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Genetic variability, correlation, path coefficient and cluster analysis in bread wheat (*Triticum aestivum* L.) under rainfed conditions

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Abstract

A study was undertaken to estimate the genetic variability, correlation, path coefficient and genetic diversity in 40 bread wheat genotypes under rainfed condition grown in randomized block design with three replications at Kisan (PG) College, Simbhaoli during *rabi* season 2021-22. The analysis of variance showed highly significant differences among the genotypes for all the characters. The highest estimates of the phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were observed for grain yield/plant, tillers/plant and biological yield/plant. Grain yield/plant, biological yield/plant and harvest index showed high heritability coupled with high genetic advance as percent of mean indicating the influence of additive gene effects. Biological yield/plant, harvest index showed positive and significant correlation with grain yield/plant and exerted positive and high direct effect on grain yield/plant. D² analysis grouped the 40 genotypes into six clusters. The maximum inter cluster distance was observed between cluster V and VI. Hence, the genotypes belonging to cluster V and VI can be utilized in crop improvement programmes and for the development of high yielding varieties under rainfed conditions.

Keywords: Genetic variability, correlation, path coefficient, cluster, bread wheat

Introduction

Wheat (*Triticum aestivum* L.) of family Poaceae is agronomically and nutritionally most important cereal crop grown worldwide. It is a self pollinated crop and second most important staple food crop of world after rice. Wheat is considered as king of cereals accounting for 20% of human consumption of calories and is an important source of protein, vitamins and minerals. Three species of wheat *i.e.* *Triticum aestivum*, *Triticum durum* and *Triticum dicoccum* are presently grown as commercial crop in India. India is the second largest producer of wheat after China. In India wheat occupies an area of 31.05 million hectare with production of about 107.18 million tons during 2019-20 (Anonymous, 2020) [1]. Uttar Pradesh is the largest wheat producing state in India and accounts for 33.97% of total area under wheat cultivation in India.

Wheat is widely cultivated in India mainly under irrigated condition; however a large area is covered under rainfed. Out of an estimated 140.3 million hectare net cultivated area of the country, 79.44 million hectare (57%) is rainfed, contributing 44% of the total food grain production (Mishra *et al.*, 2014). Hence, the productivity in rainfed region can be enhanced by the development of cultivars that are well adapted to dry conditions. The magnitude of genetic variability present in a population is essential for effective genetic improvement. Correlation and path coefficient analysis provide a better understanding of the association of different characters with grain yield. The grain yield was positively correlated with biomass yield, harvest index, thousand kernel weight, plant height and number of grains/spike (Khanal *et al.*, 2020) [13]. Khokhar *et al.*, (2021) [14] found positive direct effect of days to maturity on grain yield. Singh *et al.*, (2021) [29] reported positive direct effect of biological yield per plant on grain yield. Hence, these traits could be used in breeding for grain yield in bread wheat.

Cluster analysis helps to understand the genetic relation between the genotypes and also facilitate the selection of genetically diverse parents in hybridization programme. Hence, the present investigation was carried out to determine the genetic variability, heritability, genetic diversity and direct and indirect effects of various characters on grain yield in bread wheat under rainfed conditions.

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Materials and Methods

The experimental material consisted of forty genotypes of wheat (*Triticum aestivum* L.) (Table 1) were obtained from Indian Institute of Wheat and Barley Research Karnal, Haryana. The experiment was laid in a randomized block design with three replications during winter (*rabi*) 2021-22 under rainfed conditions at Experimental Farm of Kisan (PG) College, Simbhaoli, Hapur (UP). In each replication, the genotypes were evaluated in single row of 3m length with row to row and plant spacing of 25 cm and 10cm respectively. During experiment only pre-sowing irrigation was applied to ensure proper seed germination. The data were recorded from five randomly selected plants from each genotype on eleven distinct morphological characters *viz.*, days to heading, days to maturity, plant height (cm), number of effective tillers/plant, spike length (cm), number of spikelets/spike, number of grains/spike, 1000-grain weight (g), grain yield/plant(g), biological yield/plant (g) and harvest index (%). Standard statistical procedure were used for the analysis of variance, genotypic and phenotypic coefficient of variation, heritability and genetic advance. The path coefficient analysis was done according to the method by Dewey and Lu (1959). Cluster analysis was done based on Mahalanobis D² method (1936)^[17].

