Estimation of genetic variability, correlation and path coefficient analysis for yield and its attributes in wheat (*Triticum aestivum* L.)

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Abstract: The experiment was undertaken to estimate the genetic variability, correlation and path coefficient analysis of yield and its attributes in thirty eight wheat genotypes grown at research farm of P.G. College Ghazipur during Rabi season 2020-21. Wide genetic variation was observed among genotypes for all the characters studied considering the genetic parameters. The magnitude of phenotypic coefficients of variation (PCV) were higher than the corresponding genotypic coefficient of variation (GCV) for all the characters under investigation, indicating the influence of environmental factors on other experiment. High heritability with high genetic advance as percent of mean was observed for plant height, seed yield per plant, 100 grain weight, days to 50% flowering, biological yield, number of grain per spike and spike length. The grain yield per plant had significant and positive correlation with biological yield, spike length, and plant height. The magnitude of direct and indirect effects revealed that 100 grain weight was the most important traits followed by spike length, days to maturity and harvest index for improvement of grain yield in wheat.

Key Words: Wheat, variability, heritability, genetic advance, correlation, direct and indirect effects.

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1. Introduction

Wheat (*Triticum aestivum* L., 2n=6x=42) is a monocot plant, belongs to the tribe *triticeae*, under the grass family *poaceae*. Wheat grains has a high nutritional value with 70-75% starch, 14% water, 8-20% proteins, 2-3% non-starch polysaccharides, 2% lipids, 1.6% minerals, antioxidants *etc.* and is main staple food crop for a huge world population (Goesaert *et al.*, 2005) [12]. The growing peace of population is declining the cultivated land which is a great concern for the world's food security and alarming us to raise the grain yield production by crop improvement. The genetic variability observed in the plant population of a species is result of the both heridity effects of concerned genes and the environment. Therefore, grain yield is a complex trait and is strongly influenced by many genetic and environmental factors. Thus, direct selection for yield can be misleads and deaccelerate the pace of breeding program. Successful selection of high yielding genotypes depends on information available for genetic variability and the association of morpho-agronomic traits with grain yield. The degree of association between two or more variables is estimated by the correlation coefficient (r). The correlation analysis measures the degree of association but does not indicate the relative importance of each factor. Therefore, it is necessary to perform a more detailed examination using an analysis of the path coefficient, a statistical technique to decompose the correlation coefficient into direct and indirect effects, which facilitates the estimation of the contribution of each component (independent cause) to the grain yield (dependent variable) (Suleiman *et al.*, 2014). Keeping in mind the above facts, the present study was planned to estimate the genetic variability correlation and path coefficients analysis between grain yield and its contributing traits in wheat genotypes and to identify the yield contributing traits that could be used as selection criteria to improve grain yield.

2. Materials and Methods

The experiment was carried out in the research form of Department of Genetics and Plant Breeding, P. G. College Ghazipur. A total of 38 genotypes, including released varieties and advance breeding lines were used in the present study. The crop was sown in four rows of 3-meter length with three replicates in a Randomized Block Design (RBD) during *Rabi* 2020-21. Five plants from rows of plot were selected randomly and tagged to record the data of different morpho-agronomical traits *viz*., days to 50% flowering, days to maturity, plant height(cm), number of tillers per plant, spike length (cm), number of grains per strike, biological yield (g), 100-grain weight(g), harvest index(%) and seed yield per plant(g). Harvest index was calculated as per formula given by Donald and Humblin (1976) [8]. The mean performance of individual genotypes was used for statistical analysis. Statistical analysis of recorded phenotypic data were performed using a computer based statistical package INDOSTAT program. Analysis of variance of the observations recorded on all characteristics was carried out as per the standard procedure suggested by Fisher (1925) [11]. Genotypic and phenotypic coefficients of variation were estimated according to Burton *et al.* (1953) [4]. Heritability in broad sense was calculated as the ratio of genotypic to phenotypic variance and expressed in percentage (Falconer, 1981) [10]. Genetic advance as percent of mean of each character was worked out adopting the formula given by Johnson *et al.* (1955) [14]. Similarly, correlation coefficient and path analysis were carried out using the method suggested by Al-Jibouri *et al.* (1958) [1] and Dewey and Lu (1959) [7], respectively.

