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CONTENTS

Studies on genetic diversity and character association analysis in wheat (*Triticum aestivum* L. em. Thell)

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ABSTRACT: The experiment was conducted in the Augmented Block Design, comprised of 90 entries, along with 3 check varieties Sonalika, HD 2967 and HI 8713. Results revealed that variance was the highest for grain yield per plot and the lowest for spike length. The coefficient of variability was the highest for grain yield and the lowest for days to 75% heading. The highest heritability was recorded for tillers per meter and the lowest for 1000- grain weight. Grain yield exhibited highest genetic advance in percent of mean and lowest for days to 75% heading. However, with respect to correlation with one or other traits, grain yield was positive and significantly correlated with days to 75% heading, plant height, tillers per meter, grain per spike, spike length and grain yield per plot. Path coefficient revealed that 1000- grain weight exerted positive effect on all characters except days to 75% heading. The genotypes were classified into 7 different clusters by Non- Hierarchical Euclidean Cluster Analysis. Cluster -I had 13 genotypes whereas cluster -II had 20 genotypes, cluster- III had 8 genotypes, cluster -IV had 12 genotypes, cluster -V had 9 genotypes, cluster-VI has 15 genotypes and cluster-VII had 16 genotypes. Inter cluster distance was found maximum between cluster –III and cluster –IV and minimum was found in cluster–I and II.

Key words: Genetic Advance, heritability, path coefficient, variability

Wheat (*Triticum aestivum* L. em. Thell), also known as Bread Wheat is an allohexaploid crop (2n=6x=42), belongs to family Gramineae (Poaceae). It is most important food crop for humans from the very beginning of era of agriculture. It is known as 'King of Cereals' as it is the best staple diet for the people and can be grown in variety of soils and climates than any other crop.

According to FAOSTAT (2019-20), the largest producer of wheat is European Union (153500 metric tons) followed by China (133590 metric tons), India (102190 metric tons), Russia (74500 metric tons) & USA (52258 metric tons) etc. and bread wheat has worldwide production of about 766.4 million tons. In India, wheat production has increased to a record of 101.20 million tons for the crop year 2018-19, up by 1-3% a year ago, said by Ministry of Agriculture, during 2017-2018 wheat was grown on 29.72 million hectares of area with the production of 98.61 million tons with an average productivity of about 3318 kg/ha. In India, Uttar Pradesh has registered the highest production (30.24 million tons) followed by Punjab (17.04 million tons), Madhya Pradesh (13.93 million tons), Haryana (11.80 million tons), Rajasthan (8.92 million tons) and Bihar (5.08 million tons). These six states together contributed around 90% of the total wheat production in the country (Anonymous, 2017). In Uttarakhand, the area under wheat cultivation is about 383 thousand hectares with production of 880 thousand tons and an average productivity of 2643 kg/ha (Anonymous, 2018).

A successful selection depends upon the information on the genetic variability and association of morpho-agronomic traits with grain yield. Correlation studies along with path analysis provide a better understanding of the association of different characters with grain yield. Fonseca and Peterson (1968) based on their study highlighted the significance of components approach in formulating a successful breeding programme. The correlation coefficient gives an idea about the various linkages existing between the yield components. Path coefficient analysis separates the direct effects from the indirect effects through other related characters by partitioning the correlation coefficient (Dubey *et al.*, 1984).

Evaluation of genetic diversity among adapted, elite germplasm can provide predictive estimates of genetic variation among segregating progeny for pure line cultivar development. Knowledge about germplasm diversity and genetic relationships among breeding material could be an invaluable aid in crop improvement strategies (Mohammadi and Prasanna, 2003) and study of the genetic diversity in bread wheat is important for breeding and genetic resource conservation programs.

The experiment was done to assess the genetic diversity among the germplasm under study; to estimate the relative extent of variability for different characters among wheat germplasm; to assess the nature and magnitude of inter-character correlation; characterization of germplasm for agro-morphological traits, identification of superior lines which can be used as potential donors for yield and yield contributing characters and to assess the disease reaction on the wheat germplasm.

MATERIALS AND METHODS

The present investigation was conducted at N. E. Borlaug Crop Research Centre, Govind Ballabh Pant University of Agriculture and Technology, Pantnagar, Uttarakhand; during the *Rabi* Season 2019-20.

The present experiment comprised of 90 germplasm lines of National Genetic Stock Nursery (NGSN), obtained from National Bureau of Plant Genetic Resources (NBPGR), New Delhi. The experiment was carried out in the Augmented Block Design with 3 blocks, each containing 30 test entries along with 3 checks (randomly allocated) namely, Sonalika, HD-2967, HI 8713.

