Studies on genetic variability, correlation and path coefficient analysis for yield and yield contributing traits in ~~Bread~~ bread wheat (*Triticum aestivum* L.)

Abstract

A study was undertaken to ~~analyze~~analyse the genetic variability, correlation and estimates path coefficient ~~analysis~~ of yield and yield contributing traits in twenty-eight wheat genotypes grown at BAU Agricultural Farm, ranchi during Rabi season of 2019-2020 in three different dates of sowing with an interval of 15 days which is considered as three environments E1, E2, E3. In this field The Pooled analysis of variance revealed that the treatments were highly significant for all the characters. Wide genetic variation was observed among genotypes for ~~number of grains per spike,~~ plant height, number of grains per spike, 1000 ~~seed~~ kernel weight, Days to maturity and Flag leaf area. Considering genetic parameters, high genotypic co-efficient of variation (GCV), was observed for 1000 seed weight, no of grains per spike, plant height, flag leaf area, days to 50% flowering, days to maturity, chlorophyll content, biological yield, and harvest index. ~~w~~Whereas, low GCV was observed for ~~Spike~~ spike length, grain yield plant????, no of effective tillers, protein content. In most of the cases, phenotypic variances were higher than the genotypic variances. Environmental variance is much higher in harvest index, days to 50% flowering, low environmental variance was observed in plant height, flag leaf area, days to maturity, no of grains per spike, chlorophyll content and biological yield. High heritability with low genetic advance in per cent of mean was observed for plant height, days to maturity, chlorophyll content & harvest index which indicated the involvement of non-additive gene action for the expression of this character and selection for such trait might not be rewarding. High heritability with high genetic advance in per cent of mean was observed for grain yield per plant and no of effective tillers indicating that these traits were under additive gene control and selection for genetic improvement for these traits would be effective. Biological yield had high positive and significant correlation with plant height, number of effective tillers and number of grains per spike. Path coefficient analysis revealed maximum direct contribution towards yield per plot with sheath length followed by grains per spike.

Key words: Wheat (*Triticum aestivum* L.), correlation, path-coefficient, heritability

Introduction

Wheat (*Triticum aestivum .L*) 2n=42 is a crop of global significance. It is grown in diversified environments. It is a staple food of millions of people. Approximately one-sixth of the total arable land in the world is cultivated with wheat. Whereas paddy is mainly cultivated in Asia, wheat is grown in all the continents of the world. It supplies about 20 per cent of the food calories for the world's growing population. Global wheat production touched 763.93 million tons in 2019-20. India is the second largest producer of wheat after China. Wheat has a distinct place among the food grain crops. Carbohydrate and protein are two main constituents of wheat. On average wheat contains 11-12% protein. Wheat is grown mainly in two seasons in the world *viz.* winter and spring. Winter wheat is grown in cold countries like Europe, U.S.A., Australia, Russian federation *etc*. While spring wheat is grown in Asia and a part of U.S.A.

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Commented [ASAS1]: Please put some values spring wheat matures in 120-130 days while winter wheat takes 240-300 days for maturity. Due to this reason productivity of winter wheat is higher in comparison to spring wheat. Considering the quality wheat has been divided into two categories (1) Soft wheat and (2) Hard wheat. *Triticum aestivum* (Bread wheat) is known as soft wheat and *Triticum durum* is known as hard wheat. Therefore, there is need to exploit the existing genetic variability in wheat for developing high yielding varieties that can be adjusting and highly productive under changing climatic scenario. Grain yield, being a complex trait, depends upon component variables and their interaction. Degree and direction of relationship between two or more variables lead to estimation of correlation. Correlation studies provide better understanding of yield component which helps the plant breeder during selection (Robinson *et al*., 1951 and Johnson *et al*., 1955). Path coefficient analysis measures the direct and indirect contribution of independent variables on dependent variables and thus helps breeder in determining the yield components and understanding cause of association between two variables. The information obtains by path coefficient analysis helps in indirect selection for genetic improvement of yield because direct selection is not effective for low heritable trait like yield. Thus, the estimation of heritability and genetic advance is essential for a breeder which helps in understanding the magnitude, nature and interaction of genotype and environmental variation of the traits. With the above reference the present experiment was conducted to study the extent of genotypic and phenotypic variability among the genotypes and to estimate genetic advance, correlation coefficient among the selected characters and direct and indirect effects of component characters on yield of wheat to screen out the suitable parental groups for future- breeding program.