3. Results and Discussion

The analysis of variance for different traits revealed that the mean sum of squares due to treatments was significant for all the characters under study indicating substantial variability into material taken under study (Table-1). The presence of this variability indicated that there is a ample scope for improvement in the traits under study. The similar result have been reported by Ashish *et al.* (2020), Bhulto *et al.* (2016), Khan et al.(2017) and Phoughat et al.(2016).

3.1 Variability and heritability parameters

The extant of variability by present in the genotypes was measured in the terns of range, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability and expected genetic advance (GA) (Table 2). It is clearly marked that a significant amount of variation was present among genotypes for the character under study. The magnitude of phenotypic coefficient of variation(PCV) were higher than the corresponding genotypic coefficient of variation (GCV) for all the characters under investigation(Table 2) indicating influence of environmental factors on their expression.

3.2 Heritability and Genetic advance

The genotypic coefficient of variation does not offer full scope to estimate the variation that is heritable or environment and therefore, estimation of heritability becomes necessary. The magnitude of heritability ranged from 33.14% (days to maturity) to 91.81(spike length). Heritability estimates were high for spike length, seed yield per plant, number of grains per spike, 100 grain weight, biological yield, days to 50% flowering, number of tillers per plant, harvest index and plant height. The character days to maturity showed low heritability. The high heritability estimates would be helpful for selection and breeding of superior genotypes on the basis of phenotypic performance of quantitative characters.

However, Johnson *et al.* (1955) reported that heritability (h^2) estimates along with genetic advance where more useful than the heritability along with selecting the best genotypes. So, heritability along with high genetic advance was considered an important selection per parameter. High heritability estimates along with genetic advance as present of means were recorded for characters plant height seed yield per plant, 100-grain weight, days to 50% flowering, biological yield, number of grains per spike and spike length. This demonstrates the presence of additive gene effects indicating the effectiveness of selection for these traits in crop improvement programme. Similar results were also reported by Ashish *et al*.(2000), Branwal *et al.* (2012) and Kumar *et al*. (2014) for all the characters.

3.3 Correlation Coefficients analysis

Grain yield is a complex character and is influenced by several component characters. It is also very different to improve yield by directly selecting for grain yield per plant. So it was felt that it would be of great help in selection of the desirable genotypes for yield, if there is a certain association of grain yield with contain easily measurable plant characters. Correlation between traits could be due to linkage or pleiotropy. Correlation due to linkages can be modified through recombination, but correlation due to pleiotropy or developmental causes may not be easy to overcome. In later cases, the genetic improvement in yield is not possible without bringing an improvement in yield component traits. The inclusion of various component characters in a selection scheme is obviously not practicable and under these situations, and knowledge with respect to the association of various traits with grain yield would be of immense help in formulating an effective and efficient selection and screening programme.

Correlation among wheat genotypes showed that grain yield per plant had significant and positive correlation with biological yield per plant (g), spike length and plant height(Table 3). The 100 grain weight was positively correlated with plant height and spike length. Similarly, the association of grain yield with either one or more than one trait has also been reported by Ashish *et al* (2020), Phougat *et al.* (2017), Arya *et al*. (2017) and Desheva (2016)

3.4 Path Coefficients Analysis

Partitioning of total correlation into direct and indirect effects provide a direct and indirect contribution of characters and thus form the basis for selection to improve the yield. Considering grain yield as effect and other characters as causes, genotypic correlation coefficients were partitioned by using the method of path analysis to find out the direct and indirect effects. Shrivastava and Sharma (1976) suggested that only direct yield components should be used for selection purpose. In the present study, the magnitude of direct effects revealed that 100 grain weight was the most important trait followed by spike length, days to maturity and harvest index for improvement of grain yield (Table 4) Similar observations were found by Arya *et al*. (2017) , Ashish *et al* (2020), Phougat *et al.* (2017) . The characters plant height, number of tillers per plant spike length, showed highest positive and indirect effect on seed yield per plant via 1000 grain weight. So path analysis suggested that the 100-grain weight, biological yield, plant height, days to maturity, spike length, number of tillers per plant were the effective selection attributes doing breeding program for improvement in yield of wheat.

