Journal of AgriSearch, 10 (3): 151-157
An Open Access International Peer Reviewed Quarterly

ISSN : 2348-8808 (Print), 2348-8867 (Online)
https://doi.org/10.21921/jas.v10i03.13765

Genetic Variability, Character Association and Component Analysis in wheat

RAVI S DVIVEDI[1], BRIJESH SINGH[1], VN PATHAK[1*], S P VERMA[1] AND K K PANDEY[2]

ABSTRACT

Twenty Indigenous and exotic genotypes of wheat were analysed for variability for various agronomical and morphological characters. The highest mean was observed for days to maturity (108.51) followed by plant height (82.03), days to 50% flowering (78.31) and number of grains per spike (56.44). The estimates of PCV were slightly higher than GCV for all traits. The highest genotypic and phenotypic coefficient of variation was recorded for Flag leaf area, Spike weight, biological yield per plant and Harvest Index. High heritability (h^2) coupled with high genetic advance for biological yield per plant, Flag leaf area, Plant height and Days to 50% flowering. It revealed that by increasing the value of these traits, grain yield can be drastically increased. Path coefficient analysis revealed that maximum positive direct contribution toward yield by biological yield per plant, Harvest index, Days to 50% flowering and no. of seeds per spike. The results revealed that these traits may serve as effective selection attributes during selection in the breeding program for yield improvement in wheat. Genotypes were grouped into five distinct and non-overlapping clusters. Cluster (II) emerged with highest number of 8 genotypes. The maximum general inter-cluster distance was observed between cluster (III) and cluster (V) (566.18), and the maximum intra-cluster distance was found for cluster (IV) (360.80). Thus, crossing between the genotypes belonging to cluster pairs separated by very high inter-cluster distances as mentioned above, may result in maximum hybrid vigor and the highest number of useful segregates.

Keywords: Wheat, (Triticum aestivum L), co-relation coefficient and path analysis

ARTICLE INFO

Received on	:	12.06.2023
Accepted on	:	15.09.2023
Published online	:	30.09.2023

INTRODUCTION

Wheat (*Triticum aestivum*) is the world's largest famous energy-rich cereal crop. It covers 17% of the total cultivated land in the world. Wheat has been described as the king of cereals because of the acreage it occupies, high productivity and the prominent position it holds in the international food grain trade, it is a C3 plant grown from temperate irrigated to dry and high rainfall areas and from warm humid to dry cold environment. Undoubtedly, this wide adaptation has been possible due to the complex nature of the plants genome which provides great plasticity to the crop. The world acreage under wheat crop during 2021-22 was 221.67 million hectares with production of 778.60 million metric ton with an average production 33.08 qt/ha. In India the total area for wheat crop during 2021-22 31.68 million hectares with the production of 106.41 million metric ton and productivity was 28.05 qt/ha. In crop plants the most of the traits are quantitative in nature. Grain yield is a complex trait and highly influenced by the action and interactions of various component characters (Grafius 1960). The availability of genetic variability is the basic pre-requisite for genetic improvement through systematic breeding programme. For developing wheat varieties, indigenous and exotic germplasm is the back bone of successful breeding programme for improving yield and yields contributing traits. Nature always favors the plant having much variability in terms of promises and adaptation across the year and locations. Correlation analysis is used as effective tools to determine the relationship among different trait in genetic diverse population for encashment of crop improvement process (Dhami *et al.,* 2018). Correlation coefficient provides a better understanding of the different traits with grain yield. The study of association among various traits is useful to breeders in selecting genotypes possessing groups of desired traits. Path coefficient analysis provides a more information among variables. Path coefficient measures the magnitude of direct and indirect contribution of the components characters to a complex character and it has been defined standardized regression coefficient which split the correlation coefficient in to direct and indirect effects. Path coefficient analysis has been used by plant breeders to assist in identifying traits that are useful as selection criteria to improve yield (Dewey and Lu 1959, Ahmed *et al.,* 2003). The objective of the study to find out correlation co-efficient among various characters, direct and indirect effects and yield components on grain yield by path coefficient analysis. The D2 analysis classifies the genotypes into relatively homogeneous groups in such a way that, within the cluster

---

[1] Deptt. of Genetics & Plant Breeding, S.M.M. Town Post Graduate College Ballia, JNCU, Ballia Uttar Pardesh, India
[2] Deptt. of Agronomy, S.M.M. Town Post Graduate College, JNCU, Ballia, Uttar Pradesh, India
*Corresponding Author E-mail: vijayanand.pathak76@gmail.com

Table 1: ANOVA for 12 Characters in Wheat (*Triticum aestivum* L.)

