Genotypic and Phenotypic Correlation and Path Analysis for Growth and Yield Contributing Traits in Bread Wheat (*Triticum aestivum* L.)

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Abstract**—** *Thirty-eight advanced bread wheat lines were evaluated in Randomised Block Design with four replications at Agriculture Research Station, S. D. Agricultural University, Ladol (Gujarat) during rabi 2020-21 season to evaluate the association of yield and yield-related traits and determine the direct and indirect effects of yield-related traits on grain yield. The results of the study's correlation analysis showed grain yield per plot had highly significant and positive correlation with number of effective tiller per meter and biological yield per plot at both genotypic and phenotypic level, that indicated that these are major contributors for increasing the grain yield per plot and selection could be more effective for these traits. The estimates of genotypic correlation coefficient were higher for most of the characters than phenotypic correlation coefficient, indicating a strong inherent association among various characters. Path analysis revealed that the biological yield per plot followed by spike length had the highest positive direct effect on grain yield per plot whereas number of effective tillers per meter followed by 1000 grain weight and number of grain per spike revealed negative high direct effect on grain yield per plot. Hence, the present investigation can be helpful as selection criteria to increase grain yield in bread wheat based on these above-mentioned traits viz., biological yield per plot and spike length. These character have to be rank the first in any breeding program to improve wheat grain yield.*

***Keywords*— Correlation, path analysis, genotypic, phenotypic.**

I. INTRODUCTION

Bread wheat (*Triticum aestivum* L.) is one of the most crucial staple crops in the world, with a rich history dating back thousands of years. Its journey from ancient times to the present day has witnessed significant transformations in cultivation, breeding, and utilization. The mid-20th century witnessed a transformative phase in wheat cultivation with the advent of the Green Revolution. Scientists like Norman Borlaug developed high-yielding wheat varieties, leading to increased global wheat production. This revolution significantly impacted food security and helped alleviate hunger in many parts of the world. In recent decades, advancements in molecular genetics and biotechnology have revolutionized wheat breeding. Researchers have focused on developing varieties with improved yield, disease resistance, and nutritional content. Genetic modification and genome editing techniques are being explored to enhance wheat's adaptability to changing environmental conditions.

Globally wheat occupies an area of 222.11 million hectares with production of 778.6 million metric tonnes and productivity is 3.51 t/ha (OECD/FAO 2021/22). Wheat is cultivated in almost all the states of India but its extensive cultivation is confined to Uttar Pradesh, Madhya Pradesh, Punjab, Haryana, Rajasthan, Bihar and Gujarat. In India wheat occupies an area of 31.13 million hectares under irrigation with production of 109.59 million tonnes and productivity is 3.52 t/ha (Directorate of Economics and Statistics, DAC and FW 2021/22). While, In Gujarat wheat occupies an area of 1.3 million hectares with production of 4.3 million tonnes and productivity is 3156.29 Kg/ha (Directorate of Agriculture, Gujarat State 2020-21). Wheat is cultivated under irrigated as well as rainfed conditions. The eight-fold increase in wheat production (10.40 million tonnes in

1965-66 to 109.59 million tonnes in 2021/22) (Directorate of Economics and Statistics, DAC and FW 2019-20) during the last five decades has been a remarkable and unparalleled achievement.

Transcriptomic studies have shown that over 30000 genes are expressed in the developing wheat grain (Wan *et al.,* 2008) while, proteomic analysis of mature grain has revealed the presence of about 1125 individual components (Skylas *et al.*, 2000).

The study of different characters and their relationship with other is an important criterion design to break genetic barriers of yield. Whereas, correlation studies are helpful in determining the component of a complex trait *i.e.* grain yield. However, they do not provide an exact magnitude of direct and indirect effect towards the yield. Therefore, path coefficient analysis is an important tool to partition the correlation coefficient into direct and indirect effect of the independent variables on the dependent variables.

