

Genetic characterization and its association with grain yield in wheat (*Triticum aestivum* L.) under drought stress

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Abstract

This study was designed to identify the drought tolerant and susceptible genotypes among 160 wheat genotypes. Analysis of variance under drought condition showed mean square due to genotypes had highly significant differences for all the quantitative traits in both years and pooled data, except flag leaf width, flag leaf area those were significant only and under control condition. Mean square due to genotypes had highly significant differences for all the traits in both the years and pooled data, except plant height in the pooled data that was significant only. On the basis of grain yield per plant under both the conditions twenty one tolerant genotypes namely; DBW 39, FLW 13, FLW 7, HD 2833, HD 3093, HI 1500, HI 617, HW 2004, HW 2005, HW 2066, HW 4002, HW 4008, HW 4029, HW 4215, Lok 1, Lok 65, MACS 2496, RAJ 4037, SOKOLL, SSRT 14, VJ 99 were selected and eleven susceptible genotypes using same criteria namely; DBW 14, DBW 28, DBW 88, HD 2824, HD 2877, NW 1014, PBW 343, PBW 373, RAJ 4083, UP 2828, MACS 6272 were identified. Identified tolerant and susceptible genotypes can be used for development of mapping populations to map the QTLs for drought tolerance in wheat (*Triticum aestivum* L.).

Keywords: Morphological traits, yield traits, drought stress, wheat (*Triticum aestivum* L.)

1. Introduction

Wheat (*Triticum aestivum* L.) is one of the most important food crops across the world. It is grown under wide range of environmental conditions in terms of water regimes, climates and soil types. At present, climate changes and increased variability in precipitation giving insistence to drought stress (Trenberth, 2011). Worldwide, 70% of the cultivated wheat area experience water stress and wheat is the second most crop grown under rainfed cropping areas after maize (Portmann *et al.*, 2010). Wheat cultivation in semiarid and arid regions is increasingly constrained due to drought stresses (Gregersen *et al.*, 2013). Therefore,

enhancement in drought tolerance as well as grain yield is very important in the selection of wheat cultivars for drought stress condition. Though significant achievements have been made by breeders for raising yield potential of spring wheat under such stressful environments, greater emphasis now lie on the innovative breeding methods and tools to develop genotypes that can perform better.

The adverse effects of drought occur at the morphological, physiological and biochemical levels and are evident at all phenological stages of plant growth, at whatever stage the water shortage takes place (Kadam *et al.*, 2012). Photosynthesis is one of the main metabolic processes that

are directly affected by drought. Responses to drought include a reduction in photosynthesis, decrease in leaf expansion, stomatal closure, impaired photosynthetic machinery, premature leaf senescence, decrease in assimilate translocation, and associated reduction in crop production. Furthermore, the stress imposed by drought conditions affects water relations, such as water use efficiency, relative water content, leaf water potential, stomatal resistance, canopy temperature and rate of transpiration (Farooq *et al.*, 2009b).

In wheat greater genetic variability can be explored with available germplasm from its centres of origin and diversity (Dvorak *et al.*, 2011). In addition to cultivated wheat varieties and breeding lines, extensive variability for drought tolerance remains within wild relatives and landraces. Manipulation of this diversity for development of drought tolerance among genotypes may be achieved through genetic modification and selection for adaptive mechanisms including drought escape, dehydration avoidance, and dehydration tolerance (Blum, 2011). Grain

yield and its related traits are two most important selection criteria under moisture deficit conditions. Drought stress reduces the grain yield and an average yield loss of 17% to 70% in grain yield has been estimated due to drought stress (Nouri-Ganbalani *et al.*, 2009). More number of traits identified as being responsible for drought tolerance are heritable, additive in nature, and display continuous variation; this is an indication that there is considerable room for improvement in drought tolerance (Tuberosa and Salvi, 2006).

2. Materials and methods

The experiment was conducted in the experimental area of Norman E. Borlaug Crop Research Centre, G. B. Pant University of Agriculture and Technology, Pantnagar (Uttarakhand) during 2014-15 and 2015-16 *Rabi* season. The Crop Research Centre is situated at 29°N latitude, 79°29' E longitude and at an altitude of 243.84 m above the mean sea level. The experiment was conducted in Alpha lattice design (Patterson and Williams, 1976). The randomization of 160 cultivars was done with Crop Stat

Table 1. Analysis of variance of genetic traits under drought condition in wheat genotypes during 2014-15

Sources of variation	DF	DH	DM	DA	GFD	TLR	FLL	FLW	FLA	PH	PL	PW	SL	SLS	GS	GW	TGW	GY
Replication	1	79.68**	28.19**	48.70**	2.78**	1.88**	292.49**	0.07**	735.46**	6176.00**	0.18**	0.00**	0.50**	81.27**	10.05**	0.02**	130.56**	11.37**
Blocks(rep)	14	33.48**	7.62**	16.51**	7.73**	4.40**	68.81**	0.11**	251.23**	4146.93**	23.96**	0.00**	3.17**	3.63**	48.10*	0.31**	40.04**	2.44**
Treatments	159	9.50**	5.47**	7.06**	5.34**	4.96**	21.36**	0.05**	73.40*	4581.92**	14.36**	0.00**	2.02**	2.47**	65.41**	0.52**	60.01**	8.35**
Error	145	2.68	2.32	2.24	2.85	1.51	13.58	0.03	50.55	4221.43	2.81	0.00	1.05	1.46	22.31	0.12	7.65	0.44