Sl. No.	Source of variation	d.f	Days to 50% Flowering	Flag leaf area in cm^2	Tillers per plant	Plant height	Spikelet length	Spike weight	Days to maturity	No. of seed per spike	Biological yield	Harvest index	1000 grain weight	Grain yield
1.	Replication	3	1.01	1.13	0.45	0.96	2.24	2.14	0.84	1.86	0.01	0.43	1.46	0.32
2.	Treatment	19	201.87	297.34	7.70	229.42	3.76	20.73	138.25	245.54	312.50	138.26	62.17	27.17**
3.	Error	38	1.24	1.03	0.30	1.13	0.05	0.44	1.85	2.50	0.98	1.29	0.98	0.52

these characters. Characters which exhibited high heritability indicated that these characters were least influenced by environment and showed least GXE interaction. Only heritable component of the total variation is important in breeding. The results are in conformity with the finding of Endaic and Waines (1989).

The estimation of simple correlation coefficient between eleven characters of exotic and indigenous germplasm of wheat under study is presented in Table 5. Grain yield per plant showed highly significant and positive correlation with biological yield per plant (0.551) followed by tillers per plant (0.459) and plant height (0.409). Its showed significant correlation with Harvest index (0.344), Spike weight (0.269) and Spike length (0.267). Thus, these characters come out as most important factors in influencing grain yield in wheat. These results are similar to that of Verma *et al.* 2019. On the other hand, few quantitative traits were inter correlated with each other *viz.* biological yield per plant showed highly significant and positive correlation with plant height (0.492). Days to maturity exhibited a highly significant and positive association with days to 50% flowering (0.937), Tillers per plant (0.596), Plant height (0.394) and spike length (0383). Spike weight showed a highly significant and positive correlation with tillers per plant (0.481) and a significant association with plant height (0.284). Spike length showed highly significant and positive correlation with days to 50% flowering (0.338), tillers per plant (0.553) and plant height (0.412). Plant height showed highly significant and positive correlation with days to 50% flowering (0.450), flag leaf area (0.471) and tillers per plant (0.641). Tillers per plant showed highly significant and positive association with days to 50% flowering (0.677) and flag leaf area (0.382). Similar result was also reported by Kumar *et al.* 2019. The above discussion revealed that all the highly significant estimates of correlation coefficient observed among the important yield components. This suggests that selection would be quite efficient in improving yield and these yield components in wheat.

Path coefficient analysis is a tool to partition the observed correlation coefficient into direct and indirect effects of yield components on grain yield. Path analysis provides clearer picture of character associations for formulating efficient selection strategy. The results of path coefficient analysis carried out using simple correlation coefficients among 11 characters are given in Table 6. Results diversity is minimized and between clusters diversity is maximized. The respective genotypes from diverse clusters can be utilized in breeding programme.

MATERIALS AND METHODS

The experimental materials comprised of twenty Indigenous and exotic genotypes of wheat (Including two checks HD-3086 and PBW-502). These genotypes exhibited wide spectrum of variability for various agronomical and morphological characters. The checks used in experiment were well adapted varieties of this region, these entries were evaluated in Randomized Block Design (RBD) with three replications during *Rabi* 2019-20 at Nidhariya Agriculture Farm of Shri Murli Manohar Town Post Graduate College Ballia. Each genotype was sown in 2.5 meters length, row to row spaced 30cm and intra row spacing of 5cm all recommended cultural practiced and plant protection measures were applied to raise to healthy crop.

The data were recorded on twelve quantitative traits namely days to 50% flowering, flag leaf area (cm^{2}), plant height (cm), spike length (cm), No of seeds per spike, tillers per plant, days to maturity, spike weight (g), biological yield (g), harvest index (%), test weight (g) and grain yield/plant (g). From five randomly selected plants and days to 50% flowering and days to maturity were recorded on plot basis and all data were analyzed by standard statistical method.

RESULTS AND DISCUSSION

The analysis of variance revealed highly significant differences among the genotypes for all the quantitative characters under study (Table 1 & 2). The genotype coefficient of variation was found less than phenotypic coefficient of variation indicating the effect of environment in the development of character (Table 3 & 4). This laid the basis for large scope of selection due to the genotypic coefficient of variation as these characters were genetically potent for selection in crops like wheat. Similar results have been reported by Shah and Deora (2002) and Singh *et al.* (2013).