References

[1]. Al-Jibouri H, Miller PA, Robinson HF. Genotypic and Environmental Variances and Covariances in an Upland Cotton Cross of Interspecific Origin 1. Agronomy journal 1958;50(10):633-6.

[2]. Arya VK, Singh J, Kumar L, Kumar R, Kumar P, Chand P. Genetic variability and diversity analysis for yield and its components in wheat (Triticum aestivum L.). Indian Journal of Agricultural Research 2017;51(2):128-34.

[3]. Ashish Ashish, SK Sethi, Vikram, Divya Phougat and Antim(2020). Genetic variability, correlation and path analysis in bread wheat (Triticum aestivum) genotypes for yield and its contributing traits. Journal of Pharmacognosy and Phytochemistry 2020; 9(6): 388-391

[4]. Bhutto AH, Rajpar AA, Kalhoro SA, Ali A, Kalhoro FA, Ahmed M. Correlation and regression analysis for yield traits in wheat (Triticum aestivum L.) genotypes. Natural Science 2016;8(3):96-104.

[5]. Burton GW, Devane DE. Estimating heritability in tall fescue (Festuca arundinacea) from replicated clonal material 1. Agronomy Journal 1953;45(10):478-81.

[6]. Choudhary RA, Jat BL, Anwale R, Dhiklwal SR, Sharma KC. Studies on estimates of genetic variability and character association of yield components and protein content in pearl millet. Forage Research 2012;38:80-5.

[7]. Desheva G. Correlation and path-coefficient analysis of quantitative characters in winter bread wheat varieties. Trakia Journal of Sciences 2016;1:24-29.

[8]. Dewey DR, Lu K. A Correlation and Path-Coefficient Analysis of Components of Crested Wheatgrass Seed Production 1. Agronomy journal 1959;51(9):515-8.

[9]. Donald CM, Hamblin J. The biological yield and harvest index of cereals as agronomic and plant breeding criteria. Advances in agronomy 1976;28:361-405

[10]. Drikvand R, Bihamta MR, Najafian G, Ebrahimi A. Kernel quality association and path analysis in bread wheat. International Journal of Biology 2013;5(3):73.

[11]. Falconer DS. Introduction to quantitative genetics. Introduction to quantitative genetics. Oliver and Boyd, Edinburg, London, UK 1960,316.

[12]. Fisher RA. Statistical methods for research workers. Edinburgh. Oliver and Boyd, Edinburgh, London, UK 1925,146.

[13]. Goesaert H, Brijs K, Veraverbeke WS, Courtin CM, Gebruers K, Delcour JA. Wheat flour constituents: how they impact bread quality, and how to impact their functionality. Trends in food science & technology 2005;16(1-3):12-30.

[14]. Hussain M, Khan AS, Khaliq I, Maqsood M. Correlation studies of some qualitative and quantitative traits with grain yield in spring wheat across two environments. Pakistan Journal of Agricultural Sciences 2012;49(1):1-4.

[15]. Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans 1. Agronomy journal 1955;47(7):314-8.

[16]. Khan SA, Hassan G. Heritability and correlation studies of yield and yield related traits in bread wheat. Sarhad Journal of Agriculture 2017;33(1):103-7.

[17]. Kumar LMY, Naik VR, Biradar SS. Identification of micronutrient dense genotypes on the basis of biochemical characteristics in wheat (Triticum spp.). Karnataka Journal of Agricultural Sciences 2014;27(3):285-8.

[18]. Phougat D, Godara A, Sethi SK, Ashish, Singh V. Genetic variability and association studies for yield and its component traits in bread wheat (Triticum aestivum (L.) em.Thell) genotypes under late sown conditions. Advances in Life Sciences 2016;7(17):6842-6847.

[19]. Phougat D, Panwar IS, Saharan RP, Singh V and Anuradha. Genetic diversity and association studies for yield attributing traits in

bread wheat [Triticum aestivum (L.) em.Thell]. Research on Crops 2017;18 (1):139-144.

[20]. Shrivastava MN, Sharma KK. Analysis of path coefficients in rice. Zeitschrift fuer Pflanzenzuechtung (Germany, FR) 1976;77:174-177.

[21]. Singh, RK and Choudhary, BD Biometrical methods in quantitative genetic analysis. Kalyani Publication, New Delhi. 1977; 178-185.

