Analysis of Genetic Variability, Correlation and Path for Yield and its Attributing Traits in Wheat (*Triticum aestivum* L.)

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ABSTRACT

The current study was undertaken to analyze the genetic variability, correlation and path for yield and its attributing traits at agriculture research farm, Department of Genetics and Plant Breeding, School of Agriculture, Lovely Professional University, Punjab during during *Rabi* 2021-22 and 2022-23. Augmented design with F_2 seeds planted in ear to row fashion in 4 rows were used to study variability, correlation and path including 2 parent and its 6 F_2's for the 9 traits *viz.* plant height, spike length, number of tillers per plant, number of spikes per plant, number of spikelets per ear, number of grains per ear, biological yield, harvest index and grain yield. Finding revealed that grain yield revealed positive and highly significant correlation with number of tillers per plant (r_p= 0.8387, r_g= 0.8709) and biological yield (r_p= 0.9671, r_g= 0.9965) while positive and significant correlation with Number of spikes per plant (r_p= 0.7168, r_g= 0.7253) at both phenotypic and genotypic level. Biological yield per plant revealed highest positive direct effect (1.0642, 0.8700) with significant association with grain yield **(**0.9965, 0.9671) whereas Number of tillers reveals least positive direct effect on grain yield (0.0183, 0.0834) at both genotypic and phenotypic level. PCV was higher than GCV for all the traits indicated an influence of environment over the traits. Number of spikelets per ear recorded highest PCV and GCV followed by Grain yield. Heritability (h^2b) found higher for grain yield (84.2) followed by Number of spikelets per ear (83.4), Number of Grains per ear (82.7) and Plant height (80.1). Genetic advance (GA) recorded higher Number of spikelets per ear (35.07) followed by Grain yield (11.93). Moderate GA recorded for Plant Height (7.67) and Biological yield (6.88) whereas Spike length (0.62) recorded lowest GA. Hence, selection for these mentioned characters could bring improvement in yield and yield components.

Keywords: Correlation, Path, Phenotypic, Genotypic, Direct and indirect effect, grain yield.

1. INTRODUCTION

Wheat (*Triticum aestivum* L.) having chromosome number 2n=6x=42, [AABBDD] (hexaploid) is widely cultivated, self-pollinating annual plant belongs to the (Gramineae) family. According to Wani *et al.* [1], wheat holds great significance as it is one of the primary cereal crop used as a staple food source worldwide. In terms of global food crops, wheat ranks second after rice [2]. Wheat plays a crucial role in providing approximately 20% of the calories and protein consumed by people worldwide, contributing to the sustenance of around 40% of the global population.

According to the Food and Agriculture Organization FAO [3], global wheat production reached approximately 776.5 mt in 2020. The production was estimated to slightly increase to 778.3 mt in 2021 and then decrease to 770.3 mt in 2022. Wheat holds a crucial position not only as a key crop for food security but also as a valuable cash crop on a global scale [4]**.** The importance of wheat is reflected in the significant global trade volume. In the 2020-21 season, world wheat trade reached a record high of 186.6 mt, surpassing the previous season by 1.2 percent or 2.3 mt FAO [5]. This highlights the significant role of wheat in meeting global food demands and economic activities.

In order to establish a successful breeding program, the presence of genetic diversity within the population is crucial. Verma *et al.* [6] confirm that plants with higher genetic variability are more likely to benefit from favorable hybrid crosses and generate productive recombinants, thus leading to a broader heritability within the population during the process of genetic improvement. Estimation of heritability in combination with genetic advance are usually more useful than heritability alone for forecasting genetic gain under selection. However, a trait with a high heritability does not always have a high genetic advance Johnson [7]. Correlation reveals the degree and direction of association at phenotypic and genotypic levels btw the yield and its contributing traits. However, it should be noted that the correlation could sometimes fail to give accurate insights into the individual impact of each character on the dependent character. It is understandable that a path analysis would be necessary to determine which characters actually affect seed yield. So path analysis is used to measure the indirect and direct effects of traits [8]. It is impossible to begin an effective breeding programme without first establishing genetic variability using appropriate metrics including GCV and PCV, Genetic advance (GA) and heritability (h^2b) [9].