Table 1: List of genotypes

1. DBW 88	21. Lok 01
2. DBW 222	22. PBW 703
3. DBW 303	23. PBW 723
4. DBW 187	24. PBW 780
5. HD 3059	25. PBW 701
6. C 306	26. PBW 712
7. HD 3118	27. PBW 725
8. HD 2824	28. PBW 698
9. HD 3226	29. PBW 702
10. HD 3086	30. PBW 550
11. HUW 468	31. PBW 1763
12. HUW 234	32. PBW 677
13. K 1006	33. PBW 34
14. K 1317	34. Raj 3765
15. K 0307	35. Sumai 3
16. NIAW 1415	36. WR 544
17. NI 5439	37. DPW 621-50
18. NW 1014	38. WH 147
19. NW 5054	39. WH 730
20. NW 2036	40. WH 1105

Results and Discussion

Analysis of variance and coefficient of variation

The analysis of variance for different characters is presented in Table 2 indicating significant differences among the genotypes for all the characters under study. The estimates of mean, range, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for various characters studied are presented in Table 3. The PCV values were higher than GCV values for all the characters indicating the influence of environment on the expression of characters. High PCV and GCV values were observed for grain yield/plant (33.92) and (32.80), tillers/plant (32.76) and (29.96), biological yield/plant (30.19) and (29.46), harvest index (27.31) and (26.09) indicating better opportunity for improvement in these traits through selection.

However, moderate PCV and GCV was observed for grains/spike (14.53) and (14.08), 1000 grains weight (11.86) and (11.61), spike length (9.62) and (7.38), plant height (7.65)

and (7.05). The magnitude of PCV ranged from 3.58 for days to maturity to 33.92 for grain yield/plant. The characters with high phenotypic coefficient of variation indicated more influence of environmental factors. Similar results on variability for different characters were reported by Mohapatra *et al.*, (2019)^[21], Shah *et al.*, (2019)^[27], Yadav *et al.*, (2021)^[34], Olbana *et al.*, (2021)^[23], Prasad *et al.*, (2021)^[24], Hassani *et al.*, (2022)^[10].

Heritability and expected genetic advance

The estimates of heritability and expected genetic advance for various characters studied are shown in Table 3. Heritability estimates were highest for 1000 grains weight (95.85), followed by biological yield/plant (95.22), grains/spike (93.89), grain yield/plant (93.50), harvest index (91.31), days to heading (90.20). High heritability indicated that the characters were least influenced by environmental factors. Fellahi *et al.*, (2013)^[9], Devesh *et al.*, (2018)^[5], Thapa *et al.*, (2019)^[32] and Hayadar *et al.*, (2020) also estimated high heritability for important morphological traits. Lowest heritability was observed for spike length (58.85).

Highest value of expected genetic advance expressed as percent of mean was observed for grain yield/plant (65.34), biological yield/plant (59.23), tillers/plant (56.44) and harvest index (51.36). High heritability coupled with high genetic advance (per cent of mean) was observed for grain yield/plant, biological yield/plant and harvest index which suggested that these characters can be considered as favourable for improvement through selection. Grains/spike and 1000 grain weight showed high heritability coupled with moderate genetic advance while high heritability with low genetic advance was observed for days to heading and days to maturity. Low heritability with low genetic advance values was found for spike length and spikelets/spike indicating slow progress through selection for these characters. Similar findings were also reported by Arya *et al.*, (2017)^[2], Vaghela *et al.*, (2021)^[33] and Lamara *et al.*, (2022)^[16].