[22]. Suleiman AA, Nganya JF, Ashraf MA. Correlation and path analysis of yield and yield components in some cultivars of wheat (Triticum aestivum L) in Khartoum State, Sudan. Journal of Forest Products and Industries 2014;3(6):221-228

[23]. Wahidy S, Suresh BG, Lavanya GR. Genetic variability, correlation and path analysis in wheat germplasm (Triticum aestivum L.). International Journal of Multidisciplinary Research and Development 2016;3(7):247.

Table 1 : Analysis of variance for ten quantitative characters in wheat (*Triticum estivum* L.)

Sl. No.	**Source of Variation**	**D.F.**	**Days to 50% flowering**	**Days to maturity**	**Plant height(cm)**	**No. of tillers per plant**	**Spike length (cm)**	**No. of grains per spike**	**Biological yield (g)**	**100 grain weight**	**Harvest index(%)**	**Seed yield per plant(g)**
1	Replication	2	8.132	12.2193	221.738	21.8652	5.3677	64.527	348.48	0.41952	2.7696	27.457
2	Treatment	37	46.888***	11.5024***	206.312***	3.8101*	12.2711*	105.139*	94.58*	0.59563**	20.8026*	18.514*
3	Error	74	3.555	4.6247	28.186	2.3133	7.1685	60.281	56.48	0.27204	11.7714	10.824

* - Significant at 5% level of significance
** - Significant at 1% level of significance
*** - Significant at 0% level of significance

Table 2 : Estimates of range, mean, phenotypic coefficients of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) and genetic advance for grain yield and its attributes in wheat.

Sl. No.	Characters	Mean	Range	Coefficient of variation (cv)			Heritability (h^2)	Genetic Advance	Genetic advance(%)
				GCV	PCV	ECV			
1	**Days to 50% flowering**	78.5526	71.00-88.00	4.84	5.4	2.4	80.25%	7.0135	8.9284
2	**Days to maturity**	124.307	114.00-134.00	1.22	2.12	1.73	33.14%	1.7957	1.4446
3	**Plant height(cm)**	93.9168	70.00-118.70	8.21	9.96	5.65	67.81%	13.0712	13.9178
4	**No. of tillers per plant**	12.2932	9.28-19.95	5.75	13.64	12.37	77.41%	0.6129	4.9857
5	**Spike length (cm)**	16.6244	12.00-43.50	7.85	17.91	16.11	91.81%	1.1765	7.0769
6	**Number of grains per spike**	50.6584	13.80-73.60	7.63	17.12	15.33	98.71%	3.5512	7.0101
7	**Biological yield(g)**	37.7815	11.80-57.40	9.43	22.02	19.89	83.61%	3.1454	8.3252
8	**100 grain weight(g)**	3.8722	2.49-5.30	8.48	15.92	13.47	84.41%	0.3606	9.3126
9	**Harvest index(%)**	38.7532	26.15-45.71	4.48	9.92	8.85	70.31%	1.613	4.1622
10	**Seed yield per plant(g)**	14.4325	5-26	11.09	25.35	22.8	91.15%	1.4433	10

Table 3: Genotypic & phenotypic correlation coefficients analysis for yield and its attributing characters of different genotypes in wheat.

Traits		Days to maturity	No. of tillers per plant	Plant height(cm)	Spike length (cm)	No. of grains per spike	100 grain weight(g)	Biological yield(g)	Harvest index(%)	Grain yield per plant(g)
Days to 50% flowering	**G**	0.1893	-0.7799 **	-0.2577	-0.0167	0.5987 **	-0.582 **	-0.1474	-0.3765 *	-0.5217 **
	P	0.067	-0.638	-0.1	0.105	-0.158	-0.216	-0.145	-0.103	-0.177
Days to maturity	**G**		-0.078	-0.0288	0.1253	-0.3449 *	0.0404	-0.0926	0.3164	0.1354
	P		-0.059	-0.037	-0.02	-0.002	-0.091	-0.014	0.017	-0.058
Plant height(cm)	**G**			0.2623	0.181	-0.5736 **	0.6446 **	0.0191	0.4973 **	0.4875 **
	P			0.175	-0.009	-0.1007	0.325**	0.0108	0.124	0.247**
No. of tillers per plant	**G**				-0.4324 **	-5.00E-04	-0.4464 **	-0.6566 **	-0.3777 *	-0.4429 **
	P				-0.066	-0.044	0.0286	-0.0987	-0.049	-0.0076
Spike length (cm)	**G**					-0.0604	0.7713 **	0.4054 *	-0.0084	0.7505 **
	P					-0.039	0.204*	0.066	0.057	0.230*
No. of grains per spike	**G**						-0.0247	-0.5225 **	0.3024	0.2025
	P						0.059	-0.136	-0.039	0.0308
Biological yield(g)	**G**							0.3506 *	0.07	0.2453
	P							0.1091	0.0212	0.8425**
100 seed weight(g)	**G**								0.3369 *	0.2986
	P								0.0125	4.407
Harvest index(%)	**G**									0.136
	P									0.348