II. MATERIAL AND METHOD

The experiment was conducted on "Genotypic and Phenotypic Correlation and Path Analysis for Growth and Yield Contributing Traits in Bread Wheat (*Triticum aestivum* L.)" in *rabi* 2020-21 at Agricultural Research Station, Sardarkrushinagar Dantiwada Agricultural University, Ladol. The centre is located between latitudes 230 38' and 230 41' N and longitudes 720 41' and 720 44' E. *Triticum aestivum* L. (bread wheat) genotypes (Table 1) representing 38 different genetic origins used as the experimental material for this study. These taken from the S.D.A.U. Wheat Research Station in Vijapur, Gujarat. Four replications of the current experiment were done using a Randomized Block Design (RBD). Each genotype has a double row that is 3.0 meters long and spaced 22.5 cm apart. Twelve different traits, including days to heading (N), days to maturity (N), plant height (cm), effective tillers per meter, number of grains per spike, spike length (cm), grain yield per plot (g), biological yield per plot (g), harvest index (%), 1000 grain weight (g), protein content (%), and sedimentation value (ml), were observed for this investigation. Except for the traits of days to heading (N), days to maturity (N), number of effective tillers per meter, grain yield per plot (g), biological yield per plot (g), harvest index (%), 1000 grain weight (g), protein content (%) and sedimentation value (ml), observations were made on five randomly chosen plants from each replication. Phenotypic and genotypic correlation were estimated using the standard procedure suggested by Dewey and Lu. Path coefficient analysis was performed for character that had significant correlations with grain yield both at genotypic and phenotypic levels in order to know the direct and indirect effect of yield character on grain yield using the general formula of Al-Jibouri *et al*. by considering grain yield per plot as dependent variable.

TABLE 1
LIST OF GENOTYPES

Sr.No.	Genotypes	Sr.No.	Genotypes
1	ABV 2019-23	20	36th SAWSN-3002
2	ABV 2019-39	21	36th SAWSN-3047
3	ABV 2019-48	22	36th SAWSN-3048
4	ABV 2019-50	23	36th SAWSN-3073
5	ABV 2019-68	24	36th SAWSN-3129
6	VA 2016-22	25	36th SAWSN-3261
7	VA 2019-04	26	29th HRWSN-2040
8	VA 2019-05	27	29th HRWSN-2054
9	VA 2019-06	28	29th HRWSN-2129
10	VA 2019-16	29	DBW-187
11	VA 2019-18	30	DBW-222
12	HI-1633	31	MP-1203
13	HI-1634	32	MP-1338
14	Raj-3065	33	RWP 2018-29
15	Raj-3777	34	CG-1029
16	Raj-4079	35	WH-730
17	Raj-4083	36	LOK 1
18	17thHTWYT-38	37	GW 322
19	17th HTWYT-49	38	GW 451

III. RESULTS AND DISCUSSION

Complete knowledge on interrelationship of grain yield with other character is of paramount importance to the breeder for making improvement in complex quantitative character like grain yield for which direct selection is not much effective. Hence, mutual relationship was undertaken to determine the direction of selection and number of characters to be considered in improving grain yield. Genotypic correlation coefficient in general were higher than phenotypic correlation coefficient indicating strong inherent association between the traits.

Table 2 shown the phenotypic and genotypic relationships for morpho-agronomic features. At both the genotypic and phenotypic levels in the current study, there was a highly significant and positive correlation between grain yield per plot and the number of effective tillers per meter (rg = 0.558 and rp = 0.418) and biological yield per plot (rg = 0.919 and rp = 0.689). This showed that these traits are important for increasing grain yield per plot and that selection could be more successful for these traits. Meles et al. (2017) demonstrated a favourable and extremely significant correlation between grain yield and biological yield. At both the genotypic and phenotypic levels, the number of effective tillers per meter demonstrated a strong and positive correlation with spike length (rg = 0.345 and rp = 0.228). Grain yield per plot exhibited non-significant and negative correlation with days to maturity (rg = -0.181 and rp = -0.131), protein content (rg = -0.093 and rp = -0.020) and sedimentation value (rg = -0.015 and rp = -0.006) at both genotypic and phenotypic level. Days to heading displayed both genotypic and phenotypic non-significant and positive correlation with tillers per meter (rg = 0.105 and rp = 0.075). These findings are consistent with those made earlier (Anwar et al. 2009). At the genotypic level, there was a strong and positive correlation between grain yield per plot and 1000 grain weight (rg = 0.311) and number of grains per spike (rg = 0.322). Similar results were first noted by Khaliq et al. (2004).

