M. Trethowan, K. Sayre, L. Crossa and S. Rajaram. Plant traits related to yield of wheat in early, late, or continuous drought conditions. *Euphytica.* 1998, 100: 109-121.

[13] F. J. Betran, D. Beck, M. Banziger and G. O. Edmeades. Genetic analysis of inbred and hybrid grain yield under stress and non-stress environments in tropical maize. *Crop Sci.* 2003, 43: 807-817.

[14] J. M. Clarke, R. M. DePauw, and T. F. Townley-Smith. Evaluation of methods for quantification of drought tolerance in wheat. *Crop Sci.* 1992, 32: 728-7232.

[15] J. Mitra. Genetics and genetic improvement of drought resistance in crop plants. *Current Sci.* 2001, 80: 758-762.

[16] R. Mohammadi, M. Armion, D. Kahrizi and A. Amri. Efficiency of screening techniques for evaluating durum wheat genotypes under mild drought conditions. *Int. J. Plant Prod.* 2010, 4: 11-24.

[17] A. Nouri, A. Etminan, A. Jaime, T. D. Silva and R. Mohammadi. Assessment of yield, yield related traits and drought tolerance of durum wheat genotypes (*Triticum turjidum*var. *durum* Desf.) *Aust. J. Crop Sci.* 2011, 5: 8-16.

[18] M. Golabadi, A. Arzani and S. A. M. Maibody. Assessment of drought tolerance in segregating populations in durum wheat. *Afr. J. Agric. Res.* 2006, 5: 162-171.

[19] S. H. Azizi-Chakherchaman, H. Mostafaei, L. Imanparast and M. R. Eivazian. Evaluation of drought tolerance in lentil advanced genotypes in Ardabil region. *J Food Agric Environ.* 2009, 7: 283-288.

[20] M. M. Majidi, A. Mirlohi and F. Amini. Genetic variation, heritability and correlations of agro-morphological traits in tall fescue (*Festuca arundinacea* Schreb). *Euphytica* 2009, 167: 323-331.

[21] R. A. Johnson and D. W. Wichern. Applied Multivariate Statistical Analysis (6thEd.). Prentice-Hall International, Englewood Cliffs, NJ, USA. 2007.

[22] M. Mohammadi, R. Karimzadeh and M. Abdipour. Evaluation of drought tolerance in bread wheat genotypes under dryland and supplemental irrigation conditions. *Aust. J. Crop Sci.* 2011, 5: 487-493.

[23] A. Z. Khakwani, M. D. Dennett and M. Munir. Drought tolerance screening of wheat varieties by inducing water stress conditions. *Songklanakarin J. Sci. & Technol.* 2011, 33: 135-142.

[24] J. Anwar, G. M. Subhani M. Hussain, J. Ahmad, M. Hussain and M. Munir. Drought tolerance indices and their correlation with yield in exotic wheat genotypes. *Pak. J. Bot.* 2011, 43: 1527-1530.

[25] M. Bouslama, and W. T. Schapaugh. Stress tolerance in soybean. Part. 1: Evaluation of three screening techniques for heat and drought tolerance. *Crop Sci.* 1984, 24: 933-937.

[26] P. Gavuzzi, F. Rizza, M. Palumbo, R. G. Campaline, G. L. Ricciardi and B. Borghi. Evaluation of field and laboratory predictors of drought and heat tolerance in winter cereals. *Canadian J. Plant Sci.* 1997, 77: 523-531.

[27] SPSS Inc, 2007. SPSS for windows. Release 16.0.SPSS Inc. Chicago, IL. USA. (2006).

[28] A. Gholipouri, M. Sedghi, R. S. Sharifi and N. M. Nazari. Evaluation of drought tolerance indices and their relationship with grain yield in wheat cultivars. *Recent Res Sci. & Technol.* 2009, 1: 195-198.

[29] R. Karimizadeh, M. Mohammadi, S. Ghaffaripour, F. Karimpour and M. K. Shefazadeh. Evaluation of physiological screening techniques for drought-resistant breeding of durum wheat genotypes in Iran. *Afr. J. Biotech.*2011, 10: 12107-12117.

[30] A. Sio-Se Mardeh, A. Ahmadi, K. Poustini and V. Mohammadi. Evaluation of drought resistance indices under various environmental conditions. *Field Crop Res.* 98: 222-229.

[31] R. Talebi, F. Fayaz and N. Naji. Effective selection criteria for assessing drought stress tolerance in durum wheat (*Triticum durum* Desf.). *Gen. Appl. Plant Physiol.* 2009. 35: 64-74.

[32] K. C. Bansal, S. K. Sinha. Assessment of drought resistance in 20 accessions of *Triticum aestivum* and related species total dry matter and grain yield stability. *Euphytica.* 1991, 56: 7-14.

[33] M. Zubair, S. U. Ajmal, M. Anwar and M. Haqqani. Multivariate analysis for quantitative traits in mungbean [*Vigna radiate* (L.) Wilczek]. *Pak. J. Bot*. 2007, 39: 103-113.

[34] S. A. Mohammadi and B. M. Prasanna. Analysis of genetic diversity in crop plants- Salient statistical tools and considerations. *Crop Sci*. (2003), 43: 1234-1248.

[35] D. B. Jaynes, T. C. Kaspar, T. S. Colvin, and D. E. James. Cluster analysis of spatiotemporal corn yield pattern in an Iowa field. *Agron . J*. 2003, 95: 574-586.

[36] A. A. Leilah, and S. A. Al-Khateeb. Statistical analysis of wheat yield under drought conditions. *Elsevier*. (2005), 61: 483-496.

[37] Y. Ali, M. B. Atta, J. Akhter, P. Monneveux and Z. Lateef Genetic variability, association and diversity studies in wheat (*Triticum aestivum* L.) germplasm. *Pak. J. Bot.* 2008, 40: 2087-2097.

[38] S. Aharizad, M. Sabzi, S. A. Mohammadi and E. Khodadadi. Multivariate analysis of genetic diversity in wheat (*Titicum aestivum* L.) recombinant inbred lines using agronomic traits. *Annals Biol. Res.* 2012, 3(5): 2118-2126.

[39] Z. Ahmad, S. U. Ajmal, M. Munir, M. Zubair and M. S. Masood. Genetic diversity for morpho-genetic traits in barley germplasm. *Pak. J. Bot.* 2008, 40: 1217-1224.

AUTHOR'S PROFILE

Sanjay Singh
Ph.D. Student, Department of Agricultural Biotechnology,
Sardar Vallabhbhai Patel University of Agricultural & Technology,
(SVPUA&T), Modipuram, Meerut-250110, India
Email: sanjaydbtster@gmail.com