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Materials and methods

The experiment was conducted during Rabi season of 2019-2020 at the at western section of research farm, BAU. Kanke during *rabi*-2019-20. Birsa Agricultural University (BAU), Kanke is located at an elevation of 634 meter above mean sea level with 85°18'48.3"East longitude and 23°25'47.3"North latitude.~~.~~ The experimental material consisting 28 diverse wheat genotypes (Table 1) sown during Rabi 2019 in three different date of sowing - in Randomized Block Design (RBD) with two replications, having a plot size of 0.6m x 4m. The distance maintained between row to row and between plant to plant were 23 cm and 10 cm, respectively The different date of sowing is considered as different environments E1 (Timely sown), E2 (Late sown), E3 (Very late sown) and every sowing is done with a gap period of fifteen days. Recommended agronomic package and practices were applied to raise a healthy crop. Data were recorded on various parameters, viz., Days to 50% flowering, Chlorophyll content (%), Plant height (cm), Spike length (cm), Number of Effective tiller per plant, Protein content %, Number of ~~Grains~~ grains per spike, 1000 grain weight (g) Grain yield per Plant (g), Biological yield per plant (g), Harvest index (%). Data from five plants of each genotype were averaged replication wise and mean data was used for statistical analysis. Mean, range and coefficient of variation (CV) were also estimated. Genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV) were estimated according to Burton (1952); heritability in broad sense (h2bs) was estimated according to Burton and Devane (1953); genetic advance (GA) and genetic advance as per cent of mean (GAPM) were calculated by Johnson *et al*. (1955), correlation coefficient analysis by Robinson *et al*. (1951) and path coefficient analysis was accessed by Dewey and Lu (1959).

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Results and Discussion

The pooled analysis of variance for overall Environment (E1, E2 & E3) has been presented in (Table 2). The table revealed highly significant difference for replication and treatment mean square at 1% level of significance but for days to 50% flowering treatment mean sum of square is non-significant and for protein content replication mean sum of square is non-significant. The highest mean sum of squares due to error was observed for plant height 13.58, followed by harvest index 14.96 and no of grains per spike12.45 . The overall mean range, mean, standard error of mean along with C.D values for different characters over three environments (E1, E2 & E3) has been presented in (Table 3). The data revealed that the widest range of variability was for number of grains per spike (30.04-47.18) with mean value 39.08, (Days to maturity) 128-142 with mean value 134.2, (1000 seed weight) 31-52.47 with mean value 43.41, (Plant height) range between 92-105 with mean value of 97.68 cm, (Flag leaf area) range of variability between 14.19-24.99 with mean value of 19.09 cm^2. A perusal of the (Table 4) indicated that phenotypic variance was higher as compared to genotypic variance for all the characters studied. Highest phenotypic variance was observed in (Harvest index) 42.65 followed by (no of grains spike) 38.82, (Days to 50% flowering) 34.58. The maximum value of genotypic variance was found for (1000 seed weight) 26.94, (no of grains spike) 24.75. moderate genotypic variance was observed in (plant height) 11.67, (flag leaf area) 6.89, (days to 50% flowering) 1.10, (days to maturity) 11.69, (chlorophyll content) 3.17, (biological yield) 3.10, (harvest index) 7.00. Environmental variance is much higher in (harvest index) 35.65, (days to 50% flowering) 33.47. Moderate environmental variance was observed in (plant height) 16.76, (flag leaf area) 10.29, (days to maturity) 13.94, (no. of grains spike) 14.07, (chlorophyll content) 10.32, (biological yield) 8.05.The estimates of PCV were found higher than GCV (Table 4) for spike length, flag leaf area, grain yield per plant, no of grains per spike, biological yield and no of effective tillers, this may be due to the non-genetic factor which played an important role in the manifestation of these characters. The characters with high phenotypic coefficient of variation indicated more influence of environmental factors. Therefore, caution has to be exercised during the selection programme, because the environmental variations are unpredictable in nature and may mislead the results similar results was observed by D. K. Baranwal *et al.,* (2012) Sharma and Garg (2002) and Kumar et al. (2002). Highest phenotypic coefficient of variance was observed in (spike length) 17.80, (flag leaf area) 21.70, (grain yield plant) 23.11, (no of grains per spike) 15.94, (biological yield) 19.35, (no of effective tillers) 24.48 similar results was also observed by similar with the studies of Mohammad *et al.* (2001). Highest genotypic coefficient of variance was observed in (spike length) 15.83 , (flag leaf area) 13.74, (grain yield plant) 17.64 , (no of grains per spike) 12.73 , (biological yield) 10.20 , (no of effective tillers) 18.38 showed conformity with the findings of Panwar and Singh (2000). The highest Environmental coefficient of variation was observed in no of effective tillers, Flag leaf area and biological yield. The estimates of heritability (broad sense) and genetic advance expressed as per cent of mean have been presented in (Table 4). High heritability estimates was associated with high estimates of genetic advance (GA) for 1000 seed weight, -no of grains per spike, days to maturity and plant height which in fact demonstrate the presence of additive genes effect indicating effectiveness of selection for the improvement of these traits. Such a results showed similarity with findings of Atta *et al.* (2008) and Bhoite *et al.* (2008). Broad sense heritability was highest for 1000 seed weight (91.70), spike length (79.1), no of grains per spike (63.75), grain yield per plant (58.25) similarity with findings of Atta *et al.* (2008) and Bhoite *et al.* (2008). The estimate of genetic advance as per cent of mean was noticed for spike length (29.03), no of effective tillers (27.91), grain yield per plant (27.73). The phenotypic correlation coefficient was highly significant (Table 5) and