An efficient method for identifying both direct and indirect origins of correlations is path coefficient analysis. The results are given in Table 3 and figure 1, which show that the biological yield per plot had the most positive direct influence, followed by the days to heading, spike length, plant height, harvest index, days to maturity and protein content. Ayer et al. (2017) and Rajput, R. (2019) both reported on high positive direct effects of biological yield on grain production per plot. Plant height had a positive and negligible indirect influence that was measured by days to maturity (0.027), effective tillers per meter (0.018), grains per spike (0.061), biological yield per plot (0.045), 1000 grain weight (0.050), protein content (0.026) and sedimentation value (0.031). The direct impact of effective tillers per meter on grain yield per plot was very large (-2.073) and negative. Grain yield per plot was directly affected positively and significantly (0.441). The indirect impact of 1000 grain weight was positive and negligible, as measured by the number of effective tillers per meter (0.007) and spike length (0.047). Positive and small (0.060), the direct impact of protein content on grain yield per plot. Through the number of effective tillers per meter (-0.028), the number of grains per spike (-0.058), and the biological yield per plot (-0.088), sedimentation value showed a detrimental and negligible indirect influence.

There is a significant intrinsic relationship between different characters, as evidenced by the estimations of genotypic correlation coefficient being larger than phenotypic correlation coefficient for the majority of the characters. The results of the study's correlation analysis showed that at both the genotypic and phenotypic levels, the grain yield had a high and positive association with the number of efficient tillers per meter and the biological yield per plot. According to path analysis studies, biological yield per plot, days to heading, spike length, plant height, harvest index, days to maturity and protein content all had a positive and direct impact on grain production per plot. Based on the results, it would be reasonable to recommend that a breeder working to increase bread wheat's grain yield emphasise the traits 1000 grain weight, number of effective tillers per meter, grain yield per plot, biological yield per plot, harvest index, spike length, and number of grains per spike. Therefore, choosing individuals with these qualities will immediately aid in boosting bread wheat's grain yield.

TABLE 2
GENOTYPIC CORRELATION AND PHENOTYPIC CORRELATION COEFFICIENT FOR DIFFERENT CHARACTERS IN BREAD WHEAT

Character		DH	DM	PH	TIL/M	SL	NGS	BYP	HI	TGW	PC	SV	GYP
DH	r_g	1											
	r_p	1											
DM	r_g	0.468**	1										
	r_p	0.437**	1										
PH	r_g	-0.029	0.102	1									
	r_p	-0.028	0.077	1									
TIL/M	r_g	0.105	0.107	0.069	1								
	r_p	0.075	0.089	0.070	1								
SL	r_g	-0.008	-0.125	-0.094	0.345*	1							
	r_p	-0.016	-0.073	-0.099	0.228**	1							
NGS	r_g	-0.045	0.082	0.232	-0.277	-0.271	1						
	r_p	0.018	0.032	0.198*	-0.135	-0.122	1						
BYP	r_g	-0.112	-0.024	0.171	0.793**	0.054	0.139	1					
	r_p	-0.071	0.013	0.178*	0.601**	0.108	0.222**	1					
HI	r_g	-0.359*	-0.566**	-0.520**	-0.037	-0.003	-0.013	0.077	1				
	r_p	-0.256**	-0.370**	-0.295**	-0.006	0.057	0.039	0.065	1				
TGW	r_g	-0.531**	-0.169	0.189	0.039	-0.060	0.035	0.131	0.012	1			
	r_p	-0.496**	-0.149	0.156	0.007	-0.033	-0.138	0.125	-0.016	1			
PC	r_g	0.624**	0.040	0.098	-0.141	-0.426**	0.080	0.041	-0.130	-0.485**	1		
	r_p	0.432**	0.048	-0.023	-0.012	-0.239**	0.006	0.005	-0.068	-0.333**	1		
SV	r_g	0.722**	0.191	0.117	0.026	-0.104	0.054	0.082	-0.097	-0.577**	0.994**	1	
	r_p	0.562**	0.131	0.048	0.013	-0.128	-0.023	-0.008	-0.068	-0.412**	0.552**	1	
GYP	r_g	-0.274	-0.181	0.024	0.558**	0.149	0.322*	0.919**	0.190	0.311*	-0.093	-0.015	1
	r_p	-0.224**	-0.131	0.020	0.418**	0.112	0.200*	0.689**	0.074	0.255**	-0.020	-0.006	1