Correlation and path coefficient analysis

Correlation analysis estimates the degree and direction of the relationship between variables and are widely used in breeding selection programs. The phenotypic and genotypic correlation for all the characters is presented in Table 4. Genotypically, the grain yield/plant exhibited highly significant positive correlation with biological yield/plant (0.639), 1000 grain weight (0.467), tillers/plant (0.466), harvest index (0.428), grains/spike (0.328), spike length (0.278) and plant height (0.269). Harvest index showed negative and highly significant relationship with biological yield/plant (-0.384), tillers/plant (-0.301) and number of spikelets/spike (-0.282). Biological yield/plant exhibited positive and highly significant association with tillers/plant while a negative and highly significant correlation with days to heading and days to maturity at both phenotypic and genotypic level. Similar findings were also reported by Kandel *et al.*, (2017)^[12], Ojha *et al.*, (2018)^[22], Rathod *et al.*, (2019)^[25], Maurya *et al.*, (2020)^[19] and Semahegn *et al.*, (2021)^[26].

Path coefficient analysis measures the direct influence of one variable upon the other and allow partitioning of correlation coefficient into components of direct and indirect effects. Estimates of direct and indirect effect are presented in Table 5 and 6. Genotypic path analysis (Table 5) revealed that biological yield/plant showed maximum direct effect (1.0014)

on grain yield/plant followed by harvest index (0.8242). Days to heading, spike length and spikelets/spike also exhibited positive direct effect while days to maturity, plant height, tillers/plant, grains/spike and 1000 grain weight showed negative direct effect on grain yield/plant. Tillers/plant showed maximum indirect effect (0.7594) on grain yield/plant via biological yield/plant. Similar results were also observed by Baye *et al.*, (2020) [3], Elahi *et al.*, (2020) [7], Singh *et al.*,

(2021) [30] and Ezici *et al.*, (2022) [8].

Phenotypic path analysis (Table 6) showed that biological yield/plant had highest positive direct effect (0.9715) on grain yield/plant. Days to heading, plant height, tillers/plant, grains/spike and 1000 grain weight showed negative direct effect on grain yield/plant. Tillers/plant showed maximum indirect effect (0.6795) on grain yield/plant via biological yield/plant.

Table 2: Mean squares from analysis of variance (ANOVA) of eleven characters in forty genotypes of bread wheat

Source of variation	D.F	Days to Heading	Days to maturity	Plant Height (cm)	Tillers per plant	Spike length (cm)	No of spikelets per spike	Grains per spike	1000 grain weight (g)	Biological yield per plant (g)	Harvest index (%)	Grain yield per plant (g)
Replication	2	1.88	0.78	0.22	0.36	0.01	0.31	6.16	0.82	0.86	6.40	0.06
Treatment	39	67.57**	42.01**	89.08**	2.28**	1.75**	4.24**	139.22**	32.74**	74.28**	179.19**	7.41**
Error	78	2.36	2.32	5.01	0.14	0.33	0.64	2.96	0.47	1.22	5.51	0.17

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

Table 3: Mean, range, GCV, PCV, Heritability and genetic advance for eleven characters of bread wheat

Genotypes	Mean	Min	Max	GCV (%)	PCV (%)	Heritability (%)	Genetic advance(GA)	GA as % of mean
Days to Heading	74.13	67.00	86.00	6.29	6.62	90.20	9.12	12.30
Days to maturity	110.13	104.33	121.67	3.30	3.58	85.07	6.91	6.28
Plant Height (cm)	75.13	62.49	94.63	7.05	7.65	84.85	10.05	13.37
Tillers per plant	2.82	1.43	5.30	29.96	32.76	83.62	1.59	56.44
Spike length (cm)	9.33	7.14	10.66	7.38	9.62	58.85	1.09	11.66
No of spikelets per spike	17.17	13.13	19.63	6.38	7.90	65.19	1.82	10.60
Grains per spike	47.85	30.10	58.87	14.08	14.53	93.89	13.45	28.11
1000 grain weight (g)	28.26	19.80	32.78	11.61	11.86	95.85	6.62	23.41
Biological yield per plant (g)	16.75	5.94	30.43	29.46	30.19	95.22	9.92	59.23
Harvest index (%)	29.16	12.25	47.60	26.09	27.31	91.31	14.98	51.36
Grain yield per plant (g)	4.74	2.21	8.10	32.80	33.92	93.50	3.09	65.34