2. MATERIALS AND METHODS

The present investigation was carried out at the research farm, Department of Genetics and Plant Breeding, Lovely Professional University, Phagwara, Punjab during *Rabi* 2021-22 and 2022-23. The F_2 seeds were space planted in ear to row fashion to study variability, correlation and path including 2 parent and its 6 F_2's for the 9 traits, *viz.* plant height, spike length, number of tillers per plant, number of spikes per plant, number of spikelets per ear, number of grains per ear, biological yield, harvest index and grain yield. The experiment material consists of crosses obtained from matting of female line GS/2020-21/8049 (provided by Borlaug Institute for South Asia, BISA-CIMMYT) which are heat tolerant and susceptible to rust, with the PBW 766 male parent, which are newly released local cultivars. The list of wheat cultivars (along with Pedigree) used for study tabulated in (Table 1).

Table 1. Parents and crosses of wheat used in the experiment

S.No	Genotype	Parentage
1	**GS/2020-21/8049 (Female)**	WBLL1*2/BRAMBLING//SAAR/2*WAXWING/4/PBW343*2/KUKUNA//KRONSTAD F2004/3/PBW343*2/KUKUNA/5/2*MUCUY
2	**PBW 766 (Male)**	PBW 766 NAC/TH.AC//3*PVN/3/MIRLO/BUC/4/2*PASTOR/5/KACHU/6/KACHU
S.No	**Crosses**	**F_2 Population of GS/2020-21/8049X PBW 766**
1	**C1**	(GS/2020-21/8049 X PBW 766) 1
2	**C2**	(GS/2020-21/8049 X PBW 766) 2
3	**C3**	(GS/2020-21/8049 X PBW 766) 3
4	**C4**	(GS/2020-21/8049 X PBW 766) 4

5	**C5**	(GS/2020-21/8049 X PBW 766) 5
6	**C6**	(GS/2020-21/8049 X PBW 766)6

Using a Spacing 22.5 x 15 cm (row to row 22.5 and plant-to-plant 15 cm) in augmented Design for F2 generation. The mean value was then determined for analysis over three replications Figure in (Table 2). The formulas provided by [7] were used to compute the different genetic factors *viz.* GCV, PCV, Heritability (h^2b) and Genetic advance (GA). Using the formula provided by [10] for correlation co-efficient and [11] for path co-efficient analysis were obtained.

2.1 Estimating of correlation

Now, genotypic and phenotypic correlation coefficients were calculated using formula

$$\text{Phenotypic correlation (rp)} = \frac{\text{PCov. xy}}{\sqrt{\text{PVx. PVy}}}$$

$$\text{Genotypic correlation (rg)} = \frac{\text{GCov. xy}}{\sqrt{\text{GVx. GVy}}}$$

$$\text{rxy} = \frac{\text{Cov (x, y)}}{\sqrt{\text{V}}\text{(x) x}\sqrt{\text{V}}\text{ (y)}}$$

Where,

r_{xy} = Correlation coefficient between character x and y
$Cov_{x,y}$ = Co-variance of character x and y
V_x = Variance of character x, and
V_y = Variance of character y
r_p = Phenotypic correlation
r_g = Genotypic correlation.

2.2 Path Analysis

Path analysis splits the correlation coefficient into the measures of direct and indirect effects and measures contribution of each independent variable on the dependent variable and estimates residual effects. It helps in determining the yield and yield contributing characters.