During experiment data were recorded for days to 75% heading, plant height (cm), number of tillers per meter, spike length (cm), number of grains per spike, 1000 -grain weight and grain yield per plot. The analysis of variance for augmented design has been calculated by using Federer (1956, 1961) and (Federer and Raghavarao, 1975) and Peterson (1985).

RESULTS AND DISCUSSION

Mean sum of squares were highly significant for all the seven characters studied. The significant differences among all the genotypes indicated handsome amount of genetic variation for all the traits studied.

Variance was found highest for grain yield per plot (302550.31), followed by number of tillers per meter (2998.68), plant height (853.28), grains per spike (247.43), days to 75% heading (143.77), 1000- grain weight (98.15) and least variance is found in spike length (11.53). All the variance was found to be significant.

Grain yield per plot (16.94) showed highest PCV followed by tiller per meter (12.12), spike length (10.81), 1000- grain weight (10.45), plant height (8.18), grain per spike (7.58) and days to 75% heading (2.36) showed lowest value for PCV.

GCV was highest for grain yield (15.85), followed by tiller per meter (11.93), spike length (8.42), plant height (7.89), 1000- grain weight (6.63), grains per spike (5.61), days to 75% heading (2.20) had the lowest value for GCV.

The findings are in accordance with earlier observation of Sidharthan *et al*. (2007), Ali *et al*. (2008), Majumder *et al*. (2008), Mohsin *et al*. (2009), Ferdous *et al*. (2010), Kotal *et al*. (2010), Kumar *et al*. (2013) and Fikre *et al*. (2015).

Kumar *et al*. (2013) and Bhushan *et al*. (2013) and Kumar *et al*. (2014) estimates high GCV and PCV observed for grain yield per plant followed by tillers per plant and harvest index.

The estimates in heritability in broad sense (h^2b) showed considerable variation for different characters in table. The value of heritability ranges from 40.26% (1000- grain weight) to 96.98% (tiller per meter). Higher estimates of heritability were observed for number of tillers per meter (96.98%) followed by plant height (93%), grain yield per plot (87.48%), days to 75% heading (87.20%). Moderate estimate for spike length (60.62%), grains per spike (54.63%) and low estimate for 1000- grain weight (40.26).

Differential heritability for different genotypes in wheat were reported by Saxena *et al*. (2007), Majumder *et al*. (2008), Aydin *et al*. (2010), Ullah *et al*. (2011) and Fikre *et al*. (2015)

The genetic advance in percent of mean ranged from 4.24% (days to 75% heading) to 30.53% (grain yield per plot). Highest genetic advance is of grain yield per plot (30.53%), followed by number of tillers per meter (24.21%), plant height (15.67%), spike length (13.50%), 1000- grain weight (8.66%), grains per spike (8.54%) and days to 75% heading (4.24%) had lowest genetic advance.

Such findings were also recorded by Joshi (1984), Kumar *et al*. (1986), Sandhu and Lal (1989), Crowley *et al*. (1993), Bergale *et al*. (2002), Anwar *et al*. (2009), Pawar *et al*. (1990), Lu *et al*. (1991), Mohan *et al*. (1993), Ibrahim (1994), Paul and Ganguli (1996), Dwivedi *et al.* (2002), Mohammad *et al*. (2008), Rangare *et al*. (2010), Bhushan *et al.* (2013), Kumar *et al*. (2014) and Khan *et al.* (2010).

The positive direct effect on grain yield (dependent variable) is a function of concomitant variables (independent variables) *viz*., days to 75% heading, plant height, tillers per meter, grains per spike, 1000- grain weight and spike length. Similar results were also observed by Hirachand *et al*. (1978), Sharma and Singh (1989), Ibrahim (1994), Dwivedi *et al*. (2002), Asif *et al*. (2004), Khaliq *et al*. (2004), Sherif *et al*. (2005), Mukherjee *et al*. (2008), Singh *et al.* (2009), Gulmezoglu *et al*. (2010), Cicfi (2012) and

Table 1: Genetic variability recorded for the characters studied

Characters	G mean	Var (g)	Var (p)	Heritability (%)	GA (%)	GA% mean	GCV (%)	PCV (%)
Days to 75% heading	96.69	4.54	5.21	87.20	4.10	4.24	2.20	2.36
Plant Height	88.51	48.72	52.38	93.00	13.87	15.67	7.89	8.18
No. of tillers per meter	88.13	110.61	114.06	96.98	21.34	24.21	11.93	12.12
Grains per spike	57.62	10.44	19.10	54.63	4.92	8.54	5.61	7.58
1000-grain weight (g)	35.82	5.64	14.00	40.26	3.10	8.66	6.63	10.45
Spike length	8.86	0.56	0.92	60.62	1.20	13.50	8.42	10.81
Grain Yield (g/plot)	513.03	6609.68	7555.46	87.48	156.65	30.53	15.85	16.94

