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Association Studies for Yield and Component Traits among Nine Bread Wheat (*Triticum aestivum* L.) Genotypes and their Crosses

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ABSTRACT: In order to understand the association and contribution of 13 traits towards grain yield, the correlations and path coefficients were analysed among nine different wheat genotypes and their 36 crosses. The field experiment was conducted in the research farm region of Chaudhary Charan Singh Haryana Agricultural University, Hisar in a randomise block design with three replications. Except for days to heading and days to maturity, grain yield per plant showed a positive and significant correlation with all of the studied traits. The interdependence among these characters revealed that these are controlled by a few common genes, which can be ultimately used as selection criteria in breeding programmes. Positive selection for one characteristic would improve linked traits as well. The path coefficient study found that the degree of the positive direct effect on grain yield was largest through number of grains per spike (0.631), 100 grain weight (0.714), biological yield per plant (0.63), and harvest index (0.631) towards seed yield. Harvest index via number of productive tillers per plant (0.70); biological yield per plant via peduncle length (0.25) and number of grains per spike (0.24); number of grains per spike via spike weight (0.55) and grain weight per spike (0.48); spike weight via grain weight per spike (0.248) and number of grains per spike (0.24); spike weight via grain weight per spike (0.248) and number of grains per spike (0.24); spike weight via grain weight per spike (0.248) and number of (0.20), Spike weight and 100 grain weight had a significant positive indirect effect towards grain yield. As a result, it's reasonable to conclude that these are the major traits responsible for the improvement of wheat grain yield which is ultimately the main breeding objective in wheat improvement programmes.

Keywords: Wheat, Correlation, traits, improvement and yield.

INTRODUCTION

Wheat (*Triticum aestivum* L.) is one of the important food crops in most parts of the globe, and it ranks second after rice in Indian agriculture. Knowledge of the number, nature, and contribution of gene effects to control characteristics is critical for developing an effective wheat breeding programme. Selection for grain yield and their enhancement can only be effective if there is enough genetic variability in the breeding materials (Ali *et al.,* 2008). To boost total yield, our goal must be to maximise the effects of the components that have a positive effect while reducing the effects of the components that have a negative effect. Correlation analysis can be a effective approach for determining the interdependencies among yield and it's component traits. Genetic variability and correlation analysis help us in the identification of genetic association between various plant traits and their association with the overall productivity levels (Haydar *et al.,* 2020). The correlation coefficient is a useful statistical tool that can assist wheat breeders in selecting higher yielding crop plants.

Yield component traits, *viz* number of grains per spike (Hussain *et al.,* 2014), number of spikes per plant (Hannachi *et al.,* 2013), biological yield per plant (Shahryari *et al.,* 2013) and harvest index (Sokoto *et al.,* 2012), had a positive correlation with grain yield in bread wheat. According to Yildirim (1996), grain yield had a positive relationship with harvest index and biomass. Grain yield per plant had positive association with number of grains per spike, total dry matter per plant, and harvest index, but negatively associated to days to heading and maturity, according to Singh *et al.* (1995). They also discovered a positive association between spike length, total dry matter, harvest index and grain yield but a negative relationship between number of grains per spike and harvest index. Because correlation coefficients often explain relationships among independent variables and the degree of linear linkages among variables, they were unable to completely developed the link when a clear cause-and-effect relationship was developed between the variables (Dokuyucu *et al.,* 2002).

As a result, the direct and indirect effects of yield and its components should be recognised in breeding programmes (Turk *et al.*, 2006). The correlation coefficient can be partitioned into direct and indirect effects using the path analysis technique developed by Dewey and Lu (1959). Therefore, selection criteria for complicated traits have been developed using path coefficients. As a result, the current study was carried out to determine the correlation and path coefficient of wheat genotypes and crosses in order to identify viable and diverse sources for future breeding projects.

MATERIAL AND METHODS

Nine different wheat genotypes were used as parents in the present study, namely WH1105, HD2967, Raj3765, HD3059, HD3086, WH283, WH1124, WH1184 and WH711 which are selected based on their adaptability, yield potential, origin and diversity. In a diallel way, crosses were attempted (excluding reciprocals). The next year, at the farm area of the Department of Genetics and Plant Breeding, CCS HAU, Hisar, nine parents and their 36 crosses were sowed in a Randomized Block Design with three replications. Each entry was sown in a single 2.5 metre long row length. The space between rows and plants was kept 20cm and 10cm, respectively. All recommended agronomic practices were followed during the entire cropping season.