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positive for grain yield per plant with no of effective tillers, no of grains per spike, 1000 seed weight, plant height, biological yield and harvest index. Among component traits positive and highly significant correlation was observed between plant height and 1000 seed weight, no of grains per spike, no of effective tillers, biological yield and harvest index. The 1000-grain weight and no of grains per spike showed significant and positive correlation with yield envisages the use of these traits for yield improvement supported by earlier reports of Khan *et al*. (2010) and Khokar *et al.* (2010). The grain yield showed highly significant positive correlation with no of grains per spike (0.637), no of effective tillers (0.722), 1000 seed (0.358), the results showed conformity with the findings of Kara and Akman (2007) and highly significant negative correlation with days to maturity (-0.323). Path analysis partitions correlation coefficient (Table 6) into direct and indirect effect which probes the cause and effect relationship. Maximum direct effect on yield was exhibited by biological yield (0.727) via harvest index (0.667), no of grains per spike (0.181) and plant height (0.089). The grains per spike had positive direct effect on yield (0.181) and had relatively high correlation with no effective tillers and 1000 seed weight.

Conclusion

The correlation study revealed that grain yield had strong positive association with no of effective tillers, no of grains per spike, 1000 seed weight and grains per spike. The association studies, indicated that grain yield of wheat can be improved by selecting genotypes having higher performances for the above characters. The selection for less days to maturity would ultimately be helpful for improving grain yield. Path-coefficient analysis revealed that the maximum positive direct effect exhibited by grains per spike, no of grains per spike plant height.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

Table 1: List of 28 wheat genotypes.

(A)	Genotype	Origin	(B)	Genotype	Origin
1.	RW-5	Karnal (IIWBR)	15.	WH-1239	CCSHAU(HR)

2.	HI-1628	IARI, (Indore)	16.	HD-2932	Delhi (IARI)
3.	DBW-252	Karnal (IIWBR)	17.	HD-3237	Delhi (IARI)
4.	K-307(C)	Kanpur (U.P)	18.	LBP-2017-2	Karnal (Haryana)
5.	NIAW-3170	Niphad (M.H)	19.	DBW-14(C)	Karnal (IIWBR)
6.	RAJ-4529	Durgapura (Raj)	20.	PBW-773	Ludhiana (Punjab)
7.	NI-5439	Niphad (MH)	21.	MP-1331	Powarkheda (M.P)
8.	WH-1235	CCS HAU(HR)	22.	RIL-5138	Tata research
9.	DBW-273	Karnal (IIWBR)	23.	DBW-110	Karnal (IIWBR)
10.	BG-3(C)	Ranchi (B.A.U)	24.	M-516	AICRP (Wheat)
11.	RWP-2018-31	AICRP (Wheat)	25.	DBW-136	Karnal (IIWBR)
12.	DBW-233	Karnal (IIWBR)	26.	UP-2981	Pantnagar (U.K)
13.	MACS-6696	Pune, (ARI)	27.	HI-1621	IARI, (Indore)
14.	K-1317	Kanpur (U.P)	28.	WR-544(C)	Delhi (IARI)

Table 2: Analysis of variance for Pooled Environments (E1, E2 & E3)