The high heritability of biological yield high genetic gain followed by days to 50% flowering, flag leaf area, plant height, spikelet length, are equal and high genetic gain. Presence of additive nature of genetic variability was indicated. It can be concluded that since these characters are highly responsible for selection. Superior genotype can be evolved through selection on express of

Table 2: Mean value of various plant characters in wheat (*Triticum aestivum L.*)

Sr. No.	Variety	Days to 50% flowering	Flag leaf area in cm²	Tillers per plant	Plant height in cm	Spikelet length in cm	Spike weight in gm.	Days to maturity	No. of seed per spike	Biological yield	Harvest index	1000 grain weight	Grain yield
1	IBWSN 1082	87	51.3167	10.2667	84.8533	11.3867	7.0333	117	35.58	49.3	31.1067	32.8667	15.3267
2	STEMRRSN 6110	81.6667	49.8467	9.8667	85.5467	12.08	8.3333	117.6667	43.5633	52.63	29.6633	33.8333	15.6067
3	STEMRRSN 6060	79	51.79	10.2667	86.64	9.2467	14.3	109.3333	70.2233	46.8833	38.9667	39.4333	18.2633
4	WR 544	70	48.9567	10.3333	93.28	10.34	9.9333	102	52.6967	68.1033	32.6067	37.5667	22.15
5	GW 366	76.6667	33.6533	10.0667	89.1	11.5333	11.2	104.6667	60.03	54.5933	36.7067	41.3667	20.0433
6	SBWON 11	79	47.5567	10.8667	87.3733	11.1133	13.4667	107	58.0533	49.74	36.9033	39.5	18.9567
7	ESBWYT 32	83.3333	43.19	10.95	70.8733	11.6667	11.5667	111.6667	60.0267	59.8667	35.6067	33.5	21.3233
8	ESBWYT 24	84.3333	39.1467	10.8	76.0467	9.9067	9.9333	111.6667	47.33	46.02	34.2967	43.4667	15.7833
9	ESBWYT 48	84.6667	42.5967	9.7333	74.68	9.58	15.0667	113	68.5	45.6667	32.99	35.1667	15.18
10	HTWYT 42	74	48.32	10.2	73.9667	9.72	12.8333	102.3333	58.8333	39.27	39.91	36.9	15.6933
11	HRWSN 2101	84	45.9867	12.2	87.84	11.42	12.4333	112.3333	53.5233	39.6733	40.7167	49.2667	16.1667
12	SAWSN 3032	86	44.75	11.9333	96.74	12.5933	17.4	110.3333	70.6433	50.2533	36.5467	32.4667	18.3333
13	IBWSN 1006	83	49.4133	11.8	88.77	12.2133	15.1667	113	53.4167	64.6067	24.2467	40.8	15.6667
14	SAWYT 344	87.6667	52.97	13.4	89.6067	12.5667	13.2333	118	55.6833	40.38	39.6733	37.4667	15.9767
15	IBWSN 1081	83	28.8467	11.6	76.9267	12.5333	14.6667	112.6667	46.41	36.7267	57.1667	33.8	21
16	IBWSN 1168	82	24.4633	10.2	81.76	11.0267	12.1	112.6667	58.8933	47.3567	45.9467	39.2333	21.7667
17	ESWYT 112	70	33.3033	12.0667	83.3867	12.84	15.1	102.3333	64.2767	57.52	35.5733	44	20.4667
18	HTWYT 5	69.3333	22.3767	10.4133	81.58	10.3333	11.8667	101	59.8267	63.1667	29.46	38.4667	18.6
19	HD 3086	61.6667	32.28	7.1333	69.42	10.6	9.7667	96.6667	49.06	32.6967	37.7233	45.5667	12.4667
20	PBW 502	60	26.8067	6.4	62.36	10.08	9.7667	94.9533	62.25	33.7267	34.8933	40.9667	11.7667
21	Mean	78.3167	40.8785	10.5248	82.0375	11.139	12.2583	108.5143	56.441	48.909	36.5352	38.7817	17.5268

Table 3: Mean, Range and Coefficient of variation (%) for 12 Characters in 20 germplasm of Wheat (*Triticum aestivum* L.)