Table 4: Genotypic (G) and phenotypic (P) correlation coefficient for different characters in bread wheat

Characters		Days to heading	Days to maturity	Plant height (cm)	Tillers per plant	Spike length (cm)	No. of Spikelets per spike	Grains per spike	1000 grain weight (g)	Biological yield/plant (g)	Harvest index (%)	Grain yield per plant (g)
Days to heading	G	1.000	0.784**	0.168	-0.076	0.228*	0.271**	0.200*	0.280**	-0.065	0.222*	0.099
	P	1.000	0.672**	0.172	-0.075	0.191*	0.200*	0.201*	0.261**	-0.053	0.211*	0.101
Days to maturity	G		1.000	-0.189*	-0.105	0.165	0.234*	0.159	0.199*	-0.102	0.246**	0.099
	P		1.000	-0.144	-0.072	0.137	0.196*	0.146	0.177	-0.097	0.228*	0.098
Plant height (cm)	G			1.000	0.288**	0.298**	0.167	0.087	0.308**	0.427**	-0.112	0.269**
	P			1.000	0.305**	0.387**	0.250**	0.127	0.278**	0.423**	-0.097	0.270**
Tillers per plant	G				1.000	0.250**	0.269**	0.123	0.287**	0.758**	-0.301**	0.466**
	P				1.000	0.266**	0.287**	0.134	0.271**	0.699**	-0.267**	0.427**
Spike length (cm)	G					1.000	0.448**	0.397**	0.461**	0.402**	-0.149	0.278**
	P					1.000	0.550**	0.395**	0.349**	0.363**	-0.085	0.276**
No. of Spikelets per spike	G						1.000	0.449**	0.162	0.440**	-0.282**	0.223*
	P						1.000	0.445**	0.148	0.395**	-0.208*	0.220*
Grains per spike	G							1.000	0.005	0.433**	-0.117	0.328**
	P							1.000	0.013	0.426**	-0.093	0.332**
1000 grain weight (g)	G								1.000	0.352**	0.205*	0.467**
	P								1.000	0.333**	0.195*	0.440**
Biological yield/ plant (g)	G									1.000	-0.384**	0.639**
	P									1.000	-0.378**	0.628**
Harvest index (%)	G										1.000	0.428**
	P										1.000	0.445**
Grain yield per plant (g)	G											1.000
	P											1.000

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

Table 5: Direct effect (bold values) and indirect effect for different characters on grain yield at genotypic level

Characters	Days to Heading	Days to maturity	Plant Height (cm)	Tillers per plant	Spike length (cm)	No of spikelets per spike	Grains per spike	1000 grain weight (g)	Biological yield per plant (g)	Harvest index (%)	R with Grain yield per plant (g)
Days to Heading	0.0098	-0.0213	-0.0112	0.0024	0.0104	0.0110	-0.0067	-0.0137	-0.0650	0.1830	0.099
Days to maturity	0.0077	-0.0271	0.0126	0.0033	0.0076	0.0095	-0.0053	-0.0097	-0.1020	0.2025	0.099
Plant Height (cm)	0.0017	0.0051	-0.0667	-0.0092	0.0136	0.0068	-0.0029	-0.0151	0.4281	-0.0925	0.269**
Tillers per plant	-0.0008	0.0029	-0.0192	-0.0319	0.0114	0.0109	-0.0041	-0.0141	0.7594	-0.2484	0.466**
Spike length (cm)	0.0022	-0.0045	-0.0198	-0.0080	0.0457	0.0182	-0.0132	-0.0226	0.4027	-0.1231	0.278**
No of spikelets per spike	0.0027	-0.0063	-0.0111	-0.0086	0.0205	0.0407	-0.0150	-0.0079	0.4404	-0.2320	0.223*
Grains per spike	0.0020	-0.0043	-0.0058	-0.0039	0.0181	0.0183	-0.0333	-0.0003	0.4335	-0.0963	0.328**
1000 grain weight (g)	0.0028	-0.0054	-0.0206	-0.0092	0.0211	0.0066	-0.0002	-0.0489	0.3524	0.1688	0.467**
Biological yield per plant (g)	-0.0006	0.0028	-0.0285	-0.0242	0.0184	0.0179	-0.0144	-0.0172	1.0014	-0.3162	0.639**
Harvest index (%)	0.0022	-0.0067	0.0075	0.0096	-0.0068	-0.0115	0.0039	-0.0100	-0.3842	0.8242	0.428**