To estimate various direct and indirect effects, the following equations were used

$$\begin{aligned} r1y &= P1y + r12P2y + r13P3y + \ldots + r1IPIy \\ r2y &= r2yP1y + P2y + r23P3y + \ldots + r2IPIy \\ rIy &= rI1P1y + rI2P2y + rI3P3y + \ldots + PIy \end{aligned}$$

Where,

r_{1y} to r_{Iy} = Coefficient of correlation between factor 1 to I and dependent character y
r_{12} to $r_{I-1,I}$ = Coefficient of correlation among causal factors themselves
P_{1y} to P_{Iy} = Direct effects of characters 1 to I on character y.

2.3 Residual effect

Residual effect, which measures the contribution of the characters was obtained by

$$(\mathrm{PRY}) = \sqrt{1 - R^2}$$

Where,

$$R^2 = \sum_{ij} P_i{}^2\, Y + 2 \sum_{\substack{i \neq j \\ i > j}} P_{iy}\ P_{jy} R_{ij}$$

2.4 Estimation of GA and GAM

The genetic advance (GA) for selection intensity (K) at 5% was calculated by the formula suggested by [12].

$$GA = (K)\ (\sigma_p)\ (H^2)$$

Where,

GA = Expected genetic advance at 5% selection intensity, σ_p = Phenotypic standard deviation

H^2= Heritability and K = selection differential (K= 2.063 at 5% selection intensity).

The genetic advance as percent of the mean (GAM) was calculated by formula given by [7]

$$GAM = \frac{GA}{X} * 100$$

Where,

GAM = Genetic advance as percent of mean

GA = Genetic advance at 5% selection intensity

X= Population Mean

Heritability (H^2) was computed by formula developed by [12]

$$H^2 = \frac{\sigma 2g}{\sigma 2p} X\ 100$$

Where,

σ^2p= Phenotypic Variance σ^2g= Genotypic Variance H^2 = Heritability in broad sense

3. RESULTS AND DISCUSSION

Significant differences ($P<0.01$) were observed among the tested genotypes for all the traits investigated *viz.* plant height, spike length, number of tillers per plant, number of spikes per plant, number of spikelets per ear, number of grains per ear, biological yield, harvest index, and grain yield. These findings indicate the presence of substantial variability among the genotypes, which can be harnessed through selection and hybridization. The significant differences observed among the genotypes for the studied characteristics justify conducting further genetic analysis [13]. The substantial genetic variation among the genotypes suggests that they exhibit genetic diversity, providing an excellent opportunity for breeders to select suitable genotypes for specific traits of interest in variety development. A similar results reported by [14-16] that the analysis of variance revealed significant genetic variability among all traits for the treatments. Table 3 presents the estimated range, minimum and maximum values, along with their corresponding genotypes, mean values, and corresponding standard errors for the nine traits examined in wheat genotypes.

Table 2. ANOVA for nine traits in wheat

Characters	Replication (d.f =4)	Treatment (d.f =7)	Error (d.f =28)

Plant Height (cm)	13.22	108.10	21.51
Spike length (cm)	0.53	1.511	0.68
Number of tillers per plant	3.10	23.377	6.08
Number of spikes per plant	6.25	23.02	7.35
No. of spikelets per ear	1.60	9.585	1.657
No. of Grains per ear	33.06	171.75	73.81
Biological yield (gm)	17.43	2089.39	345.20
Harvest index (%)	22.52	56.52	37.57
Grain yield (gm)	12.00	236.55	37.28

4.1 Variability, Heritability and Genetic advance

Genetic variability parameters *viz.* GCV, PCV, Heritability (broad sense), Genetic advance and genetic advance as 5 % of mean tabulated in Table 4. PCV (Phenotypic coefficient of variance) is higher than GCV (Genotypic coefficient of variance) for all the characters that indicates an influence of environment on traits. Data pertaining to Number of spikelets per ear recorded highest PCV and GCV followed by Grain yield. The current findings are consistent with the results reported by [17], who also observed high PCV and GCV for grain yield. Similarly, moderate PCV and GCV was recorded for Number of tillers per plant followed by Number of spikes per plant. [18] also reported moderate PCV and GCV number of tillers per plant and low PCV and GCV were recorded for Plant Height, Spike length and Harvest index. The present result in agreement with [19].