Sl. No.	Characters	Mean	Range		Coefficient of variation (%)
			Minimum	Maximum	
1	Days to 50% maturity	78.31	60.00	87.66	1.42
2	Flag leaf area (cm^2)	40.87	22.37	52.97	2.48
3	Tillers per plant	10.52	6.40	13.40	5.23
4	Plant height (cm)	82.03	62.36	62.36	1.29
5	Spike length(cm)	11.13	9.24	9.24	2.17
6	Spike weight (gm.)	12.25	7.03	7.03	5.44
7	Days to maturity	108.51	94.95	94.95	1.25
8	No. of seed per spike	56.44	35.58	35.58	2.80
9	Biological yield	48.90	32.69	32.69	2.02
10	Harvest index	36.53	24.24	24.24	3.11
11	1000 grain weight	38.78	32.46	32.46	2.56
12	Grain yield	17.52	11.76	22.15	4.13

revealed that biological yield per plant (1.167) had positive and significant association with grain yield which exerted maximum direct effect on grain yield followed by harvest index (1.074), days to 50% flowering (0.308) and no of seed per spike (0.304). Thus, biological yield per plant, harvest index and days to 50% flowering emerged as major direct yield components. These traits could be considered as important traits for selection in a breeding program for higher grain yield of the bread wheat. These results are similar to those of Jee *et al.* (2019) and Singh *et al.* (2021).

On the basis of the Non-hierarchical Euclidean cluster analysis, the nineteen genotypes and one check varieties were grouped into five distinct and non-over lapping clusters as presented in Table 7. Cluster (II) emerged with highest number of 8 genotypes followed by cluster (I) having 5 genotypes; cluster (III) with 3 genotypes, cluster (IV) and (V) possessing 2 genotypes each respectively. The discrimination of varieties/lines into so many discrete clusters suggested the presence of high degree of genetic diversity in the material evaluated. Earlier workers have also reported substantial genetic divergence in the wheat genotypes (Mishra *et al.* 2015 and Yadav *et al.* 2019).

The estimates of intra and inter cluster distance have been depicted in Table 8. The maximum generalized inter cluster distance was observed between cluster (III) and cluster (V) (566.18) followed by cluster (III) and cluster (IV) (555.03).

Table 4: Grand Mean, PCV, GCV, ECV, Standard Error and CD of 12 Characters in Wheat (*Triticum aestivum* L.)

Sr. No.	Characters	Grand mean	PCV	GCV	ECV	Std. eror	h^2 Broad sense	Genetic advancement (5%)	Genetic advance as %mean	CD	
										5%	1%
1	Days to 50% flowering	78.31	10.53	10.44	1.42	0.62	0.98	16.69	21.31	1.84	2.47
2	Flag leaf area cm^2	40.87	24.43	24.31	2.48	0.57	0.98	20.36	49.82	1.68	2.25
3	Tillers per plant	10.52	15.81	14.91	5.23	0.30	0.89	3.05	29.00	0.91	1.21
4	Plant height cm	82.03	10.71	10.63	1.29	0.59	0.98	17.83	21.742	1.76	2.35
5	Spikelet length cm	11.13	10.21	9.98	2.17	0.13	0.95	2.23	20.09	0.40	0.53
6	Spike weight gm.	12.25	21.90	21.21	5.44	0.37	0.93	5.18	42.32	1.10	1.47
7	Days to maturity	108.51	6.33	6.21	1.25	0.76	0.96	13.61	12.54	2.24	3.01
8	No. of seed per spike	56.44	16.19	15.94	2.80	0.89	0.97	18.26	32.35	2.61	3.50
9	Biological yield /plant	48.90	20.93	20.83	2.02	0.55	0.99	20.89	42.71	1.63	2.19
10	Harvest index %	36.53	18.75	18.49	3.11	0.64	0.97	13.72	37.56	1.88	2.52
11	1000 grain weight	38.78	11.92	11.64	2.56	0.55	0.95	9.08	23.42	1.64	2.20
12	Grain yield	17.52	17.50	17.00	4.13	0.40	0.94	5.96	34.03	1.19	1.60

Table 5: Genotypic and Phenotypic Correlation Coefficient for 12 Characters in Wheat (*Triticum aestivum* L.)