, ** significant at 0.05 and 0.01 level of significance, respectively. Where, DH= days to heading (N), DM= days to maturity (N), PH= plant height (cm), TIL/M= number of effective tiller per meter, SL= spike length (cm), NGS= number of grain per spike, BYP = biological yield per plot (g), HI = harvest index (%), TGW = 1000 grain weight (g), PC = protein content (%), SV = sedimentation value (ml) and GYP = grain yield per plot (g)

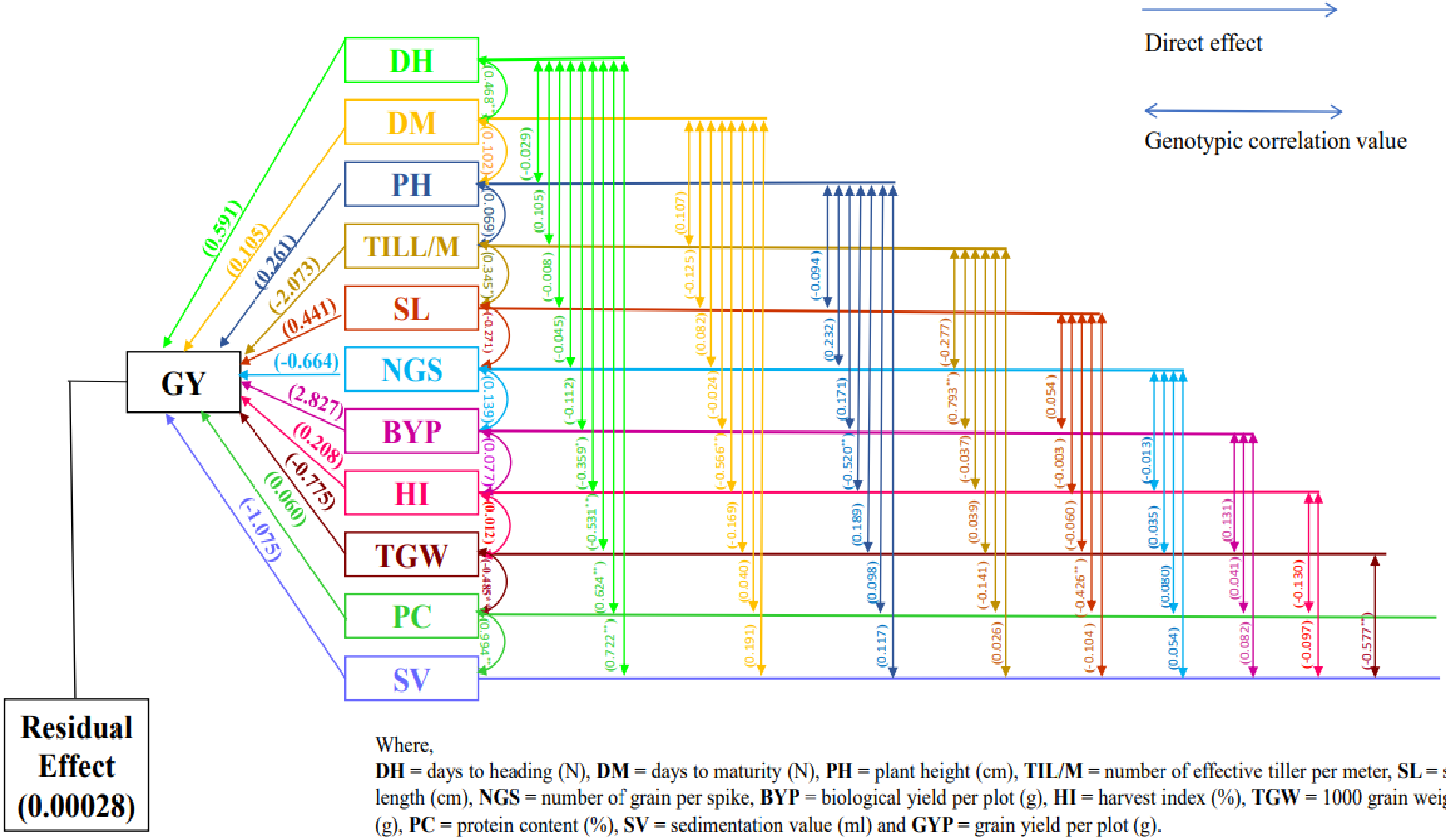
TABLE 3
DIRECT AND INDIRECT EFFECTS OF YIELD COMPONENT ON GRAIN YIELD IN BREAD WHEAT