Heritability serves as a predictor of the traits that parents will pass on to their offspring. [20] found that selection processes become easier as heritability estimates increased. The heritability (H^2) revealed the extent to which quantitative traits inherited, but it fails to disclose the extent to which genetic gain may be attained by the selection of the ideal plant from the elite populations. Therefore, the combination of heritability and genetic advance is beneficial than either factor alone [21]. Heritability (h^2b) found higher for grain yield (84.2) followed by Number of spikelets per ear (83.4), Number of Grains per ear (82.7) and Plant height (80.1). [17-18], documented similar result that high estimates of heritability. These traits exhibit a high degree of heritability, indicating that genetic factors have a strong influence on their expression. Consequently, environmental factors are likely to have a lesser impact on the development of these traits. Medium (h^2b) recorded for Number of tillers per plant (74) and Number of spikes per plant (68.1) and lower for Harvest index (32.9). Genetic advance (GA) recorded higher Number of spikelets per ear (35.07) followed by Grain yield (11.93). Moderate GA recorded for Plant Height (7.67) and Biological yield (6.88) whereas Spike length (0.62) recorded lowest GA. [22] also found similar results.

4.2 Estimation of Correlation

Assessment of the genotypic and phenotypic correlation between various traits tabulated in Table 5. Data pertaining to plant height it was found that it revealed negative and highly significant correlation with spike length (r_g= -0.8613) at genotypic level only. [23] also observed a significant positive correlation between plant height and spike length in their study. Spike length revealed positive and highly significant correlation with number of spikelets per ear (r_g= 0.9883) whereas negative and highly significant for plant height (r_g= -0.8613) at genotypic level only. Whereas negative and significant correlation was found for number of tiller per plant (r_p= -0.7068) and number of spikelets per plant (r_p= -0.7847) at phenotypic level only. Number of tillers per plant revealed positive and highly significant correlation with number of spikes per plant (r_p= 0.9409, r_g= 0.9958) and Grain yield (r_p= 0.8387, r_g= 0.8709) while positive and significant correlation with Biological yield (r_p= 0.7789, r_g= 0.7683) at both phenotypic and genotypic level. Whereas negative and significant correlation was found for spike length (r_p= -0.7068) at phenotypic level only. [15] found similar results. Number of spikes per plant revealed positive and highly significant correlation with number of tillers per plant (r_p= 0.9409, r_g= 0.9958) while positive and significant correlation with grain yield (r_p= 0.7168, r_g= 0.7253) at both phenotypic and genotypic level. Whereas negative and significant correlation was found for spike length (r_p= -0.7847) at phenotypic level only. [24] identified noteworthy associations between the plant height and number of spikelets. Biological yield revealed positive and highly significant correlation with grain yield (r_p= 0.9671, r_g= 0.9965) while positive and significant correlation with Number of tillers per plant (r_p= 0.7789, r_g= 0.7683) at both phenotypic and genotypic level. Whereas negative and significant correlation was found for harvest index (r_p= -0.7519) at phenotypic level only. Number of spikelets per ear revealed positive and highly significant correlation with Number of Grains per ear (r_p= 0.8573) at phenotypic level only while negative and significant correlation was found for harvest index (r_g= -0.8024) at genotypic level only. [22] also found similar results. Number of Grains per ear revealed positive and highly significant correlation with Number of spikelets per ear (r_p= 0.8573) at phenotypic level only while negative and significant correlation was found for harvest index (r_g= -0.7091) at genotypic level only. Harvest index revealed negative and significant correlation for grain yield (r_g= -0.9970), number of Grains per ear (r_g= -0.7091) and Number of spikelets per ear (r_g= -0.8024) at genotypic level only while, biological yield (r_p= -0.7519) for phenotypic level only. Contrary to the present study, [25] reported a positive correlation between the number of spikelets and tillers per plant with grain yield at both genotypic and phenotypic levels. Grain yield revealed positive and highly significant correlation with number of tillers per plant (r_p= 0.8387, r_g= 0.8709) and biological yield (r_p= 0.9671, r_g= 0.9965) while positive and significant correlation with Number of spikes per plant (r_p= 0.7168, r_g= 0.7253) at both phenotypic and genotypic level. [18] reported yield per head significantly correlated with harvest index. Whereas negative and highly significant correlation was found for harvest index (r_g= -0.9970) at genotypic level only. [25] and [23] reported similar results, where the genotypic correlation coefficients (r_g) were found to be higher than the corresponding phenotypic correlation coefficients (r_p) for most of the character combinations. This suggests that the observed correlations between traits are predominantly influenced by genetic factors rather than environmental factors. Genotypic correlations provide valuable insights into the underlying genetic relationships between traits, which can be useful for plant breeders in selecting desirable combinations of traits for crop improvement programs.