Sr. no.	Characters	Days to 50% flowering	Flag leaf area in cm2	Tillers per plant	Plant height in cm	Spikelet length in cm	Spike weight in gm.	Days to maturity	No. of seed per spike	Biological yield	Harvest index	1000 grain weight	Grain yield
1	Days to 50% flowering	r(g)1.000 **r(p)1.000**	0.505** **0.502****	0.716** **0.677****	0.458** **0.450****	0.348* **0.338****	0.258 **0.242**	0.948** **0.937****	-0.148 **-0.139**	0.090 **0.089**	0.110 **0.115**	-0.402** **-0.386****	0.207 **0.211**
2	Flag leaf area in cm2		r(g)1.000 **r(p)1.000**	0.399** **0.382****	0.475** **0.471****	0.053 **0.051**	0.030 **0.027**	0.508** **0.498***	-0.130 **-0.127**	0.142 **0.140**	-0.313* **-0.305***	-0.238 **-0.231**	-0.137 **-0.130**
3	Tillers per plant			r(g)1.000 **r(p)1.000**	0.671** **0.641****	0.595** **0.553****	0.534** **0.481****	0.626** **0.596****	0.034 **0.029**	0.330* **0.309***	0.139 **0.134**	-0.121 **-0.097**	0.482** **0.459****
4	Plant height in cm				r(g)1.000 **r(p)1.000**	0.419** **0.412****	0.290* **0.284***	0.407** **0.394****	0.040 **0.044**	0.497** **0.492****	-0.150 **-0.152**	-0.098 **-0.100**	0.424** **0.409***
5	Spikelet length in cm					r(g)1.000 **r(p)1.000**	0.264 **0.246**	0.391** **0.383****	-0.202 **-0.194**	0.176 **0.167**	0.135 **0.127**	-0.160 **-0.158**	0.285* **0.267***
6	Spike weight in gm.						r(g)1.000 **r(p)1.000**	0.091 **0.072**	0.699** **0.673****	0.050 **0.046**	0.256 **0.214**	-0.049 **-0.051**	0.287* **0.269***
7	Days to maturity							r(g)1.000 **r(p)1.000**	-0.309* **-0.298**	0.074 **0.069**	0.060 **0.063**	-0.412** **-0.392****	0.121 **0.120**
8	No. of seed per spike								r(g)1.000 **r(p)1.000**	0.080 **0.080**	0.020 **0.017**	0.042 **0.030**	0.195 **0.190**
9	Biological yield									r(g)1.000 **r(p)1.000**	-0.581** **-0.569****	-0.203 **-0.194**	0.562** **0.551****
10	Harvest index										r(g)1.000 **r(p)1.000**	-0.014 **-0.013**	0.327* **0.344***
11	1000 grain weight											r(g)1.000 **r(p)1.000**	-0.233 **-0.223**

*Significance at 5% level & 1% respectively

Table 6: Direct and Indirect effect at Genotypic Level of different Quantitative Characters on yield in Wheat (*Triticum aestivum L.*)

Sr. no.	Characters	Days to 50% flowe-ring	Flag leaf area in cm²	Tillers per plant	Plant height in cm	Spikelet length in cm	Spike weight in gm.	Days to matu-rity	No. of seed per spike	Biolog ical yield	Harv-est index	1000 grain weight	Grain yield
1	Days to 50% flowering	**0.308**	0.031	-0.046	0.003	0.032	-0.080	-0.198	-0.045	0.104	0.118	-0.021	0.207
2	Flag leaf area in cm²	0.156	**0.062**	-0.026	0.003	0.005	-0.009	-0.106	-0.040	0.166	-0.336	-0.012	-0.137
3	Tillers per plant	0.221	0.025	**-0.064**	0.005	0.055	-0.166	-0.131	0.010	0.385	0.149	-0.006	0.482**
4	Plant height in cm	0.141	0.030	-0.043	**0.007**	0.039	-0.090	-0.085	0.012	0.580	-0.161	-0.005	0.424**
5	Spikelet length in cm	0.107	0.003	-0.038	0.003	**0.092**	-0.082	-0.082	-0.061	0.205	0.145	-0.008	0.285*
6	Spike weight in gm.	0.080	0.002	-0.034	0.002	0.024	**-0.310**	-0.019	0.212	0.058	0.275	-0.003	0.287*
7	Days to maturity	0.292	0.032	-0.040	0.003	0.036	-0.028	**-0.209**	-0.094	0.086	0.064	-0.021	0.121
8	No. of seed per spike	-0.046	-0.008	-0.002	0.000	-0.019	-0.217	0.065	**0.304**	0.093	0.022	0.002	0.195
9	Biological yield	0.028	0.009	-0.021	0.003	0.016	-0.016	-0.016	0.024	**1.167**	-0.623	-0.011	0.562**
10	Harvest index	0.034	0.019	-0.009	-0.001	0.013	-0.079	-0.013	0.006	-0.677	**1.074**	-0.001	0.327*
11	1000 grain weight	-0.124	-0.015	0.008	-0.001	0.015	0.015	0.086	0.013	-0.237	-0.015	**0.051**	-0.233