During the entire crop time, five irrigations were applied. Five competing plants were chosen randomly from each replication in parents and F1s, and days to heading, plant height, days to maturity, grain weight per spike, spike length, number of productive tillers per plant, number of grains per spike, primary spike weight, 100 grain weight, grain yield per plant, biological yield per plant and harvest index were the traits that were investigated. According to Burton, the recorded observations were subjected to analysis of variance (ANOVA) (1952). Miller *et al.* (1958) suggested the estimation of correlation coefficients, while Wright (1934) suggested the estimation of path coefficients, which was extended by Dewey and Lu (1959). Statistical analysis was carried out by statistical software INDOSTAT Version 9.2 respectively.

RESULTS AND DISCUSSION

A. Analysis of variance (ANOVA)

Plant breeders can use variation present in the germplasm of any crop to generate new and improved cultivars with desired features for that particular crop. The genotypic variance in this study was separated into three components: parents, crosses, and parents vs crosses. The mean sums of squares owing to parents and crosses were found to be highly significant for all thirteen traits in analysis of variances (Table 1 & 2), demonstrating that there was substantial variation for all thirteen traits among genotypes and crosses. Except for the number of productive tillers per plant, peduncle length, grain yield per plant, and biological yield per plant, the mean sum squares owing to parent v/s crosses were found to be significant for almost all of the parameters.

Table 1: Analysis of variance (ANOVA) for six studied traits.

Source	d.f.	Days to heading	Days to maturity	Plant height	No. of productive tillers per plant	Spike length	Main spike weight
				(cm)		(cm)	(g)
Replicates	2	4.11	4.27	32.91	11.47**	0.01	0.29**
Genotypes	44	25.35**	24.69**	75.62**	13.90**	1.61**	0.28**
Parents	8	41.31**	30.66**	172.69**	7.15**	1.69**	0.36**
Crosses	35	22.19**	18.84**	52.45**	15.83**	1.20**	0.22**
Parent Vs. Crosses	1	8.56	181.42**	109.90**	0.13	15.11**	1.73**
Error	88	2.93	7.03	14.41	1.94	0.55	0.06

*, ** significance level when P=0.050 and P=0.01,

Table 2: Analysis of variance (ANOVA) for seven studied traits.

Source	d.f.	Grain weight per main spike(g)	No. of grains per spike	Peduncle length	100 grain weight	Grain yield per plant	Biological yield per plant	Harvest Index
				(cm)	(g)	(g)	(g)	(%)
Replicates	2	0.29**	7.92	13.74**	0.11	59.26**	97.14	107.45**
Genotypes	44	0.28**	136.54**	18.52**	0.35**	93.39**	358.42**	131.65**
Parents	8	0.36**	224.33**	33.54**	0.13**	34.31**	542.84**	42.92*
Crosses	35	0.22**	105.05**	15.49**	0.37**	109.29**	322.16**	153.49**
Parent Vs. Crosses	1	1.73**	536.0**	4.48	1.51**	9.7	152.13	76.99
Error	88	0.06	12.65	2.47	0.04	8.1	52.96	20.92

*, ** significance level when P=0.050 and P=0.01,

A. Correlation studies

The degree of genetic variability in the base population and the association between distinct traits and grain yield is the most important factors in any breeding programme. The nature of association among traits is determined using correlation and path analysis, which plays an essential role in the selection of desirable parents for hybridization in the wheat improvement programme. Except for days to heading and days to maturity all the other traits *viz,* number of productive tillers per plant, grain weight per spike, number of grains per spike, spike length, peduncle length, 100 grain weight, biological yield per plant, and harvest index showed positive and significant association with grain yield per plant (economic yield) at phenotypic level (Table 3).

Table 3: Table showing phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficient for 13 traits.