G mean: Geometgric Mean, Var (p): Phenotypic variance, Var (g): Genotypic Variance, GA: Genetic Advance, GCV: Genotypic Coefficient of Variation, PCV: Phenotypic Coefficient of Variation

Correlation analysis revealed that grain yield was positively and significantly correlated with days to 75% heading, plant height, tillers per meter, grain per spikelet, spike length and grain yield per plot.

Table 2: Correlations among the characters studied

Characters	Days to 75% heading	Plant Height (cm)	No. of tillers per meter	Grains per spike	1000- grain weight (g)	Spike length (cm)	Grain Yield (g/plot)
Days to 75% heading	1.000	0.069	-0.105	0.059	-0.293**	-0.084	-0.253*
Plant Height		1.000	-0.122	-0.111	0.056	0.165	0.142
Tillers per meter			1.000	0.306**	-0.098	-0.170	0.105
Grains per spike				1.000	0.029	-0.151	0.127
1000- grain weight(g)					1.000	-0.112	0.263*
Spike length						1.000	0.178
Grain Yield (g/plot)							1.000

*,** significant at 5% and 1% level, respectively

Path coefficient analysis revealed that 1000- grain weight (0.236) exerted high positive direct effect on grain yield followed by spike length (0.209), grains per spike (0.140), plant height (0.137) and number of tiller per meter (0.120). However, days to 75% heading (-0.171) had negative direct effect on grain yield.

Abd El-Mohsen *et al.* (2014) for grain yield and its various component characters.

All the 90 genotypes were classified into 7 non-overlapping clusters. Cluster -I had 13 genotypes whereas cluster -II had 20 genotypes, cluster- III had 8 genotypes, cluster -IV had 12 genotypes, cluster -V had 9 genotypes, cluster-VI has 15 genotypes and cluster-VII had genotypes 16 genotypes.

The maximum intra cluster distance was found for cluster-IV (2.096) which revealed maximum genetic diversity among its constituents, followed by the cluster-III (1.994), cluster-VII (1.941), cluster-II (1.927), cluster-VI (1.923), cluster-V (1.623) and cluster-I (1.532) had minimum intra cluster distance.

Inter cluster distance was found maximum distance between cluster –III and cluster –IV (4.166), followed by cluster –III and cluster-V (4.112), cluster -IV and cluster-V (3.543), cluster –IV and cluster –VI (3.344), cluster-IV and cluster-VII (3.420), cluster –V and cluster –VII (3.173) indicated that cluster –III, IV, V were distantly related to each other. Minimum cluster distance was found in cluster –I and cluster –II (2.076) followed by cluster –I and

Table 3: Path coefficient analysis with grain yield (g/plot)

Characters	Days to 75% heading	Plant Height (cm)	No. of tillers per meter	Grains per spike	1000- grain weight(g)	Spike length (cm)	Grain Yield (g/plot)
Days to 75% heading	-0.171	0.009	-0.013	0.008	-0.069	-0.018	-0.253*
Plant Height	-0.012	0.137	-0.015	-0.016	0.013	0.034	0.142
No. of tillers per meter	0.018	-0.017	0.120	0.043	-0.023	-0.036	0.105
Grains per spike	-0.010	-0.015	0.037	0.140	0.007	-0.031	0.127
1000- grain weight (g)	0.050	0.008	-0.012	0.004	0.236	-0.023	0.263*
Spike length	0.014	0.023	-0.020	-0.021	-0.026	0.209	0.178