R SQUARE = 0.9594 RESIDUAL EFFECT=0.2016

Table 7: Clustering pattern of 20 wheat genotypes on the basis of Non-hierarchical Euclidean Cluster analysis for 5 characters

Cluster	No. of Genotype	Genotypes
1	5	IBWSN- 1082, -6110, ESBWYT-32, IBWSN-1006, WR-544
2	8	STEMRRSN-6060, SBWON-11, HTWYT-42, ESBWYT-24, ESBWYT-48, SAWSN-3032, SAWYT-344, HRWSN-2101
3	3	GW-366, ESWYT-112, HTWYT-5
4	2	IBESN-1081, IBWSN-1168
5	2	HD-3086, PBW-502

Table 8: Estimates of average intra and inter-cluster distances for 6 clusters in wheat.

No of Cluster	Cluster 1	Cluster 2	Cluster 3	Cluster 4	Cluster 5
Cluster 1	**169.57**	244.46	364.63	261.45	339.89
Cluster 2		**0.00**	322.85	409.36	313.67
Cluster 3			**360.80**	553.03	566.18
Cluster 4				**0.00**	223.92
Cluster 5					**0.00**

Bold figure indicates Intra-cluster distance

Thus, crossing between the genotypes belonging to cluster pairs separated by very high inter cluster distances as mentioned above, may result maximum hybrid vigor and highest number of useful segregates. The maximum intra-cluster distance was found for cluster (IV) (360.80) followed by cluster (I) (164.57), while the minimum intra-cluster distance was recorded for cluster (II), cluster (IV) and cluster (V). These results corroborate the findings of Mishra *et al*. (2015) and Yadav *et al.* (2019).

Cluster mean analysis revealed a wide range of variation for all the traits under study (Table 9). Cluster (X) reported minimum cluster mean value for plant height (65.890). Hence, genotypes belonging to this cluster could be utilized in developing dwarf and semi – dwarf lines or this trait could be transferred into other desirable genotypes in order to reduce the plant stature. Cluster (IV) had the maximum cluster mean value for grain yield per plant. Hence, these genotypes could be utilized in yield improvement for wheat breeding programme. Cluster (III) showed maximum divergence for No. of seed per spike (61.37) These results are similar to those of Ali and Bhardwaj (2015). Other traits *viz*., tillers per plant (11.17), flag leaf area (48.545), test weight (43.26) and spike length (11.78) exhibited maximum cluster mean value in the cluster (II), (I), (V) and (IV). These findings are similar to those of, Mishra *et al.* 2015 and Saini *et al.*2017.Hence, emphasis should be given to select the above promising genetic stocks belonging to wide inter as well as intra cluster distances for hybridization programme in order to generate genetic diversity in available gene bank to enhance the production and productivity of wheat. Recently, Yadav *et al.* (2019) have utilized the molecular approach for genetic divergence and concluded that evaluation of genetic diversity and identification of wheat varieties by the Marker Assisted Selection technology is easy and early approach as compared to conventional breeding approaches.

Table 9: Clusters means for 12 characters in wheat: -

Characters	DAYS TO 50% FLOWERING	FLAG LEAF AREA IN CM2	TILLERS PER PLANT	PLANT HEIGHT IN CM	SPIKELET LENGTH IN CM	SPIKE WEIGHT IN GM.	DAYS TO MATURITY	NO. OF SEED PER SPIKE	BIOLOGICAL YIELD	HARVEST INDEX	1000 GRAIN WEIGHT	35.71GRAIN YIELD
Cluster 1	81.00	48.54	10.64	84.66	11.53	10.40	112.26	49.05	58.90	30.64	35.71	18.01
Cluster 2	82.33	46.64	11.17	84.11	10.76	13.58	110.50	60.34	44.73	37.50	39.20	16.79
Cluster 3	72.00	29.77	10.84	84.68	11.56	12.72	102.66	61.37	58.42	33.91	41.27	19.70
Cluster 4	82.50	26.65	10.90	79.34	11.78	13.38	112.66	52.65	42.04	51.55	36.51	21.38
Cluster 5	60.83	29.54	6.76	65.89	10.34	9.76	95.81	55.65	33.21	36.30	43.26	12.11