*** Significant at 5% level of significance ; ** Significant at 1% level of significance**

Table 4: Direct and Indirect effects of different characters towards yield in wheat.

Traits		Days to 50% Flowering	Days to maturity	Plant height(cm)	No. of tillers per plant	Spike length (cm)	No. of grains per spike	100 grain weight(g)	Biological yield(g)	Harvest index(%)	Correlation with seed yield/plant
Days to 50% flowering	**G**	**0.24381**	0.07805	0.13048	-0.17127	0.01159	0.33122	-1.08117	-0.11454	0.05019	-0.5217 **
	P	**-0.04321**	0.00125	0.0342	0.00291	0.00661	-0.00407	-0.18396	0.00986	-0.0014	-0.177
Days to maturity	**G**	0.04615	**0.41233**	0.01304	-0.01915	-0.08709	-0.19083	0.07509	-0.07197	-0.04217	0.1354
	P	-0.00293	**0.01846**	0.00316	0.00109	-0.00157	0.00005	-0.07776	0.00096	0.00023	-0.058
Plant height(cm)	**G**	-0.19016	-0.03215	**-0.16729**	0.17429	-0.12577	-0.31733	0.19735	0.01484	-0.06629	0.4875 **
	P	0.0276	-0.00109	**-0.05354**	-0.00508	-0.00058	0.00259	0.27615	-0.00073	0.00168	0.247**
No. of tillers per plant	**G**	-0.06284	-0.01188	-0.04388	**0.66451**	0.30049	-0.00029	-0.82926	-0.51007	0.05034	-0.4429 **
	P	0.00433	-0.00069	-0.00937	**-0.02904**	-0.00418	0.00114	0.02428	0.0067	-0.00067	-0.0076
Spike length (cm)	**G**	-0.00406	0.05167	-0.03027	-0.28731	**-0.695**	-0.0334	0.43282	0.31491	0.00112	0.7505 **
	P	-0.00456	-0.00046	0.0005	0.00194	**0.06264**	0.001	0.17352	-0.00455	0.00078	0.230*
No. of grains per spike	**G**	0.14596	-0.14222	0.09595	-0.00035	0.04196	**0.55326**	-0.04586	-0.40588	-0.0403	0.2025
	P	-0.00684	-0.00004	0.00539	0.00129	-0.00245	**-0.0257**	0.05043	0.00925	-0.00053	0.0308
Biological yield(g)	**G**	-0.1419	0.01667	-0.10783	-0.29665	-0.53607	-0.01366	**0.85762**	0.27234	-0.00932	1.0412 **
	P	0.00936	-0.00169	-0.01742	-0.00083	0.0128	-0.00153	**0.84891**	-0.0074	0.00029	0.8425**
100 seed	**G**	-0.03595	-0.0382	-0.0032	-	-	-0.28908	0.65128	**0.77679**	-0.0449	0.2986

weight(g)					0.43635	0.28175					
	P	0.00628	-0.00026	-0.00057	0.00287	0.0042	0.0035	0.09253	**-0.06791**	0.00017	4.407
Harvest index(%)	**G**	-0.0918	0.13046	-0.0832	-0.25099	0.00582	0.16729	0.12996	0.26171	**-0.13328**	0.136
	P	0.00448	0.00032	-0.00667	0.00144	0.0036	0.00102	0.018	-0.00086	**0.01348**	0.348

Residual Effect of Genotypes = -0.2913
Residual Effect of Phenotypes = 0.2798