Character	DH	DM	PH	TIL/M	SL	NGS	BYP	HI	TGW	PC	SV	Genotypic correlation with GYP
DH	**0.591**	0.049	-0.007	-0.217	-0.003	0.030	-0.317	-0.075	0.414	0.038	-0.776	-0.274
DM	0.276	**0.105**	0.027	-0.222	-0.055	-0.055	-0.068	-0.118	0.132	0.002	-0.205	-0.181
PH	-0.017	0.011	**0.261**	-0.144	-0.042	-0.154	0.485	-0.108	-0.147	0.006	-0.126	0.024
TIL/M	0.062	0.011	0.018	**-2.073**	0.152	0.184	2.242	-0.008	0.007	-0.009	-0.028	0.558^{**}
SL	-0.004	-0.013	-0.025	-0.714	**0.441**	0.180	0.153	-0.001	0.047	-0.026	0.112	0.149
NGS	-0.027	0.009	0.061	0.574	-0.119	**-0.664**	0.394	-0.003	0.151	0.005	-0.058	0.322^{*}
BYP	-0.066	-0.003	0.045	-1.644	0.024	-0.092	**2.827**	0.016	-0.102	0.003	-0.088	0.919^{**}
HI	-0.212	-0.059	-0.136	0.077	-0.001	0.009	0.218	**0.208**	-0.009	-0.008	0.104	0.190
TGW	-0.315	-0.018	0.050	0.017	-0.027	0.130	0.371	0.002	**-0.775**	-0.029	0.620	0.311^{*}
PC	0.369	0.004	0.026	0.292	-0.188	-0.053	0.117	-0.027	0.376	**0.060**	-1.068	-0.093
SV	0.426	0.020	0.031	-0.054	-0.046	-0.036	0.232	-0.020	0.447	0.060	**-1.075**	-0.015

, ** significant at 0.05 and 0.01 level of significance respectively. (Residual effect = 0.00028)

Where,

DH = days to heading (N), DM = days to maturity (N), PH = plant height (cm), TIL/M = number of effective tillers per meter, SL = spike length (cm), NGS = number of grain per spike, BYP = biological yield per plot (g), HI = harvest index (%), TGW = 1000 grain weight (g), PC = protein content (%), SV = sedimentation value (ml) and GYP = grain yield per plot (g)



Where,
DH = days to heading (N), **DM** = days to maturity (N), **PH** = plant height (cm), **TIL/M** = number of effective tiller per meter, **SL** = spike length (cm), **NGS** = number of grain per spike, **BYP** = biological yield per plot (g), **HI** = harvest index (%), **TGW** = 1000 grain weight (g), **PC** = protein content (%), **SV** = sedimentation value (ml) and **GYP** = grain yield per plot (g).

FIGURE 1: Genotypical path diagram for grain yield per plot

FIGURE 2: General view of experimental site

IV. CONCLUSION

The estimates of genotypic correlation coefficient were higher for most of the characters than phenotypic correlation coefficient, indicating a strong inherent association among various characters. The results of the study's correlation analysis showed that at both the genotypic and phenotypic levels, the grain yield had a high and positive association with the number of efficient tillers per meter and the biological yield per plot at both genotypic and phenotypic level. The grain yield showed significant positive correlation with number of grain per spike and 1000 grain weight at both genotypic and phenotypic level. This has been indicating that more attention should give to this character to improve the grain yield of bread wheat. According to path analysis studies revealed that positive and direct effect towards grain yield per plot was observed by biological yield per plot, days to heading, spike length, plant height, harvest index, days to maturity and protein content, whereas number of effective tiller per meter, sedimentation value, 1000 grain weight and number of grain per spike had showed negative direct effect on grain yield per plot. Thus, characters biological yield per plot, days to heading, spike length, plant height, harvest index, days to maturity and protein content turned out to be the major components traits for grain yield per plot and direct selection for these traits will be rewarded for improvement of grain yield in wheat. Therefore, choosing individuals with these qualities will immediately aid in boosting bread wheat's grain yield. The Residual effect in path coefficient analysis was low indicating a high contribution of independent traits to the dependent trait.

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