CONCLUSION

The analysis of variance expresses high significance for all the characters. Therefore, these characters are considerable for any further breeding program. The characters showing a highly significant positive correlation among yield and its components suggested that during selection these characters may be given due emphasis for developing high yielding varieties. Crossing between the genotypes belonging to large inter cluster distances along with higher cluster mean for majority of the yield

REFERENCES

Ahmed H M, Khan B M, Khan S, Sadiq Kissana N and Laghari S.2003. Path coefficient analysis in bread wheat. *Asian J. Plant Sci*. 2: 491-494.

Ali T and Bhardwaj DN.2015. Study of genetic divergence in wheat *(Triticum aestivum L.)*. *Agril. Communications* **3**(2):1-6.

Dewey S R and Lu K H. 1959. Correlation and path coefficient analysis of crested wheat gross seed production. *Agron. Journal* **51**: 515-518.

Dhami N B, Kandel M, Gurung S B and Shrestha J.2018. Agronomic performance and correlation analysis of finger millet genotypes (*Elusine coracana* L.). *Malaysian J. Sustain. Agric*. **2**: 16-18.

Endaic B and Waines JC.1989. Genetic Variation, heritability and path analysis and land races ob bread wheat from Southern Iran. *Euphitica* **41**: 183-190.

Grafius J E.1960. Does overdominance exist for yield in corn. *Agron. Journal* **52**: 361.

Jee C, Pathak VN, Verma SP, Verma OP, Singh OP. 2019. Association studies for grain yield and its contributing components in diverse genotypes of wheat (*Triticum aestivum* L. em. Thell). *Journal of Pharmacognosy and Phytochemistry* 8(3):1177-1180.

Kumar S, Singh B, Verma SP, Pathak VN, Jee C and Singh JP.2019. Studies on Genetic Variability, Heritability, Genetic Advance, Correlation and Path Analysis for Grain Yield and Its Contributing Traits in Indigenous Wheat (*Triticum aestivum* L.). *Int.J.Curr. Micro. biol. App.Sci.* **8**(08): 1408-16.

Mishra CN, V Tiwari, S Kumar, V Gupta, A Kumar and I Sharma. 2015. Genetic diversity and genotype by trait analysis for agromorphological and physiological traits of wheat (*Triticum aestivum* L.). *SABRAO J. Breed. and Genet.* **47 (1)**:40-48.

Saini M, Shweta and SK Paswan.2017. Genetic divergence analysis in bread wheat *(Triticum aestivum L.). Int. J. Plant Sci. (Muzaffarnagar)* **12**(2):249-252.

Shah MA and Deora VS.2002. Genetic variability and association studies in Wheat for grain and temperature tolerance parameters. *Indian J. Agril. Res.* **36**(3):123-125.

Singh JB, Verma A, Satyaprakash, Patidar I, Prakash TL, Prashad SVS, Singh AK and Mishra AN. 2013. Variability and interrelationship analysis in bread wheat under moisture stress condition. *J. Wheat Res.* **5**(2): 27-34.

Singh OP, Verma SP, Singh Brijesh, Pathak VN and Rajbhar SK.2021. Assessment of genetic variability, heritability, genetic advance and relationship of yield and its contributing traits in wheat genotypes (*Triticum aestivum* L.). *Journal of Progressive Science* 12(1&2): 24-33.

Verma SP, Pathak VN andVerma OP. 2019. Interrelationship between Yield and its Contributing Traits in Wheat (*Triticum aestivum* L). *Int. J Curr. Microbiol. App. Sci*. **8**(2): 3209-15.

Yadav S, Akdasbanu V, Dave A, Shah S and Memon Z.2019. Genetic diversity analysis of different wheat [*Triticum aestivum* (L.)] Varieties Using SSR Markers. *Int.J. Curr.Microbiol.App.Sci.* **8**(2): 839-846.

Citation:

Dvivedi RS, Singh B, Pathak V N, Verma S P and Pandey K K.2023. Genetic variability, character association and component analysis in wheat. *Journal of AgriSearch* 10(3): 151-157