4.3 Path analysis

Merely examining correlations does not offer a comprehensive understanding of how each specific trait contributes to the overall picture. Path analysis, on the other hand, proves valuable in evaluating variables by quantifying their respective contributions and distinguishing between partially indirect and direct sources of association. This analytical approach enables a comparative assessment of variables based on the magnitude of their influences. Table 6 and Figure 1 reveals the path analysis through direct and indirect effect of each trait on selected variable *viz.* grain yield. Biological yield per plant revealed highest positive direct effect (1.0642, 0.8700) with significant association with grain yield **(**0.9965, 0.9671) at both genotypic and phenotypic level. Similarly harvest index also showed highest negative indirect effect (0.2067, 0.2676) associated with biological yield (-0.2126, -0.2012), Number of spikelets per ear (-0.1658, -0.1337) and Number of grains per ear (-0.1466, -

0.1237). This result in agreement with [26-28]. Number of spikelets per ear (0.1115, 0.5200) which exhibits close association with grain yield (0.5324, 0.4622) and Number of tillers reveals least positive direct effect on grain yield (0.0183, 0.0834) at both the levels and significant association with grain yield (0.8709, 0.8387). Number of spikelets per plant and plant height showed positive direct effect on grain yield at genotypic level (0.1018 and 0.0108) and showed negative direct effect on grain yield at phenotypic level (-0.1834 and -0.1271) respectively. Number of grains per ear (-0.0074, -0.0578) and spike length (-0.0060, -0.5770) exhibited highest negative indirect effect on grain yield at both genotypic and phenotypic levels. Spike length showed highest positive indirect effect through number of spikes per plant (0.4528), number of tillers per plant (0.4078) and plant height (0.3654) at phenotypic level. Similar result in agreement with [14], [18] and [22].

CONCLUSION

Correlation reveals the degree and direction of association at phenotypic and genotypic levels btw the yield and its contributing traits. However, it should be noted that the correlation could sometimes fail to give accurate insights into the individual impact of each character on the dependent character.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

AUTHORS’ CONTRIBUTIONS

‘Author A’ designed the study and wrote the first draft of the manuscript, ‘Author C’performed the statistical analysis, ‘Author B’ wrote the protocol, ‘Author D’ managed the analyses of the study and . ‘Author E’ managed the literature searches. All authors read and approved the final manuscript.”