Traits	PH	PT	DH	SL	PL	SW	DM	NGPS	GWPS	BY	EY	HGW	HI
PH	1	0.152^{NS}	-0.065^{NS}	0.275**	0.564**	0.317**	-0.034^{NS}	0.314**	0.255**	0.317**	0.341**	-0.174*	0.060^{NS}
PT	0.382**	1	0.022^{NS}	0.277**	-0.096^{NS}	0.294**	0.074^{NS}	0.075^{NS}	0.158^{NS}	0.282**	0.247**	0.203*	0.113^{NS}
DH	-0.139^{NS}	0.569**	1	-0.035^{NS}	-0.466**	0.299**	0.617**	0.276**	0.289**	-0.104^{NS}	0.061^{NS}	0.069^{NS}	0.184*
SL	0.374**	0.120^{NS}	0.206*	1	0.129^{NS}	0.395**	0.069^{NS}	0.078^{NS}	0.214*	0.225**	0.268**	0.252**	0.159^{NS}
PL	0.643**	0.067^{NS}	-0.696**	0.304**	1	0.031^{NS}	-0.264**	0.110^{NS}	0.062^{NS}	0.210*	0.219*	-0.068^{NS}	-0.030^{NS}
SW	0.669**	0.693**	0.645**	0.751**	0.137^{NS}	1	0.355**	0.440**	0.575**	0.259**	0.249**	0.324**	0.049^{NS}
DM	-0.111^{NS}	0.458**	0.789**	0.203*	-0.402**	0.680**	1	0.276**	0.336**	0.030^{NS}	0.145^{NS}	0.192*	0.143^{NS}
NGP	0.478**	0.198*	0.385**	0.211*	0.100^{NS}	0.874**	0.432**	1	0.724**	0.311**	0.170*	-0.155^{NS}	-0.128^{NS}
GWPS	0.430**	0.515**	0.522**	0.408**	0.023^{NS}	1.042**	0.653**	0.767**	1	0.325**	0.286**	0.169*	0.008^{NS}
BY	0.337**	0.056^{NS}	-0.020^{NS}	-0.080^{NS}	0.409**	0.294**	0.014^{NS}	0.390**	0.270**	1	0.404**	0.018^{NS}	-0.460**
EY	0.453**	0.888**	0.045^{NS}	0.547**	0.362**	0.731**	0.420**	0.317**	0.587**	0.743**	1	0.302**	0.547**
HGW	-0.141^{NS}	0.406**	0.213*	0.509**	-0.050^{NS}	0.439**	0.504**	-0.238**	0.400**	0.105^{NS}	0.612**	1	0.309**
HI	0.137^{NS}	0.899**	0.156^{NS}	0.587**	-0.084^{NS}	0.425**	0.349**	-0.147^{NS}	0.179*	-0.327**	0.465**	0.491*	1

*, ** significance level when P=0.050 and P=0.01, NS= non significant PH-Plant height, DH- Days to heading, PT- Productive tillers, SL- Spike lenght, PL- Peduncle Lenght, SW- Spike weight, DM- Days to maturity, NGPS- Number of grain per spike, GWPS- Grain weight per spike, BY- Biological yield, EY- Economic(Grain) Yield, HGW- Hundered grain weight and HI- Harvest Index.

These results were comparable to those reported by Khan *et al.* (2010); Dogan *et al.* (2010). Similarly, at genotypic level except for days to heading, all the other traits showed strong positive association with grain yield per. Mohsen *et al.* (2012) discovered a favourable correlation between grain yield per plant and 100 grain weight, spike length, number of productive tillers per plant, number of spikelets per spike and number of grains per spike. Chimdesa *et al.* (2017) found that grain yield per ha was positively correlated to harvest index.

Number of productive tillers per plant, number of grains per plant, 100 grain weight, biological yield per plant, and harvest index all demonstrated a positive and significant relationship with grain yield at the genotypic as well as phenotypic level. Overall, wheat seed yield will be improved by intensive selection for number of productive tillers per plant, number of grains per spike, spike length, 100-grain weight, harvest index, and grain yield per plant. Because these six attributes are connected, *i.e.* improvement in one of them leads to the improvement in other accordingly. Similar findings were reported by Kiran *et al.* (2020).