SOV	D.F	Plant Height (cm)	Spike Length (cm)	Flag Leaf Area (cm^2)	1000 seed weight (g)	Days to 50% Flowering	Days to Maturity	Grain Yield/plant(g)	No of Grains /spike	No Effective Tillers	Chlorophyll Content (%)	Protein content (%)	Biological yield (g/plant)	Harvest Index (%)
		MEAN SQUARE												
Replication	1	44.98	2.10	0.66	0.25	1.14	0.071	1.54	0.113	0.004	13.12	0	27.34	36.85
Treatment	27	28.69 *	4.410**	18.11**	51.33 *	26.58 **	41.69 **	3.25**	64.46**	2.22**	16.08 *	4.70*	15.93 *	62.47**
Error	27	13.58	0.58	3.93	3.006	0.47	0.51	0.53	12.45	0.48	8.12	0.02	6.75	14.96

**** = significant at 1%, * = significant at 5%**

Table 3: Range and mean of different characters in wheat (*Triticum aestivum* L.) genotypes over three Environments Timely sown (E_1), late (E_2) & very late (E_3) sown conditions.

POOLED ENVIRONMENT					
Sl. No	**Characters**	**Range**	**General mean**	**SEm±**	**CD at 5%**
1	**Plant Height(cm)**	92.53-105.83	97.68	1.67	4.674
2	**Spike Length(cm)**	6.13-11.17	8.69	0.28	8.690
3	**Flag leaf area (cm^2)**	14.19-24.99	19.10	1.30	19.099
4	**1000 seed weight(g)**	31-52.47	43.42	43.41	1.783
5	**Days to 50% Flowering**	67-78	71.89	2.36	6.606
6	**Days to Maturity**	128-142	134.19	1.52	4.262
7	**Grain yield / plant (g)**	4.64-8.41	6.48	0.39	1.104
8	**No of grains/ spike**	30.04 - 47.18	39.07	1.53	4.283
9	**No. of Effective tillers**	3.08-6.1	4.65	0.32	0.895
10	**Chlorophyll Content (%)**	38.61-46.8	43.69	1.31	3.669
11	**Protein content (%)**	10.23-15.48	13.47	0.09	0.272
12	**Biological yield(g/plant)**	13.58-20.73	17.25	1.15	3.240
13	**Harvest index (%)**	3.44 - 4.71	38.32	2.43	6.817

Table 4: Pooled Genetic estimate of Environments (E1, E2 & E3)

Source of variation	Plant Height(cm)	Spike Length(cm)	Flag Leaf Area(cm^2)	1000 Seed Weight (g)	Days to 50% Flowering	Days to Maturity	Grain yield / plant(g)	No. of grains/ spike	No. of Effective tillers	Biological yield (g/plant)	Harvest Index (%)
δ^2g	11.67	1.89	6.89	26.94	1.10	11.69	1.30	24.74	0.73	3.10	7.01
δ^2ph	28.43	2.39	17.18	29.38	34.58	25.63	2.24	38.81	1.34	11.15	42.65
δ^2e	16.75	0.49	10.29	2.43	33.47	13.93	0.93	14.07	0.61	8.05	35.64
GCV	3.49	15.83	13.74	11.95	1.46	2.54	17.64	12.73	18.38	10.20	6.90
PCV	5.45	17.80	21.70	12.48	8.18	3.77	23.11	15.94	24.94	19.35	17.03
ECV	4.19	8.12	16.79	3.59	8.04	2.78	14.93	9.60	16.85	16.44	15.57
h^2	41.0	79.1	40.10	91.70	3.20	45.62	58.25	63.75	54.34	27.8	16.43
GA	4.51	2.52	3.424	10.23	0.38	4.75	1.79	8.18	1.29	1.91	2.20

Table 5: Pooled Correlation analysis for ten characters of wheat (*Triticum aestivum* L.) genotypes for environments (E_1, E_2 & E_3)