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GENOTYPES	PH	SL	NTP	NSP	BY	NSPE	NGPE	HI	GY
(GS/2020-21/8049 X PBW 766) 1	80.00	12.60	14.00	14.00	86.40	21.00	70.20	38.58	32.86
(GS/2020-21/8049 X PBW 766) 2	81.40	12.40	11.40	11.40	60.40	19.40	66.80	42.10	25.28
(GS/2020-21/8049 X PBW 766) 3	79.20	13.40	7.40	7.40	46.60	20.20	59.80	43.05	18.78
(GS/2020-21/8049 X PBW 766) 4	87.20	12.00	11.20	13.20	55.60	18.60	56.80	43.53	23.96
(GS/2020-21/8049 X PBW 766) 5	89.00	12.80	12.20	12.20	89.40	22.60	73.00	41.72	36.85
(GS/2020-21/8049 X PBW 766) 6	87.40	12.60	11.00	11.00	56.00	19.80	64.00	44.55	24.12
PBW 766	92.00	11.80	14.20	13.80	103.80	19.80	61.60	37.24	38.40
GS/2020-21/8049	87.4	11.8	13	13	60.8	18.2	57.8	47.91	28.8
Mean	**85.45**	**12.42**	**11.80**	**12.00**	**69.87**	**19.95**	**63.75**	**42.34**	**28.63**
min	79.2	11.8	7.4	7.4	46.6	18.2	56.8	37.24	18.78
max	91	13.4	14.2	14	103.8	22.6	73	47.91	38.4
C.V.	**5.42**	**6.63**	**20.90**	**22.59**	**26.59**	**6.45**	**13.47**	**14.47**	**21.32**
C.D. 5%	6.00	-	3.19	3.51	24.07	1.66	11.13	-	7.91
C.D. 1%	8.10	-	4.31	4.73	32.47	2.24	15.01	-	10.67

PH- Plant height, **SL-** Spike length, **NTP-** Number of tillers per plant, **NSP-** Number of spikes per plant, **NSPE-** Number of spikelets per ear, **NGPE-** Number of Grains per ear, **BY-** Biological yield, **HI-** Harvest index and **GY-** Grain yield

Table 3. Mean of parent and crosses for nine traits with CV, CD at 5 and 1 % respectively

Table 4. Variability (GCV & PCV), Heritability (broad sense), Genetic advance (GA) and GAM at 5% in wheat

Characters	Min	Max	Mean	GCV	PCV	h^2b	GA (5%)	GA Mean (5%)
Plant Height (cm)	79.2	91	**85.45**	4.870	5.441	80.1	7.672	8.979
Spike length (cm)	11.8	13.4	**12.42**	3.280	4.424	55	0.622	5.009
Number of tillers per plant	7.4	14.2	**11.80**	15.757	18.322	74	3.294	27.915
Number of spikes per plant	7.4	14	**12.00**	14.757	17.884	68.1	3.010	25.083
Number of spikelets per ear	46.6	103.8	**69.87**	26.676	29.206	83.4	35.071	50.191
Number of Grains per ear	18.2	22.6	**19.95**	6.312	6.940	82.7	2.359	11.826
Biological yield (gm)	56.8	73	**63.75**	6.942	9.194	57	6.885	10.799
Harvest index (%)	37.24	47.91	**42.34**	4.537	7.906	32.9	2.271	5.363
Grain yield (gm)	18.78	38.4	**28.63**	22.046	24.020	84.2	11.936	41.683

Table 5. Phenotypical and Genotypic Correlation for nine traits in wheat

		Phenotypical and Genotypic Correlation Matrix								
		PH	**SL**	**NTP**	**NSP**	**BY**	**NSPE**	**NGPE**	**HI**	**GY**
PH	r_p	**1.0000**	-0.6333	0.4832	0.4993	0.4751	-0.0599	-0.1433	-0.0115	0.5745
	r_g	**1.0000**	-0.8613 **	0.6021	0.6664	0.5501	-0.0811	-0.2107	0.0332	0.6796
SL	r_p		**1.0000**	-0.7068*	-0.7847*	-0.3074	0.5950	0.3871	-0.0477	-0.4048
	r_g		**1.0000**	-1.2255	-1.4055	-0.5855	0.9883**	0.6233	0.4326	-0.6089
NTP	r_p			**1.0000**	0.9409**	0.7789*	0.0458	0.2900	-0.3861	0.8387**
	r_g			**1.0000**	0.9958**	0.7683*	0.0717	0.3880	-0.4136	0.8709**
NSP	r_p				**1.0000**	0.6473	-0.0808	0.1440	-0.3008	0.7168*
	r_g				**1.0000**	0.6023	-0.1826	0.1556	-0.1443	0.7253*
BY	r_p					**1.0000**	0.5088	0.5100	-0.7519*	0.9671**
	r_g					**1.0000**	0.5817	0.6473	-1.0288	0.9965**
NSPE	r_p						**1.0000**	0.8573 **	-0.4997	0.4622
	r_g						**1.0000**	1.1176	-0.8024 *	0.5324
NGPE	r_p							**1.0000**	-0.4623	0.5007
	r_g							**1.0000**	-0.7091 *	0.6765
HI	r_p								**1.0000**	-0.5678
	r_g								**1.0000**	-0.9970**
GY	r_p									**1.0000**
	r_g									**1.0000**