Residual effect = 0.0533

Table 6: Direct effect (bold values) and indirect effect for different characters on grain yield at phenotypic level

Characters	Days to Heading	Days to maturity	Plant Height (cm)	Tillers per plant	Spike length (cm)	No of spikelets per spike	Grains per spike	1000 grain weight (g)	Biological yield per plant (g)	Harvest index (%)	R with Grain yield per plant (g)
Days to Heading	-0.0137	0.0035	-0.0099	0.0017	0.0047	0.0051	-0.0028	-0.0076	-0.0515	0.1713	0.101
Days to maturity	-0.0092	0.0052	0.0082	0.0017	0.0034	0.0050	-0.0020	-0.0052	-0.0938	0.1854	0.099
Plant Height (cm)	-0.0024	-0.0008	-0.0573	-0.0070	0.0095	0.0064	-0.0018	-0.0081	0.4107	-0.0793	0.270**
Tillers per plant	0.0010	-0.0004	-0.0175	-0.0229	0.0065	0.0073	-0.0019	-0.0079	0.6795	-0.2172	0.427**
Spike length (cm)	-0.0026	0.0007	-0.0222	-0.0061	0.0246	0.0140	-0.0056	-0.0102	0.3524	-0.0692	0.276**
No of spikelets per spike	-0.0027	0.0010	-0.0143	-0.0066	0.0135	0.0254	-0.0062	-0.0043	0.3835	-0.1688	0.220*
Grains per spike	-0.0027	0.0008	-0.0073	-0.0031	0.0098	0.0113	-0.0140	-0.0004	0.4139	-0.0760	0.332**
1000 grain weight (g)	-0.0036	0.0009	-0.0159	-0.0062	0.0086	0.0038	-0.0002	-0.0291	0.3237	0.1583	0.440**
Biological yield per plant (g)	0.0007	-0.0005	-0.0242	-0.0160	0.0089	0.0100	-0.0060	-0.0097	0.9715	-0.3072	0.628**
Harvest index (%)	-0.0029	0.0012	0.0056	0.0061	-0.0021	-0.0053	0.0013	-0.0057	-0.3669	0.8134	0.445**

Residual effect = 0.0597

Genetic divergence

On the basis of D^2 values, all the 40 genotypes were grouped in 6 clusters (Table 7). Among the six clusters, cluster III was the largest, comprising of 10 genotypes followed by cluster II with 8 genotypes, cluster I with 7 genotypes, cluster IV with 6 genotypes, cluster V with 5 genotypes and cluster VI with 4 genotypes. The clustering pattern revealed that the groups of genotypes which were together in a cluster also indirectly proved their stable performance.

The inter and intra cluster distance among the genotypes is presented in Table 8. The maximum intra-cluster distance was observed in cluster III (2.342) followed by cluster VI (2.197) and cluster V (2.168) indicating differences in genotypes within the cluster. The least intra-cluster distance was found in cluster I (1.939) indicating close resemblance between the genotypes presented in this cluster. The highest inter-cluster

distance was observed between cluster V and VI (6.059) indicating a high degree of genetic diversity. The lowest inter-cluster distance was observed between cluster II and III (2.413) followed by cluster I and II (2.655) indicating that these clusters were relatively less divergent.