Characters		Plant height(cm)	Spike length(cm)	Flag leaf area(cm²)	1000-seed weight(g)	Days to 50% flowering	Days to maturity	No. of grains/ spike	No. of Effective tillers	Chlorophyll Content (%)	Protein content (%)	Biological yield (g/plant)	Harvest Index (%)	Grain yield / plant(g)
Plant height(cm)	G	1	-0.017	-0.278	0.465	-1.265	-0.548	1.002	1	0.23	0.159	1.027	0.841	0.953
	P	1	0.010	-0.050	0.282 **	-0.120	-0.188 *	0.570**	0.566 **	-0.026	0.097	0.446 **	0.27 **	0.599 **
Spike length(cm)	G		1	-0.201	0.256	0.276	-0.125	0.124	0.104	0.214	0.016	0.184	0.165	0.161
	P		1	-0.116	0.209 **	0.103	-0.077	0.095	0.088	0.059	0.020	0.104	0.043	0.107
Flag leaf area(cm²)	G			1	-0.283	0.596	0.090	-0.232	-0.190	0.057	0.027	-0.284	-0.329	-0.253
	P			1	-0.163 *	0.068	0.031	-0.214 **	-0.196*	-0.045	0.017	-0.112	-0.048	-0.140
1000-seedweight(g)	G				1	-0.474	-0.267	0.544	0.531	0.158	0.231	0.402	0.709	0.493
	P				1	-0.08	-0.176 *	0.417 **	0.377**	0.050	0.215 **	0.226**	0.245 **	0.358 **
Days to 50% flowering	G					1	0.614	-0.831	-0.685 **	-0.659 **	-0.461 *	-1.029 **	-0.968 **	-0.861 **
	P					1	0.229	-0.094	-0.013	-0.094	-0.046	-0.09	0.02	-0.058
Days to maturity	G						1	-0.535	-0.464	-0.080	-0.330	-0.514	-0.403	-0.517
	P						1	-0.247 **	-0.254 **	-0.024	-0.199 **	-0.238 **	-0.167 *	-0.323 **
No. of grains/ spike	G							1	1.060	0.170	0.200	1.116	1.049	1.071
	P							1	0.751 **	0.008	0.167 *	0.449 **	0.326 **	0.637 **
No. of Effective tillers	G								1	0.172	0.173	1.072**	1.070**	1.053**
	P								1	0.095	0.128	0.484 **	0.395**	0.722 **
Biological yield (g/plant)	G											1	1.009	1.018
	P											1	-0.152 *	0.727 **
Harvest Index(%)	G												1	0.975
	P												1	0.519 **

**** = significant at 1%, * = significant at 5%**

Table 6 :Pooled Path analysis for twelve characters of wheat (*Triticum aestivum* L.) genotypes under three environments (E_1, E_2, E_3)

Characters		Plant height(cm)	Spike length(cm)	Flag leaf area(cm^2)	1000-seed weight(g)	Days to 50% flowering	Days to maturity	No. of grains/ spike	No. of Effective tillers	Chlorophyll Content (%)	Protein content (%)	Biological yield (g/plant)	Harvest Index (%)
Plant height(cm)	**P**	**0.048**	-0.000	0.000	-0.002	-0.001	0.003	0.014	0.049	-0.000	0.001	0.328	0.158
Spike length(cm)	**P**	0.000	**-0.008**	0.000	-0.002	0.001	0.001	0.002	0.007	0.001	0.000	0.076	0.024
Flag leaf area(cm^2)	**P**	-0.002	0.000	**-0.006**	0.001	0.000	-0.000	-0.005	-0.017	-0.001	0.000	-0.082	-0.027
1000-seed weight(g)	**P**	0.013	-0.001	0.001	**-0.010**	-0.001	0.003	0.010	0.033	0.001	0.002	0.166	0.139
Days to 50% flowering	**P**	-0.005	-0.000	-0.000	0.000	**0.013**	-0.004	-0.002	-0.001	-0.003	-0.000	-0.066	0.011
Days to maturity	**P**	-0.009	0.000	-0.000	0.001	0.003	**-0.017**	-0.006	-0.022	-0.000	-0.002	-0.175	-0.095
No. of grains/ spike	**P**	0.027	-0.000	0.001	-0.004	-0.001	0.004	**0.026**	0.065	0.000	0.001	0.331	0.185
No. of Effective tillers	**P**	0.027	-0.000	0.001	-0.003	-0.000	0.004	0.019	**0.087**	0.003	0.001	0.356	0.225
Chlorophyll Content (%)	**P**	-0.001	-0.000	0.000	-0.000	-0.001	0.000	0.000	0.008	**0.033**	0.001	0.011	0.069
Protein content (%)	**P**	0.004	-0.000	-0.000	-0.002	-0.000	0.003	0.004	0.011	0.003	**0.011**	0.060	0.070
Biological yield (g/plant)	**P**	0.021	-0.000	0.000	-0.002	-0.001	0.004	0.011	0.042	0.000	0.000	**0.736**	-0.086
Harvest Index(%)	**P**	0.013	-0.000	0.000	-0.002	0.000	0.003	0.008	0.034	0.004	0.001	-0.111	**0.568**

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