PH- Plant height, **SL-** Spike length, **NTP-** Number of tillers per plant, **NSP-** Number of spikes per plant, **NSPE-** Number of spikelets per ear, **NGPE-** Number of Grains per ear, **BY-** Biological yield, **HI-** Harvest index and **GY-** Grain yield

Figure 1. Genotypic and Phenotypic Path matrix of nine traits in wheat for Grain Yield

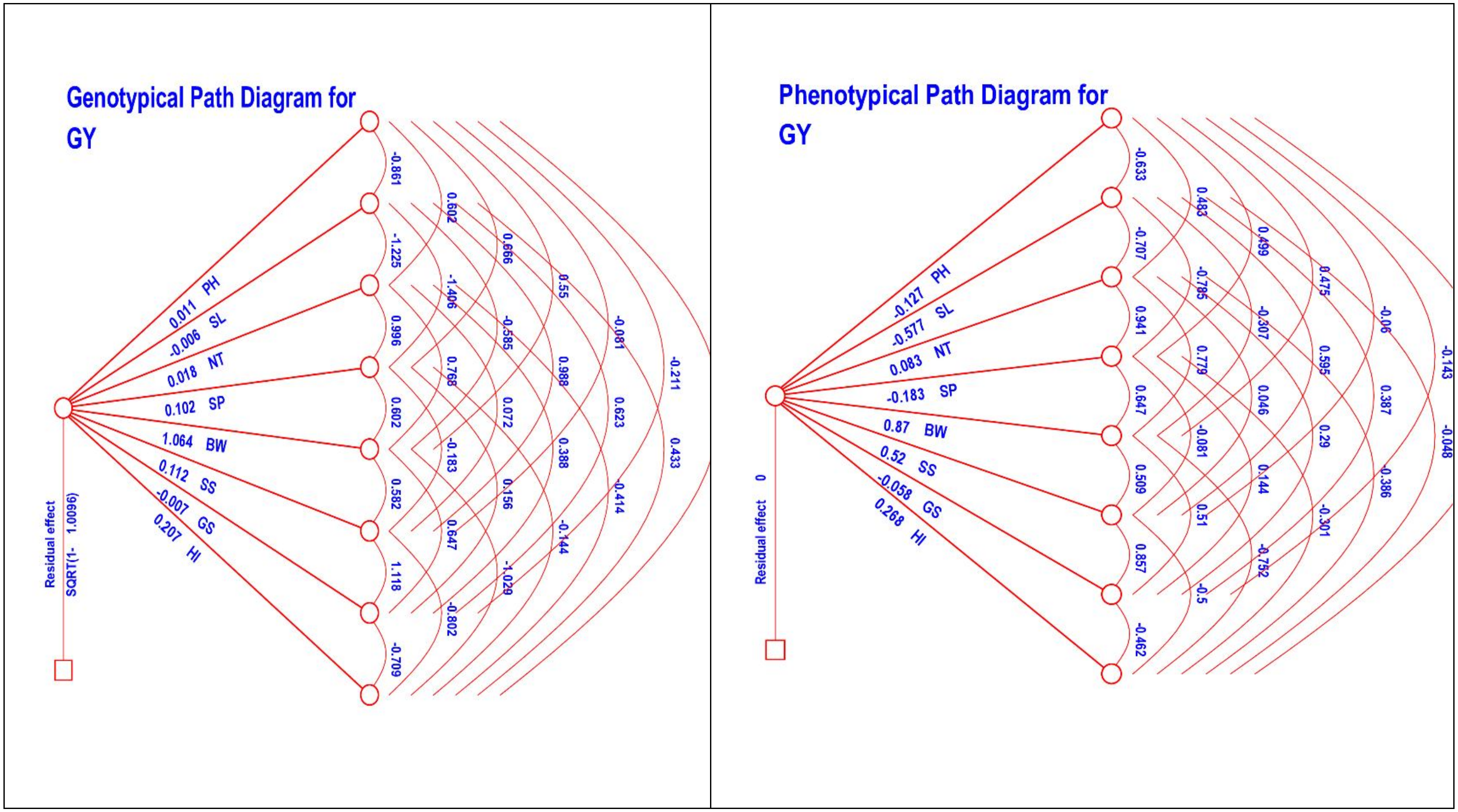

Table 6. Phenotypic and Genotypic Path matrix of nine traits in wheat for Grain Yield

Phenotypic and Genotypic Path Matrix for GY

		PH	SL	NTP	NSP	BY	NSPE	NGPE	HI	GY
PH	**P**	**-0.1271**	0.0805	-0.0614	-0.0635	-0.0604	0.0076	0.0182	0.0015	0.5745
	G	**0.0108**	-0.0093	0.0065	0.0072	0.006	-0.0009	-0.0023	0.0004	0.6796
SL	**P**	0.3654	**-0.5770**	0.4078	0.4528	0.1773	-0.3433	-0.2234	0.0275	-0.4048
	G	0.0052	**-0.0060**	0.0073	0.0084	0.0035	-0.0059	-0.0037	-0.0026	-0.6089
NTP	**P**	0.0403	-0.0590	**0.0834**	0.0785	0.065	0.0038	0.0242	-0.0322	0.8387
	G	0.0110	-0.0225	**0.0183**	0.0182	0.0141	0.0013	0.0071	-0.0076	0.8709