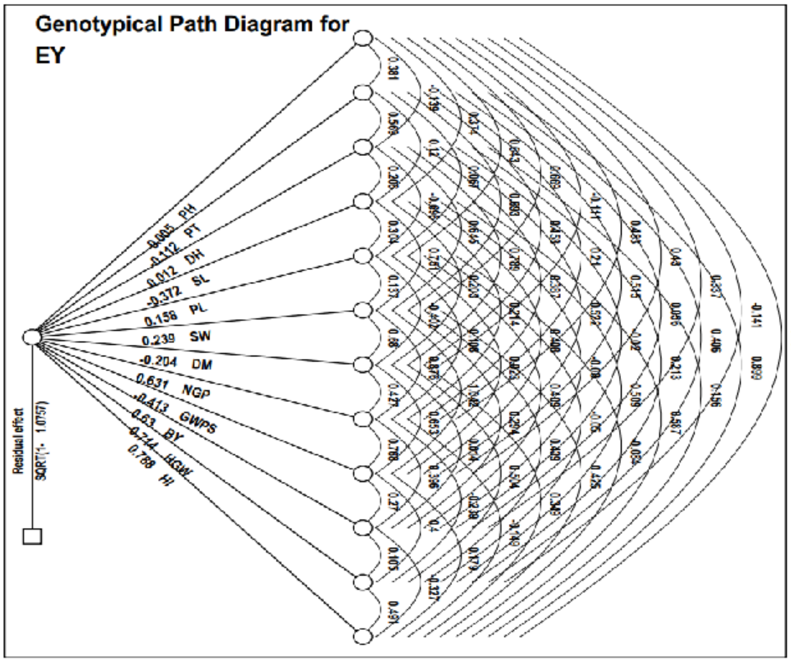

Fig. 1. Showing genotypic path diagram for grain yield in bread wheat.

The path coefficient studies revealed the contribution of several yield components to total grain yields in the genotypes under investigation. It's a quick and easy technique to figure out the direct and indirect effects of various characteristics on grain yield. The studied traits such as days to heading, plant height, days to maturity, spike length, peduncle length, number of productive tillers per plant, grain weight per spike, number of grains per spike, spike weight, 100 grain weight, biological yield per plant, and harvest index were considered independent variables, while path analysis used to determine the contribution and effect of these components on grain yield, which was the dependent variable (Fig. 1).

For grain yield per plant, path coefficient analysis revealed that traits like 100 grain weight (0.714), number of grains per spike (0.631), harvest index (0.631) and biological yield per plant (0.63) had the strong positive direct effect on seed yield. This indicates that a little increase in one of the traits listed above could have a direct impact on seed yield. Shahryari *et al*. (2013); Verma *et al.* (2013) both reported similar findings.

The traits namely, harvest index via number of productive tillers per plant (0.70); biological yield per plant via peduncle length (0.25) and number of grains per spike (0.24); number of grains per spike via spike weight (0.55) and grain weight per spike (0.48); spike weight via grain weight per spike (0.248) and number of grains per spike (0.24); spike weight via grain weight per spike (0.248) and number of grains per spike (0.48) had positive indirect effect for economic(grain) yield. Mollasadeghi *et al.* (2012) found that number of grain per spike and seed index had positive and direct effect which concluded the cause and effect relationships among several wheat genotype. Similar findings were reported by Kiran *et al.* (2020).

Sharma *et al*. (2018) calculated correlation and path coefficients to assess the significance of several agromorphological features in wheat, concluding that correlation and path coefficients were discovered in different wheat germplasm. The direct and indirect contributions of number of grains per spike, biological yield per plant, 100 grain weight, spike weight, grain weight per spike, and harvest index on seed yield were highest, according to path coefficient analysis. The results showed that no matter which character was chosen to increase seed yield, the enhancement could only be done through these characters.

Through spike weight and 100 grain weight, all of the above studied significant characters had an indirect influence. As a result, it's reasonable to conclude that these are the major traits responsible for wheat seed yield improvement. Selection for any other yield-contributing character will only have an effect on seed yield if these traits are chosen. The study of correlation is interesting because it relates to the genetic causes of correlation *via* pleiotropy, which occurs when a gene impacts two or more traits via linkage. In both circumstances, gene segregation creates simultaneous character variation, and it affects or is liked with genes of other traits. Incomplete linkage, especially in populations resulting from crosses between divergent strains, is a cause of temporary correlation.

CONCLUSION

In present study, association analysis revealed that the characters *viz,* number of productive tillers per plant, number of grains per plant, 100 grain weight, biological yield per plant, and harvest index showed positive and significant relationship with grain yield at the genotypic as well as phenotypic level. While path coefficient analysis revealed that same traits exhibited highest positive direct effect on grain yield and each must be given preference in selection along with optimum plant height and spike length while selecting the superior genotypes. Hence these characters can be directly selected for the yield improvement in bread wheat. Thus, selection of genotypes based on the associated character will be useful in development of elite breeding lines.

FUTURE SCOPE

The present experimental study will help to understand the trait association between the yield contributing traits and selection based on these traits will be helpful in the identification of superior genotypes of bread wheat.

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Conflict of Interest. None.

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