** = Significant at 1% level, * = Significant at 5% probability level, ns = Non-Significant

Table 2. Analysis of variance of genetic traits under drought condition in wheat genotypes during 2015-16

Sources of variation	DF	DH	DM	DA	GFD	TLR	FLL	FLW	FLA	PH	PL	PW	SL	SLS	GS	GW	TGW	GY
Replication	1	29.40**	75.07**	69.37**	0.11**	9.45**	277.51**	0.54**	1070.44**	45.00**	3.74**	0.00**	8.12**	72.20**	8.12**	0.00**	82.83**	0.30**
Blocks(rep)	14	32.06**	11.85**	21.18**	9.17**	3.16**	71.56**	0.12**	243.75**	237.50**	23.47**	0.00**	3.30**	3.85**	56.65**	0.22**	47.57**	1.60**
Treatments	159	10.46**	7.07**	8.17**	6.10**	5.35**	23.23**	0.06**	75.74**	171.44**	14.58**	0.00**	2.25**	2.72**	60.09**	0.54**	64.64**	8.44**
Error	145	2.51	2.48	2.21	2.53	1.15	14.17	0.03	44.67	24.07	2.84	0.00	1.04	1.43	27.48	0.14	8.03	0.49

** = Significant at 1% level, * = Significant at 5% probability level, ns = Non-Significant

Table 3. Pooled analysis of variance of genetic traits under drought condition in wheat genotypes during 2014-15 and 2015-16

Sources of variation	DF	DH	DM	DA	GFD	TLR	FLL	FLW	FLA	PH	PL	PW	SL	SLS	GS	GW	TGW	GY
Treatment	159	20.56**	12.50**	15.66**	10.73**	9.89**	45.99**	0.11**	155.21**	2847.24**	29.07**	0.00**	4.43**	5.09**	122.89**	1.05**	125.15**	16.59**
Year	1	705.61**	1762.17**	743.89**	216.20**	129.22**	138.58**	2.32**	1528.49**	8049.86**	62.71**	0.05**	50.18**	71.36**	517.72**	6.24**	152.12**	18.02**
Rep. (Year)	2	55.40**	51.05**	60.08**	1.91**	5.55**	287.66**	0.31**	913.55**	3173.08**	2.04**	0.00**	4.34**	76.81**	9.20**	0.02**	109.11**	5.60**
Blocks	7	42.10**	18.49**	23.23**	11.77**	1.13**	71.81**	0.08**	224.78**	2075.19**	19.15**	0.00**	3.69**	4.72**	77.03**	0.64**	35.95**	0.90**
Treat. x Year	159	0.47**	0.37**	0.22**	0.61**	0.63**	0.17**	0.00**	1.90**	1981.89**	0.03**	0.00**	0.05**	0.18**	3.59**	0.02**	1.18**	0.33**
Error	311	2.57	2.36	2.31	2.76	1.40	13.67	0.03	48.07	2076.28	2.86	0.00	1.06	1.55	25.71	0.13	7.62	0.45

** = Significant at 1% level, * = Significant at 5% probability level, ns = Non-Significant

DH=Days to heading, DM=Days to maturity, DA=Days to anthesis, GFD=Grain filling duration, TLR=No. of tillers per plant, FLL=Flag leaf length (cm), FLW=Flag leaf width (cm), FLA=Flag leaf area (cm²), PH=Plant height (cm), PL=Peduncle length (cm), PW=Peduncle weight (g), SL=Spike length (cm), SLS=No. of spikelets per spike, GS=No. of grains per spike, GW=Grain weight per spike (g), TGW=1000-grain weight (g), GY=Grain yield per plant (g).

v7.2 software. The design constitutes of 8x20 i.e. eight blocks each of 20 genotypes, planted in two environments; drought condition and control condition with two replications. Each entry was planted two-meter-long with three rows in each plot. The plants were spaced 10 cm each other and rows were spaced 20 cm. The experimental material was evaluated for 2 years 2014-15 and 2015-16. The plots were irrigated before sowing to ensure uniform germination. Under drought condition no irrigation was done during the crop season. Under control condition normal irrigations were given. The data were recorded on seventeen yield contributing traits viz., DH, DM, DA, GFD, TLR, FLL, FLW, FLA, PH, PL, PW, SL, SLS, GS, GW, TGW, GY. The data were subjected to analysis of variance using SAS GLM procedure release 9.3. Analyses of variance (ANOVA) for the phenotypic data were performed using PROC GLM of SAS.

3. Results and discussion

Analysis of variance for both the years and pooled data under drought condition are presented in (Tables 1, 2 and 3). Mean square of the treatments had highly significant differences for year wise and pooled data, except in case of flag leaf width, flag leaf area, plant height was non-significant in first year. Mean square of the year had highly significant differences for all the traits in pooled data except, plant height was significant only. Treatments x Years were non-significant for all the traits in pooled data. Analysis of variance for both the years and pooled under control condition are presented in (Tables 4, 5 and 6). Mean square due to treatments had highly significantly differences for all the studied traits in both the years and pooled data, except plant height in the pooled data was significant only, and plant height in the first year was non-significant also. Mean square of the year had highly significantly differences for all the characters in pooled data, except plant height was non-significant. Treatments x Years were non-significant for all the characters in pooled data. Wider range in mean values of different traits validates the genotypic differences (Ahmad *et al.*, 2011). Bhattarai *et al.*, (2017) reported highly significant variation for DM, GFD, PH, SL, GS, TGW and GY among genotypes assessed under drought condition. The

traits observed here are very important for discriminate wheat genetic resource which are essential and helpful for breeders seeking to enhancement the existing germplasm by introducing novel genetic variation for certain traits into the breeding populations (Pagnotta *et al.*, 2009; Zarkti *et al.*, 2010). Therefore, these traits have good potential in order to select and to conserve genotypes. So that, information of genetic diversity, evaluation of the genetic relationships among these genotypes can provide relevant guidelines in selecting parents and for designing new breeding strategies for wheat cultivar improvement especially for drought tolerance (Elhaddoury *et al.*, 2012). The findings of present study are also in agreement with (Sinha *et al.*, 2006; Kamboj, 2007; Baloch *et al.*, 2013) reported highly significant differences for among all the traits.

The estimates of pooled correlation coefficients under drought condition are presented in (Table 7). The grain yield per plant exhibited highly significant positive correlation with TGW (0.735), GW (0.635), GS (0.512), PH (0.317), GFD (0.273), TLR (0.266), PL (0.251). The grain yield per plant exhibited significant negative correlation with SLS (-0.233). The estimates of pooled correlation coefficients under control condition are given in (Table 8). The grain yield per plant exhibited highly significant positive correlation with TGW (0.724), GW (0.613), GS (0.610), PH (0.315), PL (0.248). The grain yield per plant exhibited highly significant positive correlation with TGW, GW, GS, PH, GFD, TLR, PL under drought condition. The grain yield is a main selection criterion under drought condition is a complex trait that determined by several physiological, biochemical processes and its associations are greatly ambiguous (Ali *et al.*, 2011). Present findings are in agreement with (Singh *et al.*, 2012) showing strong association of grain yield with yield component traits viz. TLR, GW and GS suggested that grain yield potential can be effectively improved by obtaining maximum expression of SL, GS and GW. Length of spike showed positive and significant correlation with SLS (Saefer-ul-Hassan *et al.*, 2004), GS (El-Shazly, 2000) and GY (Singh *et al.*, 2010) under control condition.

Table 4. Analysis of variance of genetic traits under control condition in wheat genotypes during 2014-15

Sources of variation	DF	DH	DM	DA	GFD	TLR	FLL	FLW	FLA	PH	PL	PW	SL	SLS	GS	GW	TGW	GY
Replication	1	0.50 ^{ns}	720 ^{ns}	2.81 ^{ns}	1.01 ^{ns}	6.32 [*]	8.03 ^{ns}	0.03 ^{ns}	45.85 ^{ns}	1340.70 ^{ns}	3.93 ^{ns}	0.00 ^{ns}	5.77 [*]	122.51 ^{ns}	261.00 ^{ns}	0.01 ^{ns}	56.91 ^{ns}	0.03 ^{ns}
Blocks(rep)	14	34.10 ^{ns}	15.20 ^{ns}	17.92 ^{ns}	4.85 [*]	2.01 [*]	15.30 ^{ns}	0.08 ^{ns}	66.09 ^{ns}	3283.89 ^{ns}	28.52 ^{ns}	0.00 ^{ns}	1.87 [*]	4.88 ^{ns}	74.41 ^{ns}	0.13 ^{ns}	27.33 ^{ns}	1.94 ^{ns}
Treatments	159	9.66 ^{ns}	7.67 ^{ns}	6.56 ^{ns}	4.66 ^{ns}	3.97 ^{ns}	26.40 ^{ns}	0.05 ^{ns}	85.55 ^{ns}	2924.67 ^{ns}	17.90 ^{ns}	0.00 ^{ns}	1.55 ^{ns}	2.49 ^{ns}	74.73 ^{ns}	0.40 ^{ns}	49.15 ^{ns}	6.33 ^{ns}
Error	145	3.23	2.65	2.12	2.31	1.05	11.78	0.03	41.82	2592.67	5.14	0.00	0.97	1.68	22.60	0.13	6.33	0.32

^{ns} = Significant at 1% level, ^{*} = Significant at 5% probability level, ns = Non-Significant

Table 5. Analysis of variance of genetic traits under control condition in wheat genotypes during 2015-16

Sources of variation	DF	DH	DM	DA	GFD	TLR	FLL	FLW	FLA	PH	PL	PW	SL	SLS	GS	GW	TGW	GY
Replication	1	14.45*	7.50 ^{ns}	2.62 ^{ns}	19.01**	41.32**	5.12 ^{ns}	0.02 ^{ns}	25.87 ^{ns}	67.52 ^{ns}	1.78 ^{ns}	0.00 ^{ns}	2.41 ^{ns}	66.61**	42.77 ^{ns}	0.16 ^{ns}	17.87 ^{ns}	0.00 ^{ns}
Blocks(rep)	14	35.18**	17.14**	24.04**	6.83**	2.66**	19.10 ^{ns}	0.10**	87.08*	202.59**	26.04**	0.00**	2.76**	4.43**	67.32**	0.15 ^{ns}	31.73**	1.35**
Treatments	159	10.81**	10.10**	8.35**	5.15**	4.42**	28.29**	0.06**	83.63**	187.56**	18.09**	0.00**	2.02**	2.48**	85.49**	0.47**	62.17**	5.57**
Error	145	3.28	2.96	2.57	2.64	1.18	13.38	0.03	43.49	26.85	3.87	0.00	1.11	1.65	25.31	0.13	6.93	0.43

**=Significant at 1% level, *=Significant at 5% probability level, ns = Non-Significant

Table 6. Pooled analysis of variance of genetic traits under control condition in wheat genotypes during 2014-15 and 2015-16

Sources of variation	DF	DH	DM	DA	GFD	TLR	FLL	FLW	FLA	PH	PL	PW	SL	SLS	GS	GW	TGW	GY
Treatment	159	21.06**	17.44**	15.11**	9.25**	7.79**	54.79**	0.12**	166.58**	1870.67*	36.27**	0.00**	3.63**	5.05**	157.88**	0.85**	110.80**	11.51**
Year	1	878.90**	2971.31**	610.35**	888.30**	87.02**	230.64**	2.24**	2111.39**	3080.02**	71.82**	0.04**	22.80**	30.62**	486.50**	7.07**	141.60**	14.15**
Rep.(Year)	2	7.25 ^{ns}	7.35 ^{ns}	2.72 ^{ns}	10.01**	23.82**	6.57 ^{ns}	0.02 ^{ns}	35.86 ^{ns}	704.11 ^{ns}	2.86 ^{ns}	0.00*	4.09*	94.56**	151.89**	0.09 ^{ns}	37.39**	0.01 ^{ns}
Blocks	7	42.70**	32.49**	31.42**	5.80**	0.40 ^{ns}	55.97**	0.19**	245.11**	1332.99 ^{ns}	20.73**	0.00*	3.42**	3.48 ^{ns}	55.76*	0.28 ^{ns}	31.85**	0.34 ^{ns}
Treat. x Year	159	0.17 ^{ns}	0.48 ^{ns}	0.21 ^{ns}	0.54 ^{ns}	0.66 ^{ns}	0.26 ^{ns}	0.00 ^{ns}	1.94 ^{ns}	1276.48 ^{ns}	0.34 ^{ns}	0.00 ^{ns}	0.10 ^{ns}	0.14 ^{ns}	3.20 ^{ns}	0.01 ^{ns}	1.19 ^{ns}	0.47 ^{ns}
Error	311	3.13	2.86	2.30	2.54	1.15	12.12	0.03	42.25	1309.76	4.47	0.00	1.02	1.77	26.15	0.14	6.31	0.37

**=Significant at 1% level, *=Significant at 5% probability level, ns = Non-Significant

DH=Days to heading, DM=Days to maturity, DA=Days to anthesis, GFD=Grain filling duration, TLR=No. of tillers per plant, FLL=Flag leaf length (cm), FLW=Flag leaf width (cm), FLA=Flag leaf area (cm²), PH=Plant height (cm), PL=Peduncle length (cm), PW=Peduncle weight (g), SL=Spike length (cm), SLS=No. of spikelets per spike, GS=No. of grains per spike, GW=Grain weight per spike (g), TGW=1000-grain weight (g), GY=Grain yield per plant (g).

The genetic divergence among 160 wheat genotypes into thirteen clusters under drought condition is given in (Table 9). The maximum number of genotypes appeared in cluster III (58 genotypes) followed by cluster IV (46 genotypes), cluster II (34 genotypes), cluster I (16 genotypes) and cluster XIII (2 genotypes). The average value of intra and inter-cluster distance for thirteen clusters are presented in (Table 10). The highest intra-cluster values

were observed in cluster IV (3.49) followed by cluster XIII (275.71), cluster III (243.01), cluster II (184.27), and cluster I (112.16). The maximum inter-cluster distances were observed between cluster XI and cluster XIII (1878.37). The cluster average values for different traits are presented in (Table 11). The genotypes of cluster XIII had maximum mean for DH (93.882) followed by cluster X (92.430) and cluster IX (90.560). The genotypes of

Table 7. Pooled correlation coefficient analysis between genetic traits under drought condition during 2014-15 and 2015-16

	DH	DM	DA	GFD	TLR	FLL	FLW	FLA	PH	PL	PW	SL	SLS	GS	GW	TGW	GY
DH	1.000	0.620**	0.889**	-0.399**	0.051	-0.087	-0.034	-0.078	0.031	-0.257**	-0.174*	0.071	0.227*	-0.056	-0.188*	-0.158	-0.122
DM		1.000	0.585**	0.267**	0.103	0.071	0.041	0.070	0.227*	-0.046	0.069	0.080	0.065	-0.049	-0.031	0.080	0.106
DA			1.000	-0.546**	0.050	-0.122	-0.046	-0.103	0.020	-0.266**	-0.177*	0.113	0.243**	-0.065	-0.230**	-0.174*	-0.143
GFD				1.000	0.050	0.212*	0.095	0.190*	0.213*	0.256**	0.273**	-0.046	-0.210*	0.023	0.231**	0.282**	0.273**
TLR					1.000	-0.139	0.103	-0.048	0.060	-0.109	-0.021	0.139	-0.027	-0.085	0.109	0.057	0.266**
FLL						1.000	0.420**	0.894**	0.086	0.328**	0.388**	0.156	-0.012	0.205*	0.221*	0.190*	0.190*
FLW							1.000	0.745**	-0.022	-0.097	0.185*	0.278**	0.048	0.123	0.169*	0.142	0.026
FLA								1.000	0.034	0.169*	0.354**	0.240**	0.004	0.178*	0.210*	0.190*	0.134
PH									1.000	0.485**	0.364**	0.222*	0.160	0.171*	0.292**	0.438**	0.317**
PL										1.000	0.724**	0.030	-0.083	0.150	0.236**	0.287**	0.251**
PW											1.000	0.325**	0.032	0.238**	0.395**	0.300**	0.200*
SL												1.000	0.425**	0.280**	0.317**	0.096	0.011
SLS													1.000	0.285**	0.074	-0.152	-0.233**
GS														1.000	0.731**	0.470**	0.512**
GW															1.000	0.676**	0.635**
TGW																1.000	0.735**
GY																	1.000

**=Significant at 1% probability level, r=0.230, *=Significant at 5% probability level, r=0.164

Table 8. Pooled correlation coefficient analysis between genetic traits under control condition during 2014-15 and 2015-16

	DH	DM	DA	GFD	TLR	FLL	FLW	FLA	PH	PL	PW	SL	SLS	GS	GW	TGW	GY
DH	1.000	0.678**	0.942**	-0.266**	-0.006	-0.119	-0.110	-0.145	0.156	-0.192*	-0.172*	0.073	0.290**	-0.059	-0.151	-0.158	-0.137
DM		1.000	0.706**	0.351**	-0.030	-0.058	-0.070	-0.083	0.236**	0.071	0.100	0.104	0.210*	-0.029	-0.022	0.096	0.039
DA			1.000	-0.331**	0.007	-0.154	-0.144	-0.187*	0.154	-0.214*	-0.207*	0.111	0.339**	-0.057	-0.153	-0.133	-0.122
GFD				1.000	-0.050	0.116	0.087	0.125	0.126	0.369**	0.400**	0.000	-0.145	0.033	0.164*	0.300**	0.208*
TLR					1.000	-0.112	0.190*	0.015	0.029	-0.142	0.001	0.127	0.116	-0.076	0.105	0.056	0.098
FLL						1.000	0.278**	0.861**	-0.068	0.388**	0.328**	0.085	-0.024	0.236**	0.251**	0.199*	0.203*
FLW							1.000	0.693**	-0.227*	-0.059	0.193*	0.301**	0.017	0.181*	0.248**	0.133	0.029
FLA								1.000	-0.144	0.260**	0.340**	0.218*	-0.004	0.261**	0.304**	0.202*	0.158
PH									1.000	0.509**	0.424**	0.162	0.072	0.122	0.241**	0.463**	0.315**
PL										1.000	0.741**	-0.033	-0.112	0.205*	0.248**	0.305**	0.248**
PW											1.000	0.255**	-0.045	0.249**	0.430**	0.363**	0.214*
SL												1.000	0.313**	0.313**	0.399**	0.200*	0.066
SLS													1.000	0.326**	0.096	-0.166*	-0.115
GS														1.000	0.756**	0.412**	0.610**
GW															1.000	0.621**	0.613**
TGW																1.000	0.724**
GY																	1.000

** = Significant at 1% probability level, $r=0.230$, * = Significant at 5% probability level, $r=0.164$

DH=Days to heading, DM=Days to maturity, DA=Days to anthesis, GFD=Grain filling duration, TLR=No. of tillers per plant, FLL=Flag leaf length (cm), FLW=Flag leaf width (cm), FLA=Flag leaf area (cm²), PH=Plant height (cm), PL=Peduncle length (cm), PW=Peduncle weight (g), SL=Spike length (cm), SLS=No. of spikelets per spike, GS=No. of grains per spike, GW=Grain weight per spike (g), TGW=1000-grain weight (g), GY=Grain yield per plant (g).

Table 9. Clustering pattern of 160 wheat genotypes for genetic traits under drought condition across the years

Cluster No.	Number of Genotypes	Genotypes
I	16	HW 2036, DRYSDALE, HW 5209, SB025, HW 4218, HD 3090, KUKRI, CETTIA, WH 1080, HD 3043, WH 711, PBW 550 HUW 510, BWL 0924, VJ01 and IC 252803CK9
II	30	RAJ 4120, BARKARE, SSRT65, SSRT16, SSRW35, VJ10, IEPACA RABBE, HD 3118, DBW 77, SB187, NI 5439, TACUPETOF2001, SB062, AUS30523, SB169, WH 1021, BABAX, SSRT02, HD 2985, SILVERSTAR, SB165, TEPOKO, BWL 1771, DHARWARDRY, HALNA, JANZ, SITTELLA, HI 1563, GRANERO INTA and HD 3121
III	58	NAC0ZARIF 76, VOROBAY, WH 542, EXCALIBUR, HI 1531, SERI M 82, SB053, HW 4219, HD 2733, SB044, RAJ 4083, WYALKATCHEM, SB003, DBW 14, HD 2824, PBW 343, UP 2828, HW 3620, MACS 6272, PBW 373, HD 3123, HD 2687, HD 2932, BWL9022, RAJ3765, BERKUT, HARTOG, SB057, RAC875, SB109, BWL 1793, LOVE-HH-129, DBW 58, AUS30518, KRICHAUFF, BWL 0814, HD 3070, DBW 50, PBN142, AUS30354, NW 1014, HD 3086, GLADIUS, HD 3091, HW 4009, PBW 502, DBW 39, Chirya 7, HW 2066, BACANORA 88, HD 2877, FLW 12, WH730, PBN 51, FLW 3, HD 3093, FLW 7 and SB010
IV	46	HI 617, HW 2004, C 306, VJ99, AUS30355, MACS 6273, HD 3122, NW 2036, HW 4008, HD 2987, HW 2039, HD 2643, HW 4002, HD 2833, Lok 65, BAW898, HI 1544, HW 4215, HW 4209, FLW 13, RAJ 4037, HD 2864, K 1016, HW 4022, BAVIACORA M 92, PBW 175, WH 157, HI 1500, UP 2691, Lok 1, WH 147, SSRW47, Lok 45, HW 4213, OTHERY EGYPT, NP 846, SSRT09, HW 1105, SSRT14, VJ30, HW 2005, DBW 28, PASTOR, SSRT17, SB069 and MACS 2496
V	1	HD 3059
VI	1	HW 4202
VII	1	DBW 88
VIII	1	HD 2967
IX	1	HD 3076
X	1	SOKOLL
XI	1	HW 4029
XII	1	HW 2009
XIII	2	ATTILA and IC 532653

Table 10. Estimates of average intra-and inter-cluster distances for 13 clusters of genetic traits under drought condition across the years

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	112.16	232.04	242.68	350.68	431.97	444.81	546.12	494.13	384.18	434.30	505.23	730.79	678.80
II		184.27	401.57	396.02	604.86	635.42	670.30	466.90	595.50	583.73	756.56	578.46	686.05
III			243.01	597.59	393.58	400.15	438.86	430.95	476.42	555.14	693.80	1058.38	779.98
IV				349.42	889.34	868.92	1044.01	932.44	706.09	687.24	701.06	693.22	919.68
V					0.00	757.45	368.67	326.37	870.53	628.03	718.54	1729.60	1158.44
VI						0.00	669.37	561.57	636.07	797.81	913.63	1279.45	911.76
VII							0.00	318.94	893.06	952.56	1129.25	1438.25	1111.47
VIII								0.00	773.73	755.32	1269.00	1374.49	828.60
IX									0.00	444.39	1256.76	1186.38	400.18
X										0.00	1000.89	1642.51	480.48
XI											0.00	1103.98	1878.37
XII												0.00	1460.65
XIII													275.71

cluster X (12.450) had maximum GY followed by cluster XI (12.440), cluster IV (9.453), cluster IX (9.450) and cluster V (9.415). The genetic divergence among 160 wheat genotypes into thirteen clusters under control condition is given in (Table 12). The maximum number of genotypes appeared in cluster III (59 genotypes) followed by cluster V (28 genotypes), cluster IV (25 genotypes), cluster I (22 genotypes), cluster II (15 genotypes) and cluster VIII (4 genotypes). The estimates of intra and inter-cluster distance for thirteen clusters are presented in (Table 13). The highest intra-cluster values were found in cluster VIII (534.13) followed by cluster V (454.62), cluster IV (343.50),

cluster III (258.79), cluster II (178.12) and cluster I (139.07). The maximum inter-cluster distances were recorded between cluster VIII and cluster X (1886.95). The cluster means for different traits under control condition are presented in (Table 14). The genotypes of cluster VIII had maximum mean for DH (97.650) followed by cluster II (91.894), cluster VI (91.250) and cluster XIII (91.825). The cluster mean for GY was highest in the genotypes of the cluster III (13.620), followed by cluster V (11.491) and cluster VIII (10.119). The findings of the cluster analysis showed that simultaneous evaluation of germplasm under drought condition and control condition could reveal

Table 11. Cluster means of genetic traits under drought condition in wheat genotypes across the years

	DH	DM	DA	GFD	TLR	FLL	FLW	FLA	PH	PL	PW	SL	SLS	GS	GW	TGW	GY
I	86.415	125.479	91.010	34.471	8.821	23.785	1.832	30.842	94.221	14.419	0.127	10.590	17.530	49.301	2.268	38.554	8.652
II	86.658	125.306	91.229	34.077	7.689	25.330	1.810	32.349	96.721	15.987	0.160	11.753	18.333	53.320	2.563	36.486	8.027
III	87.053	125.570	91.886	33.685	8.203	21.756	1.727	26.591	93.405	12.463	0.116	10.622	17.575	47.939	2.092	35.065	7.927
IV	85.412	125.192	90.313	34.879	8.069	26.310	1.828	34.122	100.341	16.561*	0.157	10.798	17.208	49.781	2.487	40.882	9.453
V	87.630	126.785	92.600	34.185	10.230	14.715*	1.650	16.745*	95.645	11.180	0.135	12.265	18.105	55.210	2.780	41.175	9.415
VI	87.230	125.115	91.705	33.410	6.285	21.905	1.365	20.265	83.355	14.765	0.100	7.965*	17.475	49.255	1.640	25.960*	7.075
VII	87.415	126.935	91.870	35.070	8.295	18.005	1.795	22.790	99.980	9.245*	0.115	12.385	18.960	32.455*	1.175*	26.040	4.125*
VIII	87.810	125.830	94.220	31.615*	9.530	19.475	1.725	23.930	91.785	13.095	0.135	12.460*	20.420*	59.660*	1.590	28.945	6.760
IX	90.560	127.080	93.970	33.115	10.530*	29.225	1.925	39.280	90.285	9.345	0.085*	10.085	18.670	49.910	2.160	38.965	9.450
X	92.430	129.445	94.645	34.800	3.880*	23.660	1.560	25.800	128.260*	15.070	0.135	11.055	19.665	51.005	2.690	45.625	12.450*
XI	79.895	123.405	85.585*	37.820*	5.665	19.440	1.350*	17.810	86.800	15.820	0.130	10.035	15.515	52.400	2.995*	45.980*	12.440
XII	79.700*	122.775*	86.080	36.690	7.075	31.385*	2.180*	48.635*	81.795*	16.155	0.160*	11.375	16.940	49.370	2.195	30.660	6.895
XIII	93.882*	132.605*	96.900*	35.708	6.190	29.510	1.875	38.618	102.455	13.470	0.148	11.195	18.303	50.665	2.180	35.835	6.840

** Highest Mean Value, * Lowest Mean Value

DH=Days to heading, DM=Days to maturity, DA=Days to anthesis, GFD=Grain filling duration, TLR=No. of tillers per plant, FLL=Flag leaf length (cm), FLW=Flag leaf width (cm), FLA=Flag leaf area (cm²), PH=Plant height (cm), PL=Peduncle length (cm), PW=Peduncle weight (g), SL=Spike length (cm), SLS=No. of spikelets per spike, GS=No. of grains per spike, GW=Grain weight per spike (g), TGW=1000-grain weight (g), GY=Grain yield per plant (g).

Table 12. Clustering pattern of 160 wheat genotypes for genetic traits under control condition across the years

Cluster No.	Number of Genotypes	Genotypes
I	22	PBW 502, WH 730, PBW 175, VJ01, HW 5209, BERKUT, HD 2932, HD 3043, SB057, PBW 550, WH 1021, DBW 58, SB025, WH 1080, DRYSDALE, HW 2036, SB165, HD 2687, KUKRI, SERI M 82, BWL 0814 and CETTIA
II	15	NAC0ZARI F 76, VOROBAY, HI 1531, EXCALIBUR, HD 2967, TACUPETO F2001, WYALKATCHEM, SB053, PBN 142, HD 3059, HD 3076, DBW 50, RAC875, HD 3090 and AUS30518
III	59	RAJ 4120, GRANERO INTA, BWL 1771, BARKARE, TEPOKO, HD 3118, NW 2036, SILVERSTAR, SSRT65, SSRW35, HD 2985, PASTOR, HD 3121, DBW 77, HI 1563, Lok 45, HD 2833, DBW 39, BABAX, SSRT17, VJ10, HUW 510, HW 2039, HD 3086, HD 2987, NI 5439, HW 4209, SB169, SB109, AUS30354, FLW 3, HW 4022, SB062, SB187, HD 2864, Chirya 7, WH 147, WH 711, AUS30523, HW 2066, HW 4218, RAJ 3765, HI 1544, IC 252803 CK9, HD 3123, WH 157, HW 1105, SITTELLA, HALNA, HW 4009, BAW898, BWL 1793, JANZ, HD 3091, PBN 51, LOVE-HH-129, HW 2005, HD 3070 and HW 4213
IV	25	DBW 14, RAJ 4083, UP 2828, HD 2733, MACS 6272, DBW 28, HARTOG, NW 1014, PBW 373, DBW 88, HD 2824, SB003, PBW 343, HD 2877, BWL 0924, HW 3620, BWL 9022, SB044, KRICHAUFF, SSRW47, SB010, GLADIUS, BACANORA 88, HW 4219 and SSRT09
V	28	HI 617, HW 2004, C 306, VJ99, NP 846, SSRT16, HW 4215, HW 4008, Lok 65, HD 3122, HD 2643, HW 4029, HW 4002, SB069, Lok 1, RAJ 4037, AUS30355, SSRT02, IEPACA RABBE, FLW 13, K 1016, HI 1500, DHARWAR DRY, FLW 7, SSRT14, OTHERY EGYPT, FLW 12 and HD 3093
VI	1	WH 542
VII	1	VJ30
VIII	4	UP 2691, SOKOLL, IC 532653 and ATTILA
IX	1	BAVIACORA M 92
X	1	MACS 6273
XI	1	HW 2009
XII	1	HW 4202

Table 13. Estimates of average intra-and inter-cluster distances for 13 clusters of genetic traits under control condition across the years

	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	139.07	260.48	261.22	389.65	487.44	348.98	340.07	840.67	678.13	429.79	467.53	483.62	950.50
II		178.12	465.45	392.12	766.36	355.59	691.17	718.94	1152.81	543.39	884.53	603.63	1337.18
III			258.79	586.36	464.84	431.58	454.21	871.37	522.44	680.97	537.84	655.74	676.10
IV				343.50	960.18	470.96	600.84	944.74	1195.16	636.01	861.10	476.40	1587.08
V					454.62	856.65	687.53	1062.29	727.86	799.15	735.73	1069.64	725.91
VI						0.00	588.13	970.49	745.46	1068.65	841.44	368.61	987.37
VII							0.00	1403.72	542.40	537.75	312.04	338.83	1205.05
VIII								534.13	1810.30	1028.41	1886.95	1213.16	1215.23
IX									0.00	1301.85	282.53	981.96	755.28
X										0.00	751.71	689.41	1795.76
XI											0.00	829.48	1399.74
XII												0.00	1559.89
XIII													0.00

the most valuable source for drought tolerance. This was in fall arrangement with CIMMYT, s approach to breeding for drought tolerance which advocated parallel testing of germplasm under both stress and non-stress conditions (Rajaram *et al.*, 1996). The results are also agreed the reports of Narouee (2006) who determined the genetic diversity of wheat landraces using cluster

analysis under rainfed condition. Fang *et al.*, (1996) used 120 wheat genotypes of wheat and clustered them into five groups on the bases of morphological traits namely; date of maturity, plant height, spike length, grains per spike, spike length, 1000-grain weight, and grain weight per spike and reported the same results under rainfed condition, similar finding were given by Ali *et al.*, (2008)

Table 14. Cluster means of genetic traits under control condition in wheat genotypes across the years

	DH	DM	DA	GFD	TLR	FLL	FLW	FLA	PH	PL	PW	SL	SLS	GS	GW	TGW	GY
I	89.171	128.691	93.954	34.739	9.837	24.341	1.796	30.676	96.314	15.786	0.160	11.716	19.539	56.949	2.813	40.965	9.885
II	91.894	130.288	96.096	34.192	10.121	21.409	1.811	27.346	101.576	13.419	0.146	12.304	20.409	60.565	2.798	39.166	9.548
III	89.917	129.340	94.118	35.222	9.407	27.980	1.858	36.613	99.590	17.496	0.184	12.117	19.403	57.583	2.888	40.812	9.809
IV	90.992	129.686	95.073	34.614	9.432	23.432	1.724	28.320	96.520	14.493	0.142	11.422	19.431	46.321*	2.092	33.691	7.772*
V	89.345	129.909	93.732	36.177	9.466	27.509	1.852	35.961	108.883	19.170	0.199	11.938	19.164	58.264	3.102	46.351	11.491
VI	91.250	128.015	95.480	32.530*	9.260	28.015	1.840	35.890	92.130	11.350*	0.150	11.180	21.830**	62.655**	2.785	32.525*	8.935
VII	86.180	123.875*	90.270	33.605	7.715*	27.295	1.835	35.150	118.475**	20.080	0.135	9.650	19.060	54.205	2.310	39.635	8.230
VIII	97.650**	136.034**	100.574**	35.458	7.754	26.097	1.741	31.764	116.656	18.690	0.175	12.041	21.064	56.443	2.695	42.470	10.119
IX	85.545	127.235	89.575	37.655	8.605	32.390	2.045**	47.095	94.635	20.445	0.215**	12.330**	20.595	62.540	3.095	36.390	9.245
X	89.025	129.100	93.165	35.935	10.895	17.095*	1.555	18.195*	109.605	22.110**	0.170	10.060	19.015*	51.305	2.620	40.325	9.850
XI	83.045*	125.735	88.075	37.655**	8.355	25.515	1.945	35.550	96.385	18.695	0.190	12.205	19.095	55.040	2.630	38.405	8.880
XII	89.280	127.690	94.380	33.310	8.300	26.480	1.480*	27.485	77.380*	17.550	0.130*	8.465*	20.110	58.980	1.945*	28.040	8.935
XIII	91.825	132.270	95.810	36.460	11.225**	37.575**	1.840	48.050**	115.680	18.755	0.200	12.195	19.950	61.355	3.805**	47.720**	13.620**

** Highest Mean Value, * Lowest Mean Value

DH=Days to heading, DM=Days to maturity, DA=Days to anthesis, GFD=Grain filling duration, TLR=No. of tillers per plant, FLL=Flag leaf length (cm), FLW=Flag leaf width (cm), FLA=Flag leaf area (cm²), PH=Plant height (cm), PL=Peduncle length (cm), PW=Peduncle weight (g), SL=Spike length (cm), SLS=No. of spikelets per spike, GS=No. of grains per spike, GW=Grain weight per spike (g), TGW=1000-grain weight (g), GY=Grain yield per plant (g).

for the improvement of wheat genotypes through cluster analysis under rainfed condition. According to Rahim *et al.*, (2010) the crosses between the genotypes having highest distance resulted high yield, the cross between these genotypes can be used in breeding programs to achieve maximum heterosis. Singh *et al.*, (2009) genotypes belonging to clusters showing higher inter cluster distance considered genetically more divergent and hybridization between these genotypes of dissimilar clusters is likely to generate broad variability with desirable sergeants.

On the basis of grain yield per plant under both the conditions twenty one tolerant genotypes viz., DBW 39, FLW 13, FLW 7, HD 2833, HD 3093, HI 1500, HI 617, HW 2004, HW 2005, HW 2066, HW 4002, HW 4008, HW 4029, HW 4215, Lok 1, Lok 65, MACS 2496, RAJ 4037, SOKOLL, SSRT 14, VJ 99 were selected and eleven susceptible genotypes using same criteria namely; DBW 14, DBW 28, DBW 88, HD 2824, HD 2877, NW 1014, PBW 343, PBW 373, RAJ 4083, UP 2828, MACS 6272 were identified. Identified tolerant and susceptible genotypes can be used for development of mapping populations to map the QTLs for drought tolerance in wheat (*Triticum aestivum* L.).

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