NSP	**P**	-0.0916	0.1439	-0.1725	**-0.1834**	-0.1187	0.0148	-0.0264	0.0552	0.7168
	G	0.0678	-0.1430	0.1013	**0.1018**	0.0613	-0.0186	0.0158	-0.0147	0.7253
BY	**P**	0.4133	-0.2674	0.6776	0.5631	**0.8700**	0.4426	0.4437	-0.6541	0.9671
	G	0.5854	-0.6231	0.8177	0.641	**1.0642**	0.6191	0.6889	-1.0949	0.9965
NSPE	**P**	-0.0312	0.3094	0.0238	-0.042	0.2645	**0.5200**	0.4458	-0.2598	0.4622
	G	-0.0090	0.1102	0.008	-0.0204	0.0649	**0.1115**	0.1246	-0.0895	0.5324
NGPE	**P**	0.0083	-0.0224	-0.0167	-0.0083	-0.0295	-0.0495	**-0.0578**	0.0267	0.5007
	G	0.0016	-0.0046	-0.0029	-0.0012	-0.0048	-0.0083	**-0.0074**	0.0053	0.6765
HI	**P**	-0.0031	-0.0128	-0.1033	-0.0805	-0.2012	-0.1337	-0.1237	**0.2676**	**-0.5678**
	G	0.0069	0.0894	-0.0855	-0.0298	-0.2126	-0.1658	-0.1466	**0.2067**	-0.9970

PH- Plant height, **SL-** Spike length, **NTP-** Number of tillers per plant, **NSP-** Number of spikes per plant, **NSPE-** Number of spikelets per ear, **NGPE-** Number of Grains per ear, **BY-** Biological yield, **HI-** Harvest index and **GY-** Grain yield