Resi = 0.0483; *,** significant at 5% and 1% level, respectively

Table 4: Number of Genotypes in each cluster

Clusters	No of genotypes	Genotypes
I	13	DBW 71, DBW 252, HI 8737 (d), HI 8805 (d), HS 611, PBW 777, TL 3011 (t), VL 3014, HI 1619, KRL 370, PBW 780, DBW 179, HI 8708 (d)
II	20	HD 3086, HI 1609, HI 1628, MACS 4058 (d), MP 1203, RAJ 3765, RAJ 4083, UAS 466 (d), HS 627, PBW 760, TL 3013, TL 3014, DBW 251, DBW 246, FLW 10, FLW 22, DWAP 1530, DWAP 1531, RAJ 4079, Sonalika
III	8	AKAW 4927, CG 1018, DBW 71, DBW 107, HD 3237, HI 1621, DWAP 1103, FLW 16
IV	12	K 1317, RAJ 3077, HS 665, UAS 462 (d), HPW 439, HS 644, HS 646, DDK 1051, DDK 1052, DDK 1053, MACS 5049, AKAW 3717
V	9	VL 3013, DM 6, DM 7, WH 117, WAPD 1505, WAPD 1508, WAPD 1516, WAPD 1519, WAPD 1524
VI	15	HI 8777, HI 8802 (d), PBW 778, WH 1232, DBW 129, DBW 150, HI 8751 (d), WH 730, GW 499, GW 1339 (d), MPO 1336 (d), RAJ 4238, TL 3012 (t), TL 3015 (t), HI 8713
VII	16	AKAW 4901, DBW 93, DBW 110, DBW 173, DBW 222, HD 3043, HD 3118, HD 3171, HD 3271, HI 1620, UAS 375, HI 1612, HI 8765 (d), DBW 221, MP 1338, HD 2967

Table 5: Inter and intra distances between the characters studied

Clusters	I	II	III	IV	V	VI	VII
I	1.532						
II	2.076	1.927					
III	2.479	2.850	1.994				
IV	2.270	2.584	4.166	2.096			
V	2.721	2.497	4.112	3.543	1.623		
VI	2.533	2.631	3.817	3.344	2.655	1.923	
VII	2.756	2.248	2.947	3.420	3.173	2.560	1.941

Table 6: Cluster Mean of the characters studied

Cluster		Days to 75% heading	Plant Height (cm)	Tillers per meter	Grains per spike	1000- grain weight (g)	Spike length (cm)	Grain Yield (g/plot)
I	Mean	97.69	86.85	68.62	57.00	38.08	8.38	406.15
	± SE	1.80	10.33	10.11	3.83	2.67	1.12	83.31
II	Mean	94.08	88.90	93.33	54.43	32.32	9.34	465.83
	± SE	3.61	6.61	16.19	5.04	3.87	1.05	118.95
III	Mean	93.62	94.00	57.75	49.25	41.56	10.12	591.75
	± SE	3.38	7.05	10.01	4.56	5.43	1.25	162.69
IV	Mean	103.25	92.58	86.08	56.00	30.76	8.33	317.67
	± SE	3.57	11.19	17.34	6.74	4.22	1.23	48.83
V	Mean	95.22	62.67	100.56	61.00	35.76	8.44	495.44
	± SE	2.59	7.14	12.89	5.20	4.18	0.88	71.42
VI	Mean	96.09	92.18	105.42	62.56	39.65	7.11	574.22
	± SE	3.34	11.72	11.90	5.30	4.14	0.97	98.66
VII	Mean	97.12	94.65	90.98	61.00	35.74	10.27	718.54
	± SE	1.96	10.66	15.37	6.15	3.65	1.10	121.18

cluster –IV (2.270), cluster –I and cluster –II (2.479), cluster –II and cluster –V (2.497), cluster –I and cluster –VI (2.533) indicated that cluster –I and II possess similar expression. The higher inter cluster distance indicated greater genetic diversity between the genotypes of those clusters, while lower cluster values between the clusters suggested that the genotypes of these clusters were not genetically diverse.

On the basis of cluster mean value, we can conclude that cluster -VII can be used as donor parent for the characters like plant height, spike length and grain yield, whereas cluster -VI can be used as donor for tillers per meter and grains per spike, cluster -IV as donor parent for character like days to 75% heading and cluster-III can be used as donor parent for characters like 1000- grain weight and spike length. Similar findings are reported by the Sanghera *et al*. (2014) and Rahman *et al*. (2015) studied genetic divergence of wheat genotypes using Mahalanobis D^2. Intercluster distances were more than intra cluster distances. The result of this study showed the high amount of genetic variation.

CONCLUSION

It is therefore present research findings concluded that the significant differences with respect to mean sum of square, genotypic and phenotypic variance, heritability, genetic advance for different characters under studied among different genotypes indicated the presence of considerable amount of genetic variation. All the characters were positively and significantly correlated. Genotypes of cluster -VII can be used as donor parent for the characters like plant height, spike length and grain yield, whereas cluster -VI can be used as donor for tillers per meter and grains per spike, cluster -IV as donor parent for character like days to 75% heading and cluster-III can be used as donor parent for characters like 1000-grain weight and spike length.

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