The cluster mean for each character is tabulated in Table 9. Highest mean values for days to heading (82.50) and days to maturity (116.78) was observed in cluster IV while least mean values for these characters was found in cluster V and VI. Cluster VI exhibited the highest mean values for tillers/plant (4.27), spikelets/spike (18.22), 1000 grain weight (30.76), biological yield/plant (24.84) and grain yield/plant (6.91). Highest mean values for grains/spike (51.49) and harvest index (34.68) was recorded in cluster IV. Cluster V exhibited lowest mean values for plant height (67.95), tillers/plant (2.23), spike length (7.82), spikelets/spike (15.40) and

grains/spike (38.82). Singh *et al.*, (2019) [28], Majid and Dar (2020), Kumar *et al.*, (2021), Tanveer *et al.*, (2021) and

Chaudhary *et al.*, (2022) also studied the genetic divergence in bread wheat.

Table 7: Clustering pattern of 40 genotypes of bread wheat on the basis of D² statistic

Cluster No.	No. of genotypes	Genotypes in cluster
I	7	DBW 303, HD 3086, HUW 468, NW 1014, NW 2036, PBW 780, WH 147
II	8	K 1317, NIAW 1415, PBW 723, PBW 698, PBW 550, PBW 701, PBW 677, DPW 621-50
III	10	HD 3118, HD 2824, HD 3226, K 1006, K 0307, NI 5439, NW 5054, PBW 34, Sumai 3, WH 730
IV	6	DBW 88, DBW 222, DBW 187, C 306, Lok 01, WH 1105
V	5	HD 3059, HUW 234, PBW 703, PBW 712, WR 544
VI	4	PBW 725, PBW 702, PBW 1763, Raj 3765

Table 8: Inter and intra-cluster (bold values) distances involving forty genotypes of bread wheat

Clusters	I	II	III	IV	V	VI
I	1.939					
II	2.655	2.080				
III	2.964	2.413	2.342			
IV	4.107	3.693	3.312	2.167		
V	3.555	4.948	4.222	5.317	2.168	
VI	4.413	2.765	2.953	4.690	6.059	2.197

Table 9: Cluster mean for eleven characters in bread wheat

Clusters	Days to Heading	Days to maturity	Plant Height (cm)	Tillers per plant	Spike length (cm)	No of spikelets per spike	Grains per spike	1000 grain weight (g)	Biological yield per plant (g)	Harvest index (%)	Grain yield per plant (g)
I	73.19	108.81	74.25	2.45	9.05	17.31	49.02	24.01	15.31	21.97	3.27
II	72.92	109.42	76.06	3.28	10.04	17.85	47.32	30.00	18.72	22.61	4.15
III	73.27	109.00	78.20	2.75	9.57	16.63	49.39	28.56	17.27	34.40	5.86
IV	82.50	116.78	73.77	2.27	9.54	17.81	51.49	30.40	14.84	34.68	5.03
V	70.53	108.73	67.95	2.23	7.82	15.40	38.82	26.26	10.38	33.27	3.38
VI	72.25	108.42	78.15	4.27	9.35	18.22	48.88	30.76	24.84	28.32	6.91

Conclusion

From the present study it is concluded that the analysis of variance showed highly significant differences among the genotypes for all the characters studied under rainfed condition. PCV values were higher than GCV values but the difference variability between these two estimates for all the characters was very close. The characters grain yield/plant, biological yield/plant and harvest index were recorded with high heritability and genetic advance values. Correlation analysis showed positive and highly significant association of grain yield with biological yield/ plant followed by thousand grain weight, tillers/plant and harvest index. Cluster analysis revealed highest inter cluster distance between cluster V and VI indicating genetic diversity